

Genome version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:17 / Search time 6.9997 Seconds

Title: US-09-661-992b-106

Perfect score: 82

Sequence: 1 PFMCGMALVAVSCLD 16

Scoring table: BLOSUM62

Gapop 10.0, Gapex 0.5

Searched: 1107863 seqs, 15876573 residues

Total number of hits satisfying chosen parameters: 1107663

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database: 1. A_Geneseq_13Jun03.*

Listing first 45 summaries

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18: /SID1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT*
19: /SID1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT*
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22: /SID1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT*
23: /SID1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT*
24: /SID1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	ID	Description
1	82	100.0	16	22	AA020445	Anti-FIX/FIXa heavy
2	82	100.0	294	23	AA020445	Human Factor-VIII
3	82	100.0	368	16	AA020445	Human Factor-VIII
4	82	100.0	729	16	AA020445	Factor-VIII heavy
5	82	100.0	729	16	AA020445	Human Factor-VIII
6	82	100.0	740	16	AA020445	Human Factor-VIII
7	82	100.0	740	16	AA020445	Human Factor-VIII
8	82	100.0	740	16	AA020445	Human Factor-VIII
9	82	100.0	740	16	AA020445	Human Factor-VIII

Result	Score	Query	Match	Length	ID	Description
10	82	100.0	740	16	AA020445	Factor-VIII heavy
11	82	100.0	740	16	AA020445	Human Factor-VIII
12	82	100.0	1383	18	AA020445	Procoagulant-activ
13	82	100.0	1383	18	AA020445	Procoagulant-activ
14	82	100.0	1383	18	AA020445	Procoagulant-activ
15	82	100.0	1454	10	AA020445	Modified factor VI
16	82	100.0	1454	10	AA020445	Sequence of 740 Ar
17	82	100.0	1454	10	AA020445	Mutant mouse huma
18	82	100.0	1454	10	AA020445	Modified factor VII
19	82	100.0	1454	10	AA020445	Modified factor VII
20	82	100.0	1454	10	AA020445	B-domain deleted f
21	82	100.0	1454	10	AA020445	Factor VIII-SQ. U
22	82	100.0	1454	10	AA020445	B-domain-deleted
23	82	100.0	1454	10	AA020445	Human factor VIII
24	82	100.0	1457	19	AA020445	Human factor VIII
25	82	100.0	1457	19	AA020445	Beta-domain delete
26	82	100.0	1459	22	AA020445	Human factor VIII
27	82	100.0	1459	22	AA020445	Human factor VIII
28	82	100.0	1459	22	AA020445	Human factor VIII
29	82	100.0	1471	18	AA020445	Human B-domain del
30	82	100.0	1471	18	AA020445	Human factor VIII
31	82	100.0	1516	9	AA020445	Modified factor VII
32	82	100.0	1516	9	AA020445	Modified factor VII
33	82	100.0	2098	17	AA020445	Factor-VIII-Homo
34	82	100.0	2332	8	AA020445	Factor VIIIc varia
35	82	100.0	2332	8	AA020445	Factor VIIIc varia
36	82	100.0	2332	8	AA020445	Factor VIIIc varia
37	82	100.0	2332	8	AA020445	Factor VIIIc varia
38	82	100.0	2332	14	AA020445	Human Factor-VIII
39	82	100.0	2332	14	AA020445	Procoagulant-activ
40	82	100.0	2332	14	AA020445	Procoagulant-activ
41	82	100.0	2332	14	AA020445	Procoagulant-activ
42	82	100.0	2332	14	AA020445	Procoagulant-activ
43	82	100.0	2332	14	AA020445	Procoagulant-activ
44	82	100.0	2332	14	AA020445	Procoagulant-activ
45	82	100.0	2332	14	AA020445	Human factor-VIII

ALIGNMENTS

RESULT 1
AA020445 standard; Peptide, 16 AA.
AA020445:
AA020445:
21-JUN-2001 (first entry)
Anti-FIX/FIXa antibody CDR.
Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant;
Factor VIII; Factor VIIIa; Factor VIIIa; Factor VIIIa;
haemorrhagic diathesis; haemorrhagic; haemorrhagic; therapy; mouse;
complementarity determining region; CDR.
Mus musculis.
WO200119927-A2.
22-MAR-2001.
13-SEP-2001; 2000MC-BP08936.
14-SEP-1999; 99AT-0001576.
(BAXT) BAXTER AG.
Schellinger F, Kerschbaum R, Palmer F, Dörner F;
WPI; 2001-200158/30.
New factor IX/factor IXa antibodies and their derivatives useful for

increasing anidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diatheses -

Claim 7, Page 74, 138pp; English.

The present sequence is that of complementarity determining region 3 (CDR3) of an antibody having anti-factor IX (FIX) or anti-activated factor IX (FIXa) activity. Such antibodies are known to be useful in the treatment of haemorrhagic diatheses. CDR3 peptide have Factor VIIIa (FVIII) cofactor activity or FIXa activating activity. Administration of the antibodies or their derivatives leads to an increase in the procoagulant activity of FVIII and FVIIIa, and thus to a more rapid blood clotting. This allows for the rapid blood coagulation even in the absence of FVIII or FVIIIa in the case of FVIII inhibitor patients. The antibodies or their derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic diatheses.

Sequence 16 AA;

Query Match 100.0%; Score 82; DB 23; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e-09;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNQGMPTALLVNSGSD 16
Db 1 PNNQGMPTALLVNSGSD 16

RESULT 2

AA679422
ID AAG79422 standard; protein; 294 AA.

XX AAG79422;

DT 25-OCT-2002 (first entry)

XX human factor VIII region 2/3.

XX Factor VIII; Factor IX; coagulation; blood; cardiovascular disorder;

XX thrombosis; atherosclerosis; restenosis.

XX Homo sapiens.

XX MO200259268-A2.

XX 01-NOV-2002.

XX 23-JAN-2002; 2002MO-US01724.

XX 23-JAN-2001; 2001US-263431P.

XX (UYSL-) UNIV SAINT LOUIS.

XX Baf3 P8, Ray P2;

XX NPI; 2002-599771/64.

XX New polypeptide inhibits interaction of blood coagulation factor VIIIA

XX with factor IXa precluding interaction of factor IXa with factor VIIIa

XX preventing or treating coagulation disorders, such as thrombosis,

XX atherosclerosis and restenosis -

XX Claim 2, Fig 7a, 61pp; English.

The sequences given in AAG79422-23 represent regions 2 and 3 of human factor VIII and IX. Region 2 comprises the interaction between N346 between K403 of factor IXa and E613 of factor VIIIa, and the interaction between K293 of factor IXa and D712 of factor VIIIa, and the interaction between E810 of factor IXa and Y713 of factor VIIIa. Fragments of these polypeptides inhibit the interaction of blood

coagulation factor VIIIa with blood coagulation factor IXa. They also inhibit the activation of blood coagulation factor X or inhibit blood coagulation. These peptide fragments are useful in preventing and/or treating coagulation disorders, in particular cardiovascular disorders such as thrombosis, atherosclerosis and restenosis.

Sequence 294 AA;

Query Match 100.0%; Score 82; DB 23; Length 294;
Best Local Similarity 100.0%; Pred. No. 2.6e-1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNQGMPTALLVNSGSD 16
Db 268 PNNQGMPTALLVNSGSD 263

RESULT 3

AA679420
ID AAG79420 standard; peptide; 368 AA.

XX AAG79420;

DT 25-MAR-2003 (updated)

XX 21-NOV-1995 (first entry)

XX human factor VIII fragment.

XX Factor VIII; blood-clotting; blood; coagulant; haemophilia A.

XX Homo sapiens.

XX MO9513301-AL.

XX 18-MAY-1995.

XX 10-NOV-1994; 94MO-DE00424.

XX 12-NOV-1993; 93DK-0001281.

XX (NOVO) NOVO-NMD2SR AS.

XX Persson E;

XX NPI; 1995-194036/25.

XX Crosslinked factor VIII polypeptide which is stable - 10 prepd. using

XX bisulphonosuccinimide(s) substrate or disuccinimide(s) substrate in the

XX presence of polysaccharide 80 to produce a coagulant with long lasting

XX activity

XX Disclosure: Page 19; 36pp; English.

XX This is a fragment corresponding to internal AAs 373-740 of human

XX Factor-VIII which may be crosslinked resulting in

XX increased stability and retention of high activity over extended

XX periods of time after activation by thrombin. The polypeptide is

XX used to produce a coagulant with long lasting activity in the absence or deficiency

XX of Factor-VIII in a subject such as haemophilia.

XX (Updated on 25-MAR-2003 to correct PW field.)

XX Sequence 368 AA;

Query Match 100.0%; Score 82; DB 16; Length 368;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PNNQGMPTALLVNSGSD 16
Db 325 PNNQGMPTALLVNSGSD 340

RESULT 4

PA (NOVO) NOVO-NORDISK AS.
 PI Ezzhan Rasmussen M, Nicolson EM, Persson E,
 DR WFI: 1995-255039/33.
 XX Novel factor VIII derivative used to treat haemophilia - and
 XX comprises a functional A2 domain containing a mutation at one or
 XX more Cys residues.
 XX
 XX Disclosure: Page 18-20; 30pp; English.
 CC The new Factor-VIII derivative comprises a functional A2 domain in
 CC which Cys-692 is replaced with Ser. For other (less preferred)
 CC substitutions at this site, see PAR7961. Alternatively, Glu-720 and/or
 CC Ser-720 may be replaced with Thr, Leu, or Asp. The amino acids in
 CC the features) The new derivative has the same amino acid sequence as the wild-
 CC type Factor-VIII but with improved stability (the activity is not wild-
 CC maintained for a longer period compared to the rapid decline of the
 CC activity of Factor-VIII). The new derivative can be used in a
 CC completely new way, for example, as a replacement by an absence or deficiency
 CC of Factor-VIII, especially haemophilia.
 XX
 XX Sequence 740 Aa:
 SQ
 Query Match 100.0%; Score 82; DB 16; Length 740;
 Best Local Similarity 100.0%; Pred. No. 8.7e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FRRNRGNTALNKSQD 16
 DB 697 FRRNRGNTALNKSQD 712
 RESULT 9
 AAR73021
 ID AAR73021 standard; peptide; 740 Aa.
 AC AAR73021:
 XX 25-MAR-2003 (updated)
 DT 21-NOV-1995 (first entry)
 XX Human Factor-VIII N-terminal fragment.
 DB
 XX Factor-VIII; blood-clotting; blood; coagulant; haemophilia-A.
 XX Homo sapiens.
 OG W09513301-A1.
 PN 18-MAY-1995.
 PD
 PF 13-NOV-1994; 94MO-DK00424.
 XX 12-NOV-1993; 93DK-0001081.
 XX (NOVO) NOVO-NORDISK AS.
 PA
 XX Persson E;
 XX WFI: 1995-194038/25.
 XX Crosslinked Factor VIII polypeptide which is stable - is prepd. using
 PT bis(sulphonosuccinimide) anhydride or dianhydride.
 PT Presence of polysorbate 80 to produce a coagulant with long lasting
 PT activity
 XX
 XX Disclosure: Page 21; 36pp; English.
 CC This is the N-terminal fragment of human Factor-VIII which may be
 CC crosslinked resulting in increased stability and retention of high
 CC activity over extended periods of time after activation by thrombin.

CC The polypeptide is used to prevent or treat diseases caused by the
 CC absence or deficiency of Factor-VIII in a subject such as
 CC haemophilia.
 CC (updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 740 Aa:
 SQ
 Query Match 100.0%; Score 82; DB 16; Length 740;
 Best Local Similarity 100.0%; Pred. No. 8.7e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FRRNRGNTALNKSQD 16
 DB 697 FRRNRGNTALNKSQD 712
 RESULT 10
 AAR74090
 ID AAR74090 standard; protein; 740 Aa.
 XX
 XX AAR74090:
 XX 25-MAR-2003 (updated)
 DT 04-NOV-1995 (first entry)
 XX Factor-VIII heavy chain N-terminal fragment.
 XX human; Factor VIII; heavy chain; N-terminal fragment;
 XX Thrombin cleavage; blood-clotting.
 XX Homo sapiens.
 OG W09513300-A1.
 PN 18-MAY-1995.
 PD
 PF 10-NOV-1994; 94MO-DK00423.
 XX 12-NOV-1993; 93DK-0001280.
 XX (NOVO) NOVO-NORDISK AS.
 PA
 XX Ezzhan Rasmussen M, R341ke M;
 XX WFI: 1995-194037/25.
 XX Factor VIII polypeptide(s) comprising a heavy chain shorter than native
 PT Factor VIII, which is able to produce recombinantly and retain coagulant
 PT activity may be used for patients who have developed antibodies to
 PT C-terminal epitopes of Factor VIII.
 XX
 XX Disclosure: Page 30-32; 51pp; English.
 CC The sequence represents N-terminal residues 1-740 of a human Factor-
 CC VIII heavy chain. The sequence contains entire A1 and A2 domains,
 CC and truncated forms (1-720 in (AAR74088) and 1-729 in (AAR74090))
 CC and truncated forms (1-720 in (AAR74088) and 1-729 in (AAR74090)). The
 CC C-terminally truncated fragments, which are produced by specific
 CC activity as full-length Factor-VIII, and may be produced specific
 CC recombinantly to reduce production costs and improve safety, giving
 CC a longer half-life and stability than for the full-length form.
 CC The fragments are used for the treatment of haemophilia A and B.
 CC antibodies against epitopes in the C-terminal part of the heavy chain.
 CC (updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 740 Aa:
 SQ
 Query Match 100.0%; Score 82; DB 16; Length 740;
 Best Local Similarity 100.0%; Pred. No. 8.7e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FRRNRGNTALNKSQD 16
 DB 697 FRRNRGNTALNKSQD 712

DB 697 PRNRGNTALLNVSQD 712

RESUME 11

AAH76902 ID AAR76982 standard; protein; 740 AA.

AAH76902 21-FEB-1996 (file entry)

Human factor VIII A2-domain derivative.

Factor VIII; human; haemophilia; thrombin; protein C; plasmin;

serine protease; recombination; therapy; deficiency.

Human sapiens.

Key Location/Qualifiers

Misc-difference 720 /label= Gln, Ser, Thr, Val, Ala

Misc-difference 720 /label= Val, Ala, Ile

MO518828-A1.

13-JUL-1995.

06-JAN-1995; 95MO-DK00009.

07-JAN-1994; 94DK-0000031.

(NOVO) NOVO-NORDISK AS.

Ezhan Rasmussen M, Nicolaisen EM, Persen E;

WPI; 1995-255040/33.

Novel factor VIII derivative with resistance to enzymatic cleavage -

and comprises a functional A2 domain where Gln720 and/or Tyr728 is

deleted/substituted.

Claim 1; Page 11-14; 26pp; English.

This sequence represents the A2 domain of a human factor VIII derivative.

Factor VIII is a large glycoprotein which is present in plasma at low

concentration. Factor VIII is an essential part of the clotting

process. Factor VIII is cleaved by thrombin and other serine proteases

by thrombin, activated protein C, plasmin, and other serine proteases

Full length factor VIII consists of three repeats of the A-domain, a

B-domain and a C-peptide. The A-domain, active factor VIII has the A1

and A2 domains. The A1 domain is cleaved by thrombin and other serine

proteases. Factor VIII containing this sequence has improved stability

and shows resistance against enzymatic activity present in mammalian

cells. This means that factor VIII containing this sequence can be used

treating diseases caused by an absence or deficiency of factor VIII (in

the same way as normal factor VIII) e.g. haemophilia. The advantage with

using a recombinant factor VIII also includes no need for lots of donors

process and there is no risk of transmission of blood-borne diseases

such as HIV.

RESUME 12

AAH33227 ID AAM33227 standard; protein; 1383 AA.

AAH33227 30-APR-1998 (file entry)

Procoagulant active human factor VIII.C (FVIII) mutant protein.

Factor VIII; human; haemophilia A; recombinant; resistance;

recombinant secretion procoagulant activity; resistance;

von Willebrand factor binding site; binding affinity;

FVIII replacement therapy.

Human sapiens.

Key Location/Qualifiers

Misc-difference 740 /note= "factor VIII heavy chain"

Misc-difference 740 /note= "factor VIII light chain"

Misc-difference 740 /note= "A1 domain"

Misc-difference 740 /note= "A2 domain"

Misc-difference 740 /note= "A2 domain"

Misc-difference 740 /note= "A2 domain"

Misc-difference 740 /note= "A2 domain"

Misc-difference 740 /note= "A2 domain"

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Misc-difference 740 /note= "A2 domain"

Misc-difference 740 /note= "A2 domain"


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PR      01-AUG-1986; 86CUS-0893375.
XX      (BIOJ) BIOGEN NY.
PA      (PASE/) PASEK M P.
XX
XX      Paek MP;
XX
XX      WPI: 1988-049866/07.
DR      N-PSDB; AAN80447.
XX
XX      New DNA sequences encoding modified factor VIII:C - with deletion of DNA
PT      encoding mutation polypeptide, useful for high yield transformation.
XX
XX      Claim 3; Page 60-61-62-63; 97p; English.
PS
XX      The PD deletion removes the DNA from Ser 741 to Ser 1657.
CC      A major part of the sequence encoding the matured polypeptide of
CC      factor VIII:C is deleted, i.e. Gln 744 - Asp 1563.
CC      The full length factor VIII:C cDNA has two changes with respect to the
CC      Genbank sequence 1990 application 604577:
CC      C70 to C74 and C75 to C77. The first change is amino acid residue 1880
CC      (Phe to Leu). The product is produced in approx. 20 times higher
CC      yields than previous recombinant produced factor VIII:C and are more
CC      easily purified. The peptide
CC      is used for treating haemophilia A, both
CC      See also AAN80444 and AAN80446.
CC      (Updated on 25-MAR-2003 to correct PA field.)
XX
XX      Sequence 1424 AA;
SQ

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Query Match 100.0%; Score 82; DB 9; Length 1424;

Best local similarity 100.0%; Pseq. No. 1.9e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 PNNNGTALTKVSSCD 16
        |||||
Db      697 PNNNGTALTKVSSCD 712

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Search completed: November 7, 2003, 07:27:05
Job time : 7.89987 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd

CM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 0.720961 Seconds
(without statistics)

652.278 Million cell updates/sec

Title: US-09-661-992B-5

Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62

[illegible]

Searched: 127863 seqs, 47026705 r

Total number of hits satisfying chosen parameter

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing:	Minimum Match 04
	Maximum Match 10

Listing First 45

Database : SwissProt_41:*

Pred. No. is the number of

and is derived by analysis

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

[illegible]

ALIGNMENTS

RESULT 1
 F026 MYCTD STANDARD, PRT: 583 AA.
 AD 0109761
 DT 10-OCT-1996 (Rel. 34, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Purative fatty-acid-CoA ligase fadD6 [NC 6.2.1.-] (Acyl-CoA
 synthetase)
 GN FAD06 OR RW293 OR MY999 OR MYC338.19.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 PX NC01_TaxID=1773;
 RP SEQUENCE FROM N.A.
 RX STEAIN-33787;
 RX MEDLINE=923587; PubMed=9634330;
 RA Gordon S.V., Eisenberg K., Brown S., Barry C.E., Iii, Terasa P.,
 RA Badcock K., Baseman D., Gorm D., Chillingworth T., Connor R.,
 RA Bayes R., Devlin J., Felwell J., Gentile S., Hamlin N., Holroyd S.,
 RA Oliver S., Olesinski J., Quinn M., Reinhardt M., Sengenès R.,
 RA Butler S., Seeger K., Skellern S., Squares S., Squares R.,
 RA Bulston J.B., Taylor K., Whithead S., Barrett B.G.,
 RT Complete genome analysis of Mycobacterium tuberculosis from the
 RL Nature 393:337-344(1998).
 RN (12) <http://www.ncbi.nlm.nih.gov/PMOBS/summary.fcgi?seq=12>
 RC STRAIN=CMC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson S., Deboy R., Dodson R., Gelin M.T., Haft D., Hickey E., G.L.,
 RA Delcher A.L., Umayahara C., Adams J., Kocniak R., Still J., Smith A.,
 RA Binkai N.
 RT Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT submitted (Apr-2001) to the EMBL/Genbank/DBS databases.
 CC -I- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
 CC FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use, but the EMBL/Genbank/DBS databases are not to be used for
 CC modified and this statement is not removed, usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)
 CC or send an email to licenses@db-eu.sib.ch.
 DR EMBL: Z747697; CAA9395.1; AAT INIT.
 DR EMBL: AB007123; AAA67127.1;
 DR TIGR: MT2399;
 DR TIGR: 12330;
 DR InterPro: IPR000873; AMP-bind.

[illegible][illegible]

Gencore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 3.29773 Seconds

Sequence: 1 YKNSPMRY 10
765,326 Million colt updates/sec

Title: US-09-661-992b-5

Perfect score: 58

Sequence: 1 YKNSPMRY 10

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Searched: 830525 seqs, 28605604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: sp.bacteria.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.fungi.*
5: sp.fungi.*
6: sp.fungi.*
7: sp.fungi.*
8: sp.fungi.*
9: sp.fungi.*
10: sp.fungi.*
11: sp.fungi.*
12: sp.fungi.*
13: sp.fungi.*
14: sp.fungi.*
15: sp.fungi.*
16: sp.fungi.*
17: sp.fungi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	44	75.9	120	11 Q92068	Q92068 mus musc
2	43	74.1	120	11 Q92068	Q92068 mus musc
3	43	74.1	120	11 Q92068	Q92068 mus musc
4	42	72.4	833	3 Q13620	Q13620 echinosac
5	41	70.7	389	8 Q9827	Q9827 galliaric
6	41	70.7	453	16 P74064	P74064 synchocys
7	40	69.0	221	5 Q9VTH9	Q9VTH9 synchocys
8	40	69.0	1312	16 Q98N66	Q98N66 rhizobium
9	39	67.2	401	16 Q98N66	Q98N66 rhizobium
10	39	67.2	559	13 Q98N66	Q98N66 rhizobium
11	39	67.2	559	13 Q98N66	Q98N66 rhizobium
12	39	67.2	559	13 Q98N66	Q98N66 rhizobium
13	39	67.2	559	13 Q98N66	Q98N66 rhizobium
14	39	67.2	559	13 Q98N66	Q98N66 rhizobium
15	39	67.2	559	13 Q98N66	Q98N66 rhizobium
16	39	67.2	559	13 Q98N66	Q98N66 rhizobium

17	38	67.2	600	13 Q93386	Q93386 bacillus
18	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
19	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
20	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
21	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
22	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
23	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
24	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
25	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
26	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
27	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
28	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
29	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
30	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
31	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
32	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
33	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
34	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
35	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
36	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
37	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
38	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
39	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
40	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
41	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
42	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
43	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
44	38	65.5	402	16 Q9VH68	Q9VH68 bacillus
45	38	65.5	402	16 Q9VH68	Q9VH68 bacillus

ALIGNMENTS

Result No.	Query	Length	DB ID	Description
1	Q92068	120	11 Q92068	Q92068 mus musc
2	Q92068	120	11 Q92068	Q92068 mus musc
3	Q92068	120	11 Q92068	Q92068 mus musc
4	Q92068	120	11 Q92068	Q92068 mus musc
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6	Q92068	120	11 Q92068	Q92068 mus musc
7	Q92068	120	11 Q92068	Q92068 mus musc
8	Q92068	120	11 Q92068	Q92068 mus musc
9	Q92068	120	11 Q92068	Q92068 mus musc
10	Q92068	120	11 Q92068	Q92068 mus musc
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19	Q92068	120	11 Q92068	Q92068 mus musc
20	Q92068	120	11 Q92068	Q92068 mus musc
21	Q92068	120	11 Q92068	Q92068 mus musc
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23	Q92068	120	11 Q92068	Q92068 mus musc
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45	Q92068	120	11 Q92068	Q92068 mus musc

Query	Length	DB ID	Description
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2	120	11 Q92068	Q92068 mus musc
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40	120	11 Q92068	Q92068 mus musc
41	120	11 Q92068	Q92068 mus musc
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44	120	11 Q92068	Q92068 mus musc
45	120	11 Q92068	Q92068 mus musc


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RESULT 11
ID 098287 PRELIMINARY; PRT; 491 AA.
AC 098287-2001 (TRENDArel. 17, Created)
DT 01-JUN-2001 (TRENDArel. 17, Last sequence update)
DE 01-MAR-2003 (TRENDArel. 23, Last annotation update)
DB Cytoplasmic polyadenylation element-binding protein Ebfot form.
GN EBFOT, Ebfotens (Human)
OC Bkaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OK NCBI_Taxid=9606;

RP SEQUENCE FROM N.A.
RX MEDLINE=2115222; PubMed=11233249;
RX MEK U.P.; Charleworth A., Smith G.D., MacLicoi A.M.;
RT "A cytoplasmic polyadenylation element binding protein."
RT Gene 263:113-121(2001).
DR BML:AF292403; AAK01240.1; -.
DR PROSITE; P550102; RRM; 1; rec_mec.
SQ SEQUENCE 491 AA; 54562 MW; 56140FBD82262 CRC64;

Query Match
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSNPGGYV 10
DB 280 GSNPGGYV 288

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RESULT 13
ID 098285 PRELIMINARY; PRT; 559 AA.
AC 098285-2001 (TRENDArel. 16, Created)
DT 01-MAR-2001 (TRENDArel. 16, Last sequence update)
DE 01-MAR-2003 (TRENDArel. 23, Last annotation update)
DB Cytoplasmic polyadenylation element binding protein.
GN CPBB
OC Carassius auratus (Goldfish).
OC Bkaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes;
OC Cyprinodontiformes; Cyprinodontiformes.
OK NCBI_Taxid=7957;

RP SEQUENCE FROM N.A.
RX MEDLINE=9711433; PubMed=8952099;
RX Gebauer F., Richter J.D.;
RT "Mouse cytoplasmic polyadenylation element binding protein: An
RT evolutionary conserved protein that interacts with the cytoplasmic
RT Poly. Proc. Natl. Acad. Sci. U.S.A. 93:14602-14607(1996).
DR BML:Y08260; CAA69588.1; -.
DR WDB:W0110844; CPBB.
DR PROSITE; P550102; RRM; 1; rec_mec.
DR SNAWT; SMO0350; RRM; 1; rec_mec.
SQ SEQUENCE 551 AA; 61917 MW; CB795885A313F6 CRC64;

Query Match
Best Local Similarity 67.2%; Score 39; DB 13; Length 599;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSNPGGYV 10
DB 354 GSNPGGYV 362

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RESULT 14
ID 070166 PRELIMINARY; PRT; 561 AA.
AC 070166-1997 (TRENDArel. 02, Created)
DT 01-FEB-1997 (TRENDArel. 02, Last sequence update)
DE 01-FEB-1997 (TRENDArel. 23, Last annotation update)
DB Cytoplasmic polyadenylation element-binding protein (CPBB).
GN CPBB.
OC Mus musculus (Mouse).
OC Bkaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Cyprinodontiformes; Cyprinodontiformes; Cyprinodontiformes;
OC Cyprinodontiformes; Cyprinodontiformes.
OK NCBI_Taxid=10090;

RP SEQUENCE FROM N.A.
RX MEDLINE=9711433; PubMed=8952099;
RX Gebauer F., Richter J.D.;
RT "Mouse cytoplasmic polyadenylation element binding protein: An
RT evolutionary conserved protein that interacts with the cytoplasmic
RT Poly. Proc. Natl. Acad. Sci. U.S.A. 93:14602-14607(1996).
DR BML:Y08260; CAA69588.1; -.
DR WDB:W0110844; CPBB.
DR PROSITE; P550102; RRM; 1; rec_mec.
DR SNAWT; SMO0350; RRM; 1; rec_mec.
SQ SEQUENCE 561 AA; 61917 MW; CB795885A313F6 CRC64;

Query Match
Best Local Similarity 66.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GSNPGGYV 10
DB 354 GSNPGGYV 362

```

```

RESULT 15
Q9BZ8H PRELIMINARY, PRT, 566 AA.
SD Q9BZ8H
AC Q9BZ8H
DT 01-JUN-2001 (TRIMBLrel. 17, Created)
DT 01-JUN-2001 (TRIMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRIMBLrel. 17, Last sequence update)
DE Cyclolemic polyadenylation element-binding protein long form.
GN CPEB1.
OS Homo sapiens (human)
OC Chordata; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo
OC NCBI_TaxID=9606;
CX NCBI_TaxID=9606;
RS SEQUENCE FROM N.A.
RC TISSUE=Ovary, and Brain;
RX MEDLINE=211522; PubMed=1223249;
RA "Identification of a novel N-terminal G-D, WASH-coil A-M,
RT "Identification and characterization of the gene encoding human
RL Gene 563:113-121 (2001)
RL 1223249
DR InterPro: IPR000504; RNA_rec_mot.
SQ
SD PROSITE: PS50102; PRT; 2
SD PROSITE: 566 AA; 62594 MW; 9E41B5B0C59DA87 CRC64;
SQ
Query Match 67.2%; Score 39; DB 4; Length 566;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 QNSPGSPAY 10
DB 356 QNSPGSPAY 363

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Search completed: November 7, 2003, 07:34:27
 CDD time : 6.39773 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw method

Run on: November 7, 2003, 07:21:17, Search time 4,11242 seconds

369,069 Million cell updates/sec

US-09-661-992b-5

Sequence: 1 YVNSPEYAF 10

Scoring table: BLASTNC62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: A_Geneset_10Nov03.*

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4: /SID01/gcgdata/genseq/genseq-emb1/AA1993.DMT*

5: /SID01/gcgdata/genseq/genseq-emb1/AA1994.DMT*

6: /SID01/gcgdata/genseq/genseq-emb1/AA1995.DMT*

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22: /SID01/gcgdata/genseq/genseq-emb1/AA2001.DMT*

23: /SID01/gcgdata/genseq/genseq-emb1/AA2002.DMT*

24: /SID01/gcgdata/genseq/genseq-emb1/AA2003.DMT*

Prod No. is the number of results predicted by change to have a score greater than or equal to the score of the results printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	16	22	AA200444
2	58	100.0	242	22	AA200433
3	42	72.4	656	22	AA66460
4	42	72.4	2201	22	AA63166
5	40	69.0	119	23	AA08366
6	39	67.2	119	23	AA08366
7	39	67.2	119	23	AA08366
8	39	67.2	119	23	AA08366
9	37	63.8	151	23	AA01013

10	37	63.8	258	22	AA668781
11	37	63.8	365	19	AA698684
12	37	63.8	365	23	AA695556
13	37	63.8	117	23	AA030518
14	36	62.1	117	23	AA030518
15	36	62.1	118	22	AA600681
16	36	62.1	130	22	AA615277
17	36	62.1	133	21	AA610268
18	36	62.1	183	21	AA610268
19	36	62.1	198	22	AA600682
20	36	62.1	216	21	AA694429
21	36	62.1	216	21	AA694429
22	36	62.1	251	22	AA691380
23	36	62.1	271	22	AA641266
24	36	62.1	280	24	AA011773
25	36	62.1	287	22	AA691460
26	36	62.1	287	22	AA691460
27	36	62.1	484	23	AA600557
28	36	62.1	710	21	AA690940
29	36	62.1	767	22	AA697298
30	36	62.1	767	22	AA697298
31	35	60.3	63	21	AA610161
32	35	60.3	63	21	AA699954
33	35	60.3	69	21	AA692222
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35	35	60.3	82	21	AA615559
36	35	60.3	90	21	AA635552
37	35	60.3	96	21	AA619669
38	35	60.3	108	21	AA619669
39	35	60.3	108	21	AA619669
40	35	60.3	113	21	AA632223
41	35	60.3	113	21	AA632223
42	35	60.3	119	22	AA618844
43	35	60.3	119	22	AA618844
44	35	60.3	119	22	AA618844
45	35	60.3	119	22	AA618844

ALIGNMENTS

RESULT 1	AA620388	standard: Peptide, 10 aa.
AC	AA620388:	
XX	21-UN-2001 (f1rcr entry)	
XX	Anti-FIX/FIXa antibody 193/A03 CBR.	
DE	Factor IX: FIX; Factor IXa: FIXa; antibody; procoagulant; fibrinolytic A;	
XX	hemorrhagic diathesis; hemostatic; amyolytic; therapy; mouse;	
XX	complementarily determining region, CDR.	
XX	Mus musculus.	
XX	WO200119992-A2.	
XX	22-UN-2001.	
XX	13-SEP-2000; 2000WO-EP08936.	
XX	14-SEP-1999; 99AT-0001976.	
XX	(BAXT) BAXTER AG.	
XX	Schellinger F, Kerschbawer R, Falkner F, Dornier F,	
XX	WPI; 2001-290156/30.	
XX	New Factor IX/factor IXa antibodies and their derivatives useful for	

PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as haemophilia A and haemorrhagic diathesis
XX
PS Claim 7; Page 74; 138pp; English.

New factor IX/factor IXa antibodies and their derivatives useful for increasing antidiolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis

The present sequence is that of complementarily determining region 3 of the *FIX* gene. This antibody multibody expressed by clones hybridoma 93/703. This antibody multibody is specific for *FIX* anti-activated Factor IX (*FIXa*) the invention. It is an example of anti-*FIX*/*FIXa* antibodies of the invention. Such antibodies and their derivatives (including those that comprises the present CD33 peptide) are useful in the treatment of haemorrhagic disorders and in the treatment of haemophilia A and haemophilia B. The antibodies or *FIXa* derivatives leads to an increase in the procoagulant activity of *FIXa*, even in the presence of FVIII inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIII, and in the case of FVIII inhibitors patients. The antibodies or their derivatives are useful in the treatment of haemorrhagic disorders, creating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic diathesis.

The present sequence is that of complementarity determining or anti-activated Factor IX (FXa) activity. Such antibodies and their derivatives (including those that comprise the present CD33 peptide) have Factor VIII (FVIII) cofactor activity or FVIII activating activity. Administration of the antibodies or their derivatives in the presence of FVIII, or the cofactor activity of FVIII, gives in the presence of FVIII, the anticoagulant activity of FVIII, even in the presence of FXa, in the absence of FVIII or FVIII, and in the cases of FVIII inhibitor patients. The antibodies or their derivatives are used in a claimed pharmaceutical composition for the treatment of thrombotic disorders, especially haemophilic A and haemorrhagic diathesis.

Query Match	100.0%;	Score 58;	DB 22;	Length 10;
Best Local Similarity	100.0%;	Pred. No. 0.0012;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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      Every Match      100.0%; Score 58; DB 22; Length 16;
      First Local Similarity 100.0%; Pred. No. 0.002;
      Conserved 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1	YGNSPKGFAY	10
Db	1	YGNSPKGFAY	10

4 YGNSPKGPAY 13

ABB20444 standard; Peptide; 16 AA

0433
AAB20433 standard; Protein; 242 AA.

AC AAB204447

DT 21-JUN-2001 (first entry)
XX

Anti-ETV/ETVα antibody 103

[illegible]

1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Figure 1**
 10. **Figure 2**
 11. **Figure 3**
 12. **Figure 4**
 13. **Figure 5**
 14. **Figure 6**
 15. **Figure 7**
 16. **Figure 8**
 17. **Figure 9**
 18. **Figure 10**
 19. **Figure 11**
 20. **Figure 12**
 21. **Figure 13**
 22. **Figure 14**
 23. **Figure 15**
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 74. **Figure 66**
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 90. **Figure 82**
 91. **Figure 83**
 92. **Figure 84**
 93. **Figure 85**
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 217. **Figure 209**

KM Factor Ia; F1a; factor Ia; F1a; antibody; procogulant;
 KM Factor VII cofactor; blood coagulation disorder; haemophilia A
 KM haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse
 KM complementarity determining region; CDR.
 XX

Chimeric - Mus musculus.
Chimeric - Scombrae.
Factor VIII cofactor; blood coagulation disorder; haemophilia A; haemorrhagic diathesis; haemostatic; amidiolytic; therapy; mouse.

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LOCATIONS/QUALITIES

KEY

Miles-differences?

EM

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/notice= "any amino acid"

Region 98.

/note= "any amino acid"

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/notes= "any aminn acc'd"

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105 040 / YACOV M BRINCY

[illegible]

/label= VL

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/label= CDR3

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MO200119992-A

33-448-2001

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66-9870-1339; 29A

PA (BAXT) BAXTER AG.

PI Scheifflinger F, Kern

10000 100000 1000000 10000000 100000000 1000000000

CC systematic cytokine damage.
 CC NB: The sequence data for this patent did not form part of the printed
 CC publication and is not available in the public domain. The sequence data
 CC at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 116 AA;

Query Match 67.2%; Score 39; DB 23; Length 116;
 Best Local Similarity 77.8%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 1 YGNSPKGFA 9
 65 YGNSPKGFA 73

RESULT 8
 AAAY3866
 ID AAAY3866 standard; Peptide; 129 AA.
 AC AAAY3866;

DT 11-FEB-2000 (first entry)

XX Heavy chain (VH) gene sequence of bacillus anthracis antibody 7-1.

XX Heavy chain; VH; IgG; monoclonal antibody; spore; Bacillus;

XX VH gene usage; anthrax.

XX Mus sp.

XX MO955642-A1.

XX 04-NOV-1999.

XX 27-APR-1999; 99MO-US09122.

XX 29-APR-1998; 980US-0069628.

XX (UDB-1) DBS FOUND.

XX Kearney JF.

XX WPI; 2000-013435/01.

XX Monoclonal antibody specific for Bacillus spores, used to detect
 XX anthrax.

PS Example 13; Page 53-54; 64pp; English.

XX AAAY3862-75 represent the amino acid sequences of the heavy chain
 CC (VH) gene sequences from antibodies produced by different hybridomas. The
 CC spores. The antibodies are produced by different hybridomas. The
 CC specification describes monoclonal antibodies (especially IgG
 CC antibodies) that are highly specific and can discriminate between the
 CC spores of the Bacillus anthracis and Bacillus pasteurii. The antibodies
 CC mice to Bacillus spores. The humoral immune response to Bacillus
 CC shows a conservation of VH gene usage which is distinct for each spore.
 CC peptide fragments derived from the antibodies are also capable of
 CC used to detect Bacillus spores in a field sample. It is particularly
 CC uses for detecting anthrax in a field sample.

XX Sequence 129 AA;

Query Match 65.5%; Score 38; DB 21; Length 129;
 Best Local Similarity 70.0%; Pred. No. 56;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 1 YGNSPKGFA 10
 77 YGNSPKGFA 86

RESULT 9
 AB001013
 XX AB001013 standard; Protein; 151 AA.
 AC AB001013;

DT 05-SEP-2002 (first entry)

XX Human breast specific protein SEQ ID NO: 56.

XX Human; breast specific protein; breast cancer; gene therapy; breast disease;
 XX cycloclastic.

XX Homo sapiens.

XX WC00240672-A2.

XX 23-MAY-2002.

XX 20-NOV-2001; 2001MO-US45079.

XX 20-NOV-2000; 2000US-249989P.

XX 22-NOV-2000; 2000US-249533P.

XX (D1AD-) DIADENUS INC.

XX Salceda S, Macina RA, Reclon H, Chatterkey R, Sun Y, Liu C;
 XX WPI; 2002-500220/53.

XX Novel breast-specific polypeptides and polynucleotides encoding
 XX polypeptide, useful for identifying, diagnosing, monitoring, staging,
 XX imaging and treating breast cancer and non-cancerous disease states in
 XX breast.

XX Claim 11; Page 219; 243pp; English.

XX The present invention provides human breast specific coding sequences and
 CC and treating breast cancer and for detecting
 CC sequence is a breast specific polypeptide of the invention.

XX Sequence 151 AA;

Query Match 63.8%; Score 37; DB 23; Length 151;
 Best Local Similarity 75.0%; Pred. No. 99;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 2 GNSPKGFA 9
 6 GNSPKGFA 13

RESULT 10

AB067818
 ID AB067818 standard; Protein; 258 AA.

AC AB067818;

DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 31135.

XX Drosophila; developmental biology; cell signaling; insecticide;
 XX pharmaceutical.

XX Drosophila melanogaster.

XX WC000171042-A2.

XX 27-SEP-2001.

[illegible]

XX 06-SEP-2000.
 PD 21-FEB-2000; 2000EP-0200610.
 XX 26-FEB-1999; 599US-0122487.
 XX (GAST) GENSET.
 PI Dumas Milne Edwards J., Duclert A., di Giordano J.
 XX WPI: 2000-500381/45.
 DR N-PSDB; AK002108.
 XX
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 PS Claim 13; SEQ ID 6183; 71bp + CD-ROM; English.
 XX
 XX The present sequence is a polypeptide encoded by one of a large number
 CC of cDNAs that have been isolated from human and non-human tissues and
 CC were prepared from total human RNA or poly(A) RNA derived from 30
 CC different tissues. EST sequences usually correspond mainly to the 3'
 CC untranslated region (UTR) of the mRNA because they are often obtained
 CC from cDNA libraries. The present sequence is a full length cDNA for
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and can be
 CC those cases where longer cDNA sequences have been obtained. The full 5'
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
 CC DNAs. 5' ESTs are also used in diagnostic forensic gene therapy and
 CC chromosome mapping procedures. They are used to obtain upstream and
 CC regulatory sequences and to design expression and secretion vectors.
 SQ Sequence 92 Aa;
 XX
 XX Query Match 62.1%; Score 36; DB 21; Length 92;
 Best Local Similarity 60.0%; Pred. No. 68;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 YONSPPSEAY 10
 DB 46 TTKKTRAGPFI 55
 XX
 XX RESULT 14
 XX ABO03818 standard; Protein; 117 Aa.
 XX ABO03818;
 AC ABO03818;
 XX 24-JUN-2002 (first entry)
 XX
 DE Human ORFX protein sequence SEQ ID NO:7618.
 XX
 XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 XX hyperproliferative disorder; psoriasis; benign lymphoma;
 XX degenerative disorder; osteoarthritis; neurodegenerative disorder;
 XX cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 XX hypertransion; hypochylidemia; cholesteryl ester storage disease;
 XX autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myaschemia gravis.
 KW
 XX Homo sapiens.
 XX
 XX W0200192523-A2.
 XX
 XX 06-DEC-2001.
 XX
 XX 29-MAY-2001; 2001MO-US10836.
 XX
 XX 30-MAY-2000; 2000US-206132P.
 XX
 XX

PR 29-JUN-2000; 2000US-228716P.
 XX
 XX (CDRA) CURAGEN CORP.
 XX Shinkens SA, Leach MD;
 XX WPI: 2002-106308/14.
 DR N-PSDB; ABN19570.
 XX
 XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders -
 XX Disclosure; SEQ ID 7618; 1037bp; English.
 XX
 XX The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-1191 (see Table 1
 CC of the CDRA) and polynucleotides encoding the human ORFX protein
 CC for treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with an ORFX-associated disorder. ORFX polynucleotides
 CC are useful for diagnosing, preventing and treating a disease or disorder
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC storage disease, hypertension, hypochylidemia, cholesteryl ester
 CC lupus erythematosus, hypertransion, hypochylidemia, cholesteryl ester
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC diseases and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorder, or periodontal tissue, and for gut
 CC repletion or regeneration and treatment of lung or liver fibrosis
 CC and hyperproliferative diseases and conditions resulting from
 CC systemic cytokine damage.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WFO
 CC at http://wfo.int/pub/published_pat_sequences.
 SQ Sequence 117 Aa;
 XX
 XX Query Match 62.1%; Score 36; DB 23; Length 117;
 Best Local Similarity 75.0%; Pred. No. 11602;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YONSPPSE 8
 DB 43 YONSPPSE 50
 XX
 XX RESULT 15
 XX ABO00681 standard; Protein; 118 Aa.
 XX ABO00681;
 XX 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #672.
 XX
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 KW
 XX Homo sapiens.
 XX
 XX W0200175067-A2.
 XX
 XX 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001MO-US08631.
 XX
 XX

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: November 7, 2003, 07:30:19, Search time 8.7719 Seconds

(without alignment)
195.799 Million cell updates/sec

Title: US-09-661-992b-5

Perfect score: 58

Sequence: 1 YGNSKNGY 10

Scoring table:

BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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1: /cgn2_6/prodata/2/pubaa/us07_pincmb.pep:*
2: /cgn2_6/prodata/2/pubaa/pcr_new_pup.pep:*
3: /cgn2_6/prodata/2/pubaa/us06_new_pup.pep:*
4: /cgn2_6/prodata/2/pubaa/us07_new_pup.pep:*
5: /cgn2_6/prodata/2/pubaa/us07_new_pup.pep:*
6: /cgn2_6/prodata/2/pubaa/pcr05_pincmb.pep:*
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8: /cgn2_6/prodata/2/pubaa/us09_pincmb.pep:*
9: /cgn2_6/prodata/2/pubaa/us09_pincmb.pep:*
10: /cgn2_6/prodata/2/pubaa/us09_pincmb.pep:*
11: /cgn2_6/prodata/2/pubaa/us09_pincmb.pep:*
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13: /cgn2_6/prodata/2/pubaa/us10_pincmb.pep:*
14: /cgn2_6/prodata/2/pubaa/us10c_pincmb.pep:*
15: /cgn2_6/prodata/2/pubaa/us10c_pincmb.pep:*
16: /cgn2_6/prodata/2/pubaa/us10c_pincmb.pep:*
17: /cgn2_6/prodata/2/pubaa/us10c_pincmb.pep:*
18: /cgn2_6/prodata/2/pubaa/us60_pincmb.pep:*
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SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	63.8	151	US-10-001-887-96	Sequence 96, App1
2	63.8	151	US-10-001-887-96	Sequence 118, App
3	63.8	306	US-10-153-668-130	Sequence 143, App1
4	63.8	306	US-09-809-391-636	Sequence 696, App
5	63.8	365	US-09-882-171-656	Sequence 696, App
6	63.8	365	US-09-882-171-656	Sequence 288, App
7	62.1	396	US-10-515-320-245	Sequence 135, App
8	62.1	1038	US-10-156-761-1535	Sequence 135, App
9	60.3	521	US-10-037-855-7154	Sequence 7184, App1
10	60.3	521	US-10-788-686-1270	Sequence 12, App1
11	60.3	1357	US-09-852-870a-12	Sequence 12, App1
12	58.6	290	US-09-852-870a-12	Sequence 953, App1
13	58.6	290	US-09-764-864-933	Sequence 40, App1
14	58.6	294	US-09-764-864-933	Sequence 18, App1
15	58.6	324	US-10-272-415-18	Sequence 18, App1

Pred. No. 18 is the number of results predicted by chance to have a
score of 58.6 or higher. The score of the result being a predicted
and is derived by analysis of the total score distribution.

Result No.	Score	Query Length	DB ID	Description
16	58.6	443	US-09-801-366-174	Sequence 174, App
17	58.6	839	US-10-231-035-6	Sequence 6, App1
18	58.6	923	US-10-156-761-1435	Sequence 1435, App
19	58.6	923	US-10-156-761-1435	Sequence 46, App1
20	58.6	144	US-09-866-425-6	Sequence 5, App1
21	58.6	144	US-10-041-406-5	Sequence 23, App1
22	58.6	144	US-10-162-435-23	Sequence 23, App1
23	58.6	144	US-10-162-435-23	Sequence 46, App1
24	58.6	243	US-09-852-870a-12	Sequence 12, App1
25	58.6	243	US-09-852-870a-12	Sequence 12, App1
26	58.6	238	US-09-530-133-46	Sequence 36, App1
27	58.6	238	US-09-530-133-46	Sequence 36, App1
28	58.6	238	US-09-530-133-46	Sequence 36, App1
29	58.6	340	US-09-812-821-7143	Sequence 11464, App
30	58.6	340	US-09-812-821-7143	Sequence 11464, App
31	58.6	855	US-10-156-761-1464	Sequence 7923, App
32	58.6	927	US-10-032-483-7923	Sequence 5007, App
33	58.6	927	US-10-032-483-7923	Sequence 5007, App
34	58.6	203	US-08-781-9866-5207	Sequence 3, App1
35	58.6	238	US-10-156-117-3	Sequence 3, App1
36	58.6	238	US-10-156-117-4	Sequence 4, App1
37	58.6	238	US-10-156-117-4	Sequence 1382, App
38	58.6	297	US-10-238-075-1382	Sequence 8843, App
39	58.6	324	US-09-853-386-73	Sequence 138, App
40	58.6	394	US-09-853-386-73	Sequence 138, App
41	58.6	420	US-09-853-386-73	Sequence 11565, App
42	58.6	420	US-09-853-386-73	Sequence 11565, App
43	58.6	420	US-09-853-386-73	Sequence 16, App1
44	58.6	438	US-10-091-032-16	Sequence 16, App1
45	55.2	32	US-10-091-032-16	Sequence 16, App1

ALIGNMENTS

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RESULT 1
US-10-001-887-96
Sequence 96, Application US/10001887
GENERIC INFORMATION
APPLICANT: Salceda, Susana
APPLICANT: Medina, Roberto
APPLICANT: Reigman, Hevry
APPLICANT: Sun, Yongqiang
APPLICANT: Liu, Chenghua
TITLE OR INVENTION: Compositions and Methods Relating to Breast Specific Gen
CURRENT APPLICATION NUMBER: US/10/001,887
PRIOR APPLICATION NUMBER: 2001-11-20
PRIOR FILING DATE: 2001-11-20
PRIOR PUBLICATION: 60/245,996
PRIOR FILING DATE: 2000-11-22
PRIOR PUBLICATION: 60/252,563
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Percentin version 3.1
US-10-001-887-96
TYPER: PRT
ORGANISM: Homo sapien
US-10-001-887-96
Query Match
Best Local Similarity 63.8%; Score 37; DB 14; Length 151;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Cy 2 YGNSKNGY 9
Db 6 GGNKGRFA 13
RESULT 2
US-10-153-668-118
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Sequence 118, Application us/10153668
Publication No. US2001092616A1
GENERAL INFORMATION:
APPLICANT: MITSUBISHI
APPLICANT: MITSUBISHI
APPLICANT: MITSUBISHI, Shuji
TITLE OF INVENTION: STATE Activating Gene
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/293,112
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: JP 2001-157043
PRIOR FILING DATE: 2001-05-28
PRIOR APPLICATION NUMBER: JP 2001-26681
PRIOR FILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-10-10
NUMBER OF SEQ ID NOS: 488
SOFTWARE: PatentIn Ver. 2.0
SD: 120
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-660-118
Query Match
Best Local Similarity 63.8%; Score 37, DB 15, Length 249,
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0.
Cy 1 YGSPKGFAY 10
Db 151 FSGHPKGFAY 160
RESULT 3
US-10-153-668-120
Publication No. US2001092616A1
GENERAL INFORMATION:
APPLICANT: HONDA, Goichi
APPLICANT: HONDA, Goichi
APPLICANT: MITSUBISHI
APPLICANT: MITSUBISHI, Kenya
TITLE OF INVENTION: STATE Activating Gene
FILE REFERENCE: 1154-020P us/10153,668
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/293,112
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 60/316,031
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/328,403
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: JP 2001-157043
PRIOR FILING DATE: 2001-05-28
PRIOR APPLICATION NUMBER: JP 2001-26681
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: JP 2001-313175
NUMBER OF SEQ ID NOS: 488
SOFTWARE: PatentIn Ver. 2.0
SD: 120
LENGTH: 249
TYPE: PRT
ORGANISM: Homo sapiens
US-10-153-668-120

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Query Match
Best Local Similarity 63.8%; Score 37, DB 15, Length 306,
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0.
Cy 1 YGSPKGFAY 10
Db 208 FSGHPKGFAY 217
RESULT 4
US-09-609-391-696
Sequence 696, Application us/0980391
Publication No. US20030049619A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION: 166 Human Secreted proteins
FILE REFERENCE: F2002P2 us/09809,391
CURRENT FILING DATE: 2003-03-15
PRIOR APPLICATION data removed - consult PAM or file wrapper
NUMBER OF SEQ ID NOS: 761
SOFTWARE: PatentIn Ver. 2.0
SD: 120
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
US-09-609-391-696
Query Match
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0.
Cy 1 YGSPKGFAY 10
Db 267 FSGHPKGFAY 276
RESULT 5
US-09-682-171-696
Sequence 171, Application us/09882171
Publication No. US2003017556A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION: 166 Human Secreted proteins
FILE REFERENCE: F2002P2 us/09809,391
CURRENT FILING DATE: 2003-03-15
PRIOR APPLICATION data removed - consult PAM or file wrapper
NUMBER OF SEQ ID NOS: 761
SOFTWARE: PatentIn Ver. 2.0
SD: 120
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
US-09-682-171-696

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PRIOR APPLICATION NUMBER: 60/056, 881
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/056, 909
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/056, 875
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/056, 862
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/056, 887
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/056, 908
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/048, 964
 PRIOR FILING DATE: 1997-08-22
 PRIOR APPLICATION NUMBER: 60/057, 650
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: 60/056, 884
 PRIOR FILING DATE: 1997-09-05
 PRIOR FILING DATE: 1997-08-22
 PRIOR FILING DATE: 1997-09-05

Query Match 63.8%; Score 37; DB 15; Length 365;
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGNSPGFAY 10
 Db 267 FSGHSHH 276

RESULT 6
 Sequence 285, Application US/10239220
 Publication No. US2003008274A1
 GENERAL INFORMATION:
 APPLICANT: FLSM, Amy
 APPLICANT: FLSM, Amy
 TITLE OF INVENTION: Compositions affecting programmed cell
 death and their use in the modification of plant development
 PRIORITY INFORMATION: US/10/219,220
 CURRENT FILING DATE: 2002-08-14
 PRIOR APPLICATION NUMBER: U.S. No. US2003008274A1 09/325,932
 PRIOR FILING DATE: 1999-06-04
 SOFTWARE: PARSED for Windows Version 3.0
 SEQ ID NO 285
 LENGTH: 373
 ORGANISM: Pinus radiata
 US-10-219-220-285

Query Match 63.1%; Score 36; DB 15; Length 373;
 Best Local Similarity 60.0%; Pred. No. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGNSPGFAY 10
 Db 305 YGNSPGFAY 314

RESULT 7
 Sequence 153, Application US/1019220
 Publication No. US2003008274A1
 GENERAL INFORMATION:
 APPLICANT: FLSM, Amy
 APPLICANT: FLSM, Amy
 TITLE OF INVENTION: Compositions affecting programmed cell
 death and their use in the modification of plant development
 PRIORITY INFORMATION: US/10/219,220
 CURRENT FILING DATE: 2002-08-14

PRIOR APPLICATION NUMBER: U.S. No. US2003008274A1 09/325,932
 PRIOR FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 290
 SOFTWARE: PARSED for Windows Version 3.0
 SEQ ID NO 135
 LENGTH: 396
 TYPE: PRT
 ORGANISM: Pinus radiata
 US-10-219-220-135

Query Match 62.1%; Score 36; DB 15; Length 396;
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGNSPGFAY 10
 Db 328 YGNSPGFAY 337

RESULT 8
 Sequence 153, Application US/10156761
 Publication No. US2003011901B1
 GENERAL INFORMATION:
 APPLICANT: OWSA, SATOSHI
 APPLICANT: IEDA, DAVID
 APPLICANT: IEDA, DAVID
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHITAKI
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 TITLE REFERENCE: 245-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-05-30
 SEQ ID NO 1355
 LENGTH: 1038
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 US-10-156-761-1355

Query Match 62.1%; Score 36; DB 15; Length 1038;
 Best Local Similarity 60.0%; Pred. No. 1.9e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGNSPGFAY 8
 Db 254 YGNSPGFAY 261

RESULT 9
 Sequence 7154, Application US/10032585
 Publication No. US20030180953A1
 GENERAL INFORMATION:
 APPLICANT: BARRY, GREGOR D.
 APPLICANT: BARRY, GREGOR D.
 APPLICANT: HOWARD, BUSEY
 APPLICANT: CHARLES, BOONE
 TITLE OF INVENTION: Drug Target Discovery
 PRIORITY INFORMATION: US/10/032,585
 CURRENT FILING DATE: 2001-12-20
 NUMBER OF SEQ ID NOS: 8000
 SOFTWARE: PARSED for Windows Version 3.1
 SEQ ID NO 7154
 LENGTH: 521
 TYPE: PRT

ORGANISM: Candida albicans
US-10-032-585-7154

Query Match 60.3% Score 35; DB 12; Length 521;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSKPEF 8

DB 225 YGNSKPEF 232

RESULT 10
US-10-284-668-12

Sequence 12; Application US/10284668

Publication No. US20030106100A1

GENERAL INFORMATION:

APPLICANT: Sprague, James, Jose

APPLICANT: Sprague, Franziska

ABOL, Garret

TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES

PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES

CORRESPONDENCE ADDRESS: NAME

STREET: 1261 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/284,668

FILING DATE: 29-Oct-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/835,667

FILING DATE: 24-Jul-1997

REFERENCE/DOCKET NUMBER: Agrevo-4

TELEPHONE: 212-596-9000

TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

SEQUENCE: amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

US-10-284-668-12

Query Match 60.3% Score 35; DB 15; Length 1197;

Best Local Similarity 75.0%; Pred. No. 2e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNSPKGF 8

DB 45 GNSPKGF 51

RESULT 11

US-09-738-626-4750
Sequence 4750; Application US/09738626

Publication No. US20020197605A1

GENERAL INFORMATION: SATOHSHI

APPLICANT: SATOHSHI

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APPLICANT: SATOHSHI

US-09-738-626-4750

Sequence 4750; Application US/09738626

Publication No. US20020197605A1

GENERAL INFORMATION: SATOHSHI

APPLICANT: SATOHSHI

APPLICANT: SATOHSHI

APPLICANT: SATOHSHI

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APPLICANT: SATOHSHI

APPLICANT: SATOHSHI

APPLICANT: SATOHSHI


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RESULT 13
US-09-764-864-953
; Sequence 953; Application US/09764864
; Patent No. US002013793A1
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and antibodies
; FILE REFERENCE: P123
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application date removed - consult P14M or file wrapper
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: SeqScribe ver. 2.0
; SEQ ID NO 95
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-953

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Query Match      58.6%; Score 34; DB 10; Length 200;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      3 NSPKGF 8
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DB      34 NSPKGF 39

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RESULT 14
US-09-769-787-40
; Sequence 40; Application US/09769787
; Publication No. US20030091577A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Microbial Technics Inc
; APPLICANT: Hanksco, Philip
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PNC/P11290
; CURRENT APPLICATION NUMBER: US/09/769,787
; CURRENT FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 40
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-769-787-40

```

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Query Match      58.6%; Score 34; DB 11; Length 284;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY      2 GNSPKGF 10
        |||||
DB      42 GPKVSKGF 50

```

```

RESULT 15
US-10-272-419-18
; Sequence 18; Application US/10272419
; Publication No. US20030089403A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, QIZONG
; APPLICANT: THOMAS, STUART
; APPLICANT: THOMAS, STUART
; TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
; TITLE OF INVENTION: INTERMEDIATES
; FILE REFERENCE: C1341-A
; CURRENT APPLICATION NUMBER: US/10/272,419

```

```

; CURRENT FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 09/282,553
; PRIOR FILING DATE: 1999-02-19
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Microscopic Office 97
; SEQ ID NO 18
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Acetabacter sp.
US-10-272-419-18

```

```

Query Match      58.6%; Score 34; DB 15; Length 324;
Best Local Similarity 62.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY      1 YGNSPKGF 8
        |||||
DB      31 FSNPKGF 38

```

```

Search completed: November 7, 2003, 08:16:49
Job time : 10.7717 secs

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GenCore version 5.1.6
Copyright (c) 1995 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 Search file 1.4662 seconds

288,098 Million cell updates/sec

File: US-09-661-992b-5

Sequence: 1 YMSKSCFAY 10

Scoring table: BLOSUM62

Gapop 10.0, Capact 0.5

Searched: 328717 seqs 4231088 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: 1: /gen2/6/prodata/1/isa/55 COMB pep: *
2: /gen2/6/prodata/1/isa/55 COMB pep: *
3: /gen2/6/prodata/1/isa/65 COMB pep: *
4: /gen2/6/prodata/1/isa/65 COMB pep: *
5: /gen2/6/prodata/1/isa/65 COMB pep: *
6: /gen2/6/prodata/1/isa/65 COMB pep: *

Pred. No. is the number of results predicted by chance to have a
score as high as the observed score. The P-value is the probability
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	63.8	35	4	US-09-149-476-096	Sequence 696, App1
2	63.8	35	4	US-09-149-476-096	Sequence 696, App1
3	62.1	36	4	US-09-133-001C-5402	Sequence 19973, A
4	62.1	36	4	US-09-133-001C-5402	Sequence 19973, A
5	62.1	36	4	US-09-133-001C-5402	Sequence 19973, A
6	62.1	36	4	US-09-133-001C-5402	Sequence 19973, A
7	60.3	35	4	US-09-606-304-12	Sequence 12, App1
8	60.3	35	4	US-09-606-304-12	Sequence 12, App1
9	60.3	35	4	US-09-606-304-12	Sequence 12, App1
10	60.3	35	4	US-09-606-304-12	Sequence 12, App1
11	60.3	35	4	US-09-606-304-12	Sequence 12, App1
12	60.3	35	4	US-09-606-304-12	Sequence 12, App1
13	60.3	35	4	US-09-606-304-12	Sequence 12, App1
14	60.3	35	4	US-09-606-304-12	Sequence 12, App1
15	60.3	35	4	US-09-606-304-12	Sequence 12, App1
16	60.3	35	4	US-09-606-304-12	Sequence 12, App1
17	60.3	35	4	US-09-606-304-12	Sequence 12, App1
18	60.3	35	4	US-09-606-304-12	Sequence 12, App1
19	60.3	35	4	US-09-606-304-12	Sequence 12, App1
20	60.3	35	4	US-09-606-304-12	Sequence 12, App1
21	60.3	35	4	US-09-606-304-12	Sequence 12, App1
22	60.3	35	4	US-09-606-304-12	Sequence 12, App1
23	60.3	35	4	US-09-606-304-12	Sequence 12, App1
24	60.3	35	4	US-09-606-304-12	Sequence 12, App1
25	60.3	35	4	US-09-606-304-12	Sequence 12, App1
26	60.3	35	4	US-09-606-304-12	Sequence 12, App1
27	60.3	35	4	US-09-606-304-12	Sequence 12, App1
28	60.3	35	4	US-09-606-304-12	Sequence 12, App1

ALIGNMENTS

```

RESULT 1
US-09-149-476-096
/ GenCore version 5.1.6
/ Patent No 6420556
/ GENCORE INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE: IDENTIFICATION OF HUMAN SECRETED PROTEINS
/ FILING DATE: 1997-03-07
/ CURRENT FILING DATE: 1998-09-08
/ CURRENT APPLICATION NUMBER: US-09/149,476
/ EARLIER APPLICATION NUMBER: PCT/US98/04493
/ EARLIER APPLICATION NUMBER: 60/040,162
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,333
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,621
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,336
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,163
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,600
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,615
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,597
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,502
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,633
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,583
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,617
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,618
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,603
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,592
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,581
/ EARLIER FILING DATE: 1997-03-07
/ EARLIER APPLICATION NUMBER: 60/040,584
/ EARLIER FILING DATE: 1997-03-07

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Sequence 16, App1
Sequence 3188, A
Sequence 57, App1
Sequence 3102, A
Sequence 30103, A
Sequence 21, App1
Sequence 32, App1
Sequence 5068, App
Sequence 15, App1
Sequence 28771, A
Sequence 16, App1
Sequence 5048, App
Sequence 2, App1

[illegible]

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/ EARLIER APPLICATION NUMBER: 60/057,669
/ PARENT NO: 1991-09-05, 610
/ EARLIER FILING DATE: 1997-06-13, 610
/ EARLIER APPLICATION NUMBER: 60/061,060
/ EARLIER FILING DATE: 1997-10-02

```

```

Query Match 63.8%; Score 37; DB 4; Length 365;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

Cy 1 YKSPHNGA 9
Db 267 FSGHNGKAF 976

```

```

RESULT 2
US-09-252-991A-2215
/ Sequence 3215; Application US/09252991A
/ GENERAL INFORMATION:

```

```

/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ DESCRIPTION: SEQUENCES FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136

```

```

/ CURRENT APPLICATION NUMBER: US/09/252,991A

```

```

/ CURRENT FILING DATE: 1999-02-18

```

```

/ PRIOR APPLICATION NUMBER: US 60/074,788

```

```

/ PRIOR FILING DATE: 1998-07-27

```

```

/ PRIOR APPLICATION NUMBER: US 60/094,190

```

```

/ NUMBER OF SEQ ID NOS: 33142

```

```

/ LENGTH: 426

```

```

/ TYPE: PRT

```

```

/ ORGANISM: Pseudomonas aeruginosa

```

```

US-09-252-991A-32215

```

```

Query Match 63.8%; Score 37; DB 4; Length 426;
Best Local Similarity 66.7%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Cy 1 YKSPHNGA 9
Db 233 YANPHNGA 241

```

```

RESULT 3
US-09-252-991A-19973
/ Sequence 19973; Application US/09252991A
/ GENERAL INFORMATION:

```

```

/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ DESCRIPTION: SEQUENCES FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136

```

```

/ CURRENT APPLICATION NUMBER: US/09/252,991A

```

```

/ CURRENT FILING DATE: 1999-02-18

```

```

/ PRIOR APPLICATION NUMBER: US 60/074,788

```

```

/ PRIOR FILING DATE: 1998-07-27

```

```

/ PRIOR APPLICATION NUMBER: US 60/094,190

```

```

/ NUMBER OF SEQ ID NOS: 33142

```

```

/ LENGTH: 149

```

```

/ TYPE: PRT

```

```

/ ORGANISM: Pseudomonas aeruginosa

```

```

US-09-252-991A-19973

```

```

Query Match 62.1%; Score 36; DB 4; Length 149;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Cy 1 YKSPHNGA 9
Db 141 YKSPHNGA 149

```

```

RESULT 4
US-09-325-932A-153
/ Sequence 153; Application US/09325932A
/ GENERAL INFORMATION:

```

```

/ APPLICANT: Labban, Annette
/ TITLE OF INVENTION: Compositions affecting programmed cell
/ DESCRIPTION: death and their use in the modification of forestry pla
/ FILE REFERENCE: 1022

```

```

/ CURRENT APPLICATION NUMBER: US/09/325,932A

```

```

/ CURRENT FILING DATE: 1999-06-04

```

```

/ PRIOR APPLICATION NUMBER: US 60/064,964

```

```

/ PRIOR FILING DATE: 1998-08-29

```

```

/ NUMBER OF SEQ ID NOS: 5674

```

```

/ LENGTH: 396

```

```

/ TYPE: PRT

```

```

/ ORGANISM: Plinus radiata

```

```

US-09-325-932A-153

```

```

Query Match 62.1%; Score 36; DB 4; Length 365;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

Cy 1 YKSPHNGA 10
Db 328 YKSPHNGA 337

```

```

RESULT 5
US-09-134-001C-5402
/ Sequence 5402; Application US/09134001C
/ GENERAL INFORMATION:

```

```

/ APPLICANT: Genetic-Stream et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHY
/ DESCRIPTION: COCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: GTC-007

```

```

/ CURRENT APPLICATION NUMBER: US/09/134,001C

```

```

/ CURRENT FILING DATE: 1997-11-08

```

```

/ PRIOR APPLICATION NUMBER: US 60/055,779

```

```

/ PRIOR FILING DATE: 1998-08-29

```

```

/ NUMBER OF SEQ ID NOS: 5674

```

```

/ LENGTH: 484

```

```

/ TYPE: PRT

```

```

/ ORGANISM: Staphylococcus epidermidis

```

```

US-09-134-001C-5402

```

```

Query Match 62.1%; Score 36; DB 4; Length 484;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Cy 1 YKSPHNGA 9
Db 353 FSNHNGA 361

```

```

RESULT 6
US-09-252-991A-29931
/ Sequence 29931; Application US/09252991A
/ GENERAL INFORMATION:

```

```

/ APPLICANT: Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDO
/ DESCRIPTION: MONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

```

FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252.991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR FILING DATE: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 3142
 SEQ ID NOS: 1
 LENGTH: 473
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-2931

Query Match 60.3%; Score 35; DB 4; Length 474;
 Best Local Similarity 85.7%; Pct. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

3 GSNKQFA 9
 245 MARKER 251

RESULT 7
 US-08-836-567-12
 Patent No. 6130367
 GENERAL INFORMATION:
 APPLICANT: Kosseam, Jens
 APPLICANT: Spitzberg, Franziska
 APPLICANT: NetGenetic
 TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
 TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & NEAVE
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10020
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION NUMBER: release #1.0, version #1.30
 APPLICATION NUMBER: US/08/836,567
 FILING DATE: 24-JUL-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION NO:
 APPLICATION NUMBER: PCT/EP95/04415
 FILING DATE: 09-NOV-1995
 PRIOR APPLICATION DATA: DE P 44 41 408.0
 FILING DATE: 10-NOV-1994
 NAME: Haley Jr., James F.
 ATTORNEY/AGENT INFORMATION: Agrevo-4
 REFERENCE/DOCKET NUMBER:
 TELEPHONE: 212-596-9000
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1197 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 US-08-836-567-12
 Query Match 60.3%; Score 35; DB 3; Length 1197;

Best Local Similarity 85.7%; Pct. No. 4.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

2 GSNKQFA 8
 45 GSNKQFA 51

RESULT 8
 US-09-606-304-12
 Patent No. 6483010
 GENERAL INFORMATION:
 APPLICANT: Kosseam, Jens
 APPLICANT: Spitzberg, Franziska
 APPLICANT: NetGenetic
 TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRAN
 TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: FISH & NEAVE
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10020
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION NUMBER: release #1.0, version #1.30
 APPLICATION NUMBER: US/09/606,304
 FILING DATE: 28-JUN-2000
 CLASSIFICATION: 800
 PRIOR APPLICATION NO:
 APPLICATION NUMBER: 08/836,567
 FILING DATE: 24-JUL-1997
 NAME: Haley Jr., James F.
 ATTORNEY/AGENT INFORMATION: Agrevo-4
 REFERENCE/DOCKET NUMBER: 27,794
 TELEPHONE: 212-596-9000
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1197 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 US-09-606-304-12
 Query Match 60.3%; Score 35; DB 4; Length 1197;
 Best Local Similarity 85.7%; Pct. No. 4.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 TITLE OF INVENTION: Synchase
 2 NUMBER OF SEQUENCES: 15
 3 CORRESPONDENCE ADDRESS
 4 ADDRESSEE: McGregor & Adler, LLP
 5 STREET: 8011 Candle Lane
 6 CITY: Houston
 7 STATE: TX
 8 COUNTRY: USA
 9 ZIP: 77071
 10
 11 COMPUTER READABLE FORM:
 12 FILE TYPE: 3.5 floppy disk
 13 OPERATING SYSTEM: Macintosh
 14 SOFTWARE: Microsoft Word 6.0.1 for Macintosh
 15 CURRENT APPLICATION DATA:
 16 FILING DATE: 09/08/98
 17 FILING DATE: NO. 998128member 12, 1997
 18 CLASSIFICATION: 800
 19 PRIOR APPLICATION DATA:
 20 FILING DATE: 09/08/98
 21 FILING DATE: NO. 998128member 12, 1997
 22 ATTORNEY/AGENT INFORMATION:
 23 FILING DATE:
 24 NAME: Benjamin Aaron Adler, Ph.D., J.D.
 25 REGISTRATION NUMBER: 55,423
 26 TELECOMMUNICATION INFORMATION:
 27 TELEPHONE: (713) 777-2321
 28 TELEFAX: (713) 777-6908
 29 IMPROVED FOR SEQ ID NO: 1
 30 SEQUENCE CHARACTERISTICS: 35;
 31 LENGTH: 1230 amino acid residues
 32 TYPE: amino acid
 33 MOLECULE TYPE: linear
 34 DESCRIPTION: amino acid
 35 HYDROTICITY: no
 36 ANTI-GENES: no
 37 ANTI-GENES: no
 38 US-08-968-512C-35
 39
 40 Query Match 60.3%; Score 35; DB 2; Length 1230;
 41 Local Similarity 85.7%; Pct. No. 4.2e+02;
 42 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 43
 44 Oy 2 GINSPEC 8
 45 Db 78 GINSPEC 84

1 CURRENT APPLICATION DATA:
 2 APPLICATION NUMBER: US/08/750,152A
 3 FILING DATE: 09/08/98
 4 FILING DATE: NO. 435
 5 PRIOR APPLICATION DATA:
 6 APPLICATION NUMBER:
 7 FILING DATE:
 8 ATTORNEY/AGENT INFORMATION:
 9 FILING DATE:
 10 NAME: ROBINSON, WILLIAM R.
 11 REGISTRATION NUMBER: 24,618
 12 TELECOMMUNICATION INFORMATION:
 13 TELEPHONE: 703-413-3000
 14 INFORMATION FOR SEQ ID NO: 1
 15 SEQUENCE CHARACTERISTICS: 2;
 16 LENGTH: 1257 amino acids
 17 TYPE: amino acid
 18 MOLECULE TYPE: protein
 19 US-08-750-152A-2
 20
 21 Query Match 60.3%; Score 35; DB 2; Length 1257;
 22 Local Similarity 80.4%; Pct. No. 4.3e+02;
 23 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 24
 25 Oy 1 YONSPECAN 10
 26 Db 883 FANPESCAN 892
 27
 28 RESULT 11
 29 US-08-467-472C-12
 30 Sequence 12, Application US/08467472C
 31 Patent No. 6028168
 32 GENERAL INFORMATION:
 33 APPLICANT: ROBINSON, WILLIAM R.
 34 TITLE OF INVENTION: LANTHIONINE-BINDING PEPTIDES
 35 NUMBER OF SEQUENCES: 24
 36 CORRESPONDENCE ADDRESS: LANTHIONINE-BINDING PEPTIDES
 37 STREET 99 PARK AVENUE
 38 CITY: NEW YORK
 39 STATE: NY
 40 COUNTRY: USA
 41 ZIP: 10016
 42 COMPUTER READABLE FORM:
 43 MEDIUM TYPE: 3.5" floppy disk
 44 OPERATING SYSTEM: MS-DOS version 6.2
 45 SOFTWARE: ASCII
 46 CURRENT APPLICATION DATA:
 47 APPLICATION NUMBER: US/08/467,472C
 48 FILING DATE: 08-08-1995
 49 CLASSIFICATION: 514
 50 PRIOR APPLICATION DATA:
 51 APPLICATION NUMBER: US 07/742,908
 52 FILING DATE: 08-08-1991
 53 APPLICATION NUMBER: 58,123,606
 54 FILING DATE: 28-JANUARY-1993
 55 ATTORNEY/AGENT INFORMATION:
 56 NAME: ROBINSON, WILLIAM R.
 57 REGISTRATION NUMBER: 24,618
 58 TELECOMMUNICATION INFORMATION:
 59 TELEPHONE: (212) 697-3555
 60 TELEFAX: (212) 557-9635
 61 INFORMATION FOR SEQ ID NO: 12:
 62 SEQUENCE CHARACTERISTICS:
 63 TYPE: AMINO ACID
 64 TOPOLOGY: LINEAR
 65 MOLECULE TYPE:

DESCRIPTION: PEPTIDE
 HYPOTHETICAL: N/A
 FRAGMENT TYPE: INTERNAL
 ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
 ORIGINAL SOURCE: INC., 3700 MARKET STREET, PHILADELPHIA, PA 19104
 TMSD SOURCE: 1
 POSITION IN GENOME: N/A
 FEATURES:
 NAME/KEY: N/A
 LOCATION: N/A
 IDENTIFICATION METHOD: N/A
 OTHER INFORMATION: water is removed and
 OTHER INFORMATION: a -S- bridge is present between Cys and Ser
 PUBLICATION INFORMATION:
 AUTHORS: JUNG, GUNTHER
 TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
 JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
 JOURNAL: SYMPOSIUM
 VOLUME: ESCOM (LEIDEN 1990)
 ISSUE: 865 - 869
 DATE: 1990
 DOCUMENT NUMBER:
 FILING DATE: DATE:
 FILING DATE: DATE:
 RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SRR
 PUBLICATION INFORMATION:
 AUTHORS: CHIRIA, TETSUO
 JOURNAL: BIOPOLYMERS
 VOLUME: JOHN WILEY AND SONS, INC.
 ISSUE: SUPPLEMENTARY
 PAGES: 511 - 519
 DATE: 1991
 DOCUMENT NUMBER:
 FILING DATE: DATE:
 PUBLICATION DATE: IN SEQ ID NO: 12: CYS-SRR
 PUBLICATION INFORMATION:
 AUTHORS: BEAN, MARK F.
 TITLE: IDENTIFICATION OF A THIOETHER
 TITLE: IN PRODUCT
 TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
 TITLE: BY THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
 JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
 JOURNAL: SYMPOSIUM
 VOLUME: ESCOM (LEIDEN 1990)
 ISSUE: 443 - 445
 DATE: 1990
 DOCUMENT NUMBER:
 FILING DATE: DATE:
 RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SRR
 RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
 US-08-467-472C-12
 Query Match
 Best Local Similarity 59.6%; Score 34; DB 3; Length 9;
 Matches 5; Conservative 2; Mismatches 0; Indels 0;
 DB 1 YOUNSPRG 7
 3 FANSFPG 9

RESULT 12

US-09-384-061-12
 / Sequence 12, Application US/09384061
 / Patent No. 6268339
 GENERAL INFORMATION:
 TITLE OF INVENTION: MURRAY
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESSES: LUT HANFERN & DELAMUNTY
 STREET 59 PARK AVENUE
 CITY: NEW YORK
 STATE: NY
 COUNTRY: USA
 COMPUTER REMARKS FORM:
 MEDIUM TYPE: 3.5" FLOPPY DISC
 COMPUTER: COMPAQ - IBM COMPATIBLE
 SOFTWARE: MS-DOS version 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/384,061
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/467,472
 FILING DATE: 28-JANUARY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: ROBINSON, WILLIAM R.
 REFERENCE/DOCKET NUMBER: LBR-9122B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 697-3355
 TELEFAX: (212) 597-5635
 TELEX: NONE
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9
 TYPE: AMINO ACID
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PEPTIDE
 HYDROLYZABLE: N/A
 ANTI-SENSE: N/A
 FRAGMENT TYPE: INTERNAL
 ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
 ORIGINAL SOURCE: INC., 3700 MARKET STREET, PHILADELPHIA, PA 19104
 IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
 POSITION IN GENOME: N/A
 FEATURE:
 LOCATION: N/A
 IDENTIFICATION METHOD: N/A
 OTHER INFORMATION: water is removed and
 OTHER INFORMATION: a -S- bridge is present between Cys and Ser
 PUBLICATION INFORMATION:
 AUTHORS: JUNG, GUNTHER
 TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
 JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
 JOURNAL: SYMPOSIUM
 VOLUME: ESCOM (LEIDEN 1990)
 ISSUE: 865 - 869
 DATE: 1990
 DOCUMENT NUMBER:
 FILING DATE: DATE:
 PUBLICATION DATE: IN SEQ ID NO: 12: CYS-SRR
 RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SRR
 PUBLICATION INFORMATION:

```

US-09-34-061-12
AUTHOR: SHITA, TETSUO
TITLE: CHEMISTRY OF LANTHANONE PEPTIDES
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DOCUMENT NUMBER:
PUBLICATION DATE:
FILING DATE:
IN SEQ ID NO: 12; CYS-5ER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
BY-PRODUCT
TITLE: BY THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12; CYS-5ER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-09-34-061-12
Query Match
56.6%; Score 34; DB 3; Length 9;
|||||;
1 YKSGSG 7
Matches 5; Conservative 2; Mismatches 0; Indels
DB 3 PMSGSD 9

RESULT 13
US-08-068-207A-464
Sequence 461, Application US/0868207A
PDB: 1YKSGSG
SEQUENCE:
APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Stoddard, Robert
TITLE OF INVENTION: No. 634828e1 Compounds
NUMBER OF SEQUENCES: 552
ADDRESS: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
METHOD TYPE: Diskette
OPERATING SYSTEM: IBM
SOFTWARE: PASSED FOR Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA: 610/17670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:

```

```

NAME: Shima, Edward R.
RESIDATION NUMBER: 89,891
RESIDATION ADDRESS: 610-270-4478
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEX: 610-270-5090
INFORMATION FOR SEQ ID NO.: 464
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
TOPOLOGY: single
MOLECULE TYPE: No. 6348328e
US-08-858-207A-464

Query Match:
Best Local Similarity 58.6%; Score 34; DB 5; Length 111.
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0

DB 42 GENBANK 50

RESULT 14
PC/TUS94/00844-11
Sequence 11: Application PC/TUS9400844
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method of Controlling Plant Pathogenic Fungi
INVENTOR: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Windows 3.11, Release #1.0, Version #1.25 (EPC)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/00844
FILING DATE:
PRIORITY DATA:
PREVIOUS APPLICATION DATA:
APPLICATION NUMBER: US 08/010403
FILING DATE: 29-JUN-1993
INFORMATION FOR SEQ ID NO.: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PC-TUS94-00844-11

Query Match:
Best Local Similarity 85.7%; Pred.No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

DB 69 GSNPGF 75

RESULT 15
US-09-648-004-18
Sequence 18: Application US/09648004
GENERAL INFORMATION:
APPLICANT: CHEN, QIANG
APPLICANT: THOMAS, STUART
INVENTOR: NIKOLAIAN, VASSILINA
TITLE OF INVENTION: A METHOD FOR THE PRODUCTION OF ADIPIC ACID AND
INTERMEDIATES
FILE REFERENCE: C1-1441-A
CURRENT APPLICATION NUMBER: US/09/648,004

```


; CURRENT FILING DATE: 2000-04-25
 ; PRIOR APPLICATION NUMBER: 09/252,553
 ; PRIOR FILING DATE: 1999-02-19
 ; INVENTOR: BEO ID NO: 31
 ; SOFTWARE: MICROSOFT OFFICE 97
 ; SEQ ID NO 18
 ; LENGTH: 324
 ; TYPE: RT Acinetobacter sp.
 ; ORIGIN: US-09-648-004-18

Query Match 58.6%; Score 34; DB 4; Length 324;
 Match 12.5%; Pred. No. 1.5e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGF 8
 DB 31 FSVTFQGF 38

Search completed: November 7, 2003, 07:30:05
 CPU time: 2.4692 secs

GenCode version 5.1.6
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OK protein - protein search using sw model

Run on: November 7, 2003, 07:21:18 Search time 1.55407 seconds

(without alignment)
742,581 Million cell updates/sec

Title: US-09-661-992b-6

Perfect score: 72

Sequence: 1 DGGHGGSSPDY 12

Scoring table: BLOSUM62

Gappe 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 263308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Labeling first 45 summaries

Database: PIR 76:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the local score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	50	65.4	173	T31469	glycine/proline-rich
2	47	65.3	205	F87623	hypothetical prote
3	46	65.1	173	F87623	protein imported
4	44	61.1	475	C64557	hypothetical prote
5	44	61.1	475	A90672	hypothetical prote
6	44	61.1	475	B85322	hypothetical prote
7	43	59.7	215	T1207	hypothetical prote
8	43	59.7	235	T3380	hypothetical prote
9	43	59.7	304	T02651	lysophospholipase
10	43	59.7	304	T02651	lysophospholipase
11	42	58.3	1163	T38624	prostate cat. oxph
12	41	56.9	492	A24863	FMN2 protein - yea
13	41	56.9	492	A24863	FMN2 protein - yea
14	41	56.9	702	S49004	FMN2 protein - yea
15	40	55.6	425	PH1733	Ig heavy chain V r
16	40	55.6	425	PH1733	Ig heavy chain V r
17	40	55.6	33	PH1742	Ig heavy chain V r
18	40	55.6	33	PH1739	Ig heavy chain V r
19	40	55.6	80	B45466	glycine/tyrosine-r
20	40	55.6	109	B45475	glycine/tyrosine-r
21	40	55.6	126	GIHNRU	Ig heavy chain V r
22	40	55.6	137	H32513	Ig heavy chain V r
23	40	55.6	137	H32513	Ig heavy chain V r
24	40	55.6	139	T04410	strongly acidic ser
25	40	55.6	143	T04410	strongly acidic ser
26	40	55.6	286	A45350	multisubunit nucle
27	40	55.6	289	T96770	protein RNA-bindin
28	40	55.6	290	C27115	K-kinogen, LHM p
29	40	55.6	315	A71215	major acute phase

30	40	55.6	328	2	B87535	hypothetical prote
31	40	55.6	373	2	B84447	hypothetical prote
32	40	55.6	378	2	T49164	zinc transporter-1
33	40	55.6	382	2	T49164	zinc transporter-1
34	40	55.6	1227	2	T49465	probable RNA-bind
35	39	54.2	94	2	B49945	conserved hypotet
36	39	54.2	94	2	B49945	conserved hypotet
37	39	54.2	102	2	S06412	chloron protein a1
38	39	54.2	111	2	S25047	Ig heavy chain V r
39	39	54.2	273	2	A42332	hypothetical prote
40	39	54.2	312	2	A25559	synapophycin - hu
41	39	54.2	321	2	A25559	probable exporte
42	39	54.2	321	2	A25559	probable exporte
43	39	54.2	385	2	S51720	single stranded D
44	39	54.2	399	2	B83398	hypothetical prote
45	39	54.2	480	2	D83086	conserved hypotet

ALIGNMENTS

QUERY 1
T31469
Glycine/proline-rich protein - Arabidopsis thaliana
M:Alserato names protein K10A8_130
C:Query: 18-Aug-2000 sequence revision 18-Aug-2000 %text_change 18-Aug-2000
C:Accession: T31469
R:Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asanishi, E.; Kocani, H.; Tabata
submitted to the protein sequence database, August 2000
A:Accession: T31469 255394
A>Status: preliminary
A:Molecule type: DNA
A:Cross-references: EMBL:AL39151
A:Experimental source: Cultivar Columbia; BAC clone K10A8
A:Map position: 5
A:Map coordinates: 1-205
A:Note: K10A8_130

Query Match 69.44; Score 50; DB 2; Length 173;
Matched 80.04; Pred. No. 0.84; 1; Index 0;
Matches 0; Conservative 0; Negative 1; Indels 0;
Gap 0;
DB 36 GUYGGSSPDY 45

QUERY 2
F87623
hypothetical protein C3024 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Query: 20-Apr-2001 sequence revision 20-Apr-2001 %text_change 20-Apr-2001
R:Nitzman W.C.; Feldblyum, T.V.; Paulsen, I.T.; Neilson, K.E.; Eisen, J.; Heidelberg,
B.; Land, M.R.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.B.;
A:Reference number: A87249; PMID:21173697; PMID:11259647
A:Accession: F87623
A>Status: preliminary
A:Molecule type: DNA
A:Cross-references: 1-205 <DDB>
A:Cross-references: GB:A8005673; NID:G1424664; PTD:ANK24986.1; GSDDB:GN00148
A:Gene: C3024

Query Match 65.34; Score 47; DB 2; Length 205;
Best Local Similarity 70.04; Pred. No. 3;

Matches 7: Conservative 1: Mismatches 2: Indels 0: Gaps 0:

QY 3 GNGYSSFPY 12
|||||
DB 163 GNGYSSFPY 172

RESULT 3
protein [imported] - *Strombocidium mellicol* (strain 1021) magaplasmaid pygma
C/Spectra: *Strombocidium mellicol*
CDate: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
R/Barnett, M.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barto-Whitler, F.; Burt
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A/Title: Nucleotide sequence and predicted functions of the entire *Strombocidium mellicol*
A/Accession: D95384
A/Reference number: AF5262; MIMD:2139509; PMID:11681432
A/Status: preliminary
A/Molecule type: DNA
A/Accession: D95384
A/Cross-references: GB:AB004569; PID:AN65638.1; PID:g14524124; GSP08:GN00165
R/Experimental source: strain 1021, magaplasmaid pygma
R/Gillbert, F.; Flann, T.M.; Long, S.R.; Fisher, A.; Abola, A.P.; Ampe, F.; Barto-Whitler,
F.; Hyman, R.H.; Jones, T.; Komp, C.; Abola, A.P.; Barto-Whitler, F.; Burt, R.P.;
Science 293, 668-672, 2001
A/Authors: Kahn, D.; Kahn, M.T.; Kallam, S.; Keating, D.H.; Klee, E.; Komp, C.; Lalauze,
Hochuli, V.; Vandenhoef, M.; Votholler, F.J.; Weidner, S.; Wallis, D.H.; Wong, K.; Yeh, K.;
A/Reference number: A96039; MIMD:2136234; PMID:11747404
A/Contents: annotation
A/Genetics: 1176
A/Genome: Plasmid

Query Match 61.1%; Score 44; DB 2; Length 456;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7: Conservative 1: Mismatches 0: Indels 0: Gaps 0;

QY 4 HGQYSSFD 11
|||||
DB 168 HGQYSSFD 195

RESULT 4
probable iron-sulfur protein ykgf - *Escherichia coli* (strain K-12)
C/Spectra: *Escherichia coli*
CDate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
R/Balciunas, F.B.; Plunkett III, G.; Bloch, C.A.; Ferns, N.T.; Burland, V.; Riley, M.; Co
A/Title: The complete genome sequence of *Escherichia coli* K-12.
Science 277, 1453-1462, 1997
A/Reference number: AF4740; MIMD:9716601; PMID:9270503
A/Accession: C64151
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Accession: C64151
A/Cross-references: GB:AE000137; GB:U00096; NID:92367708; PIRN:JAC73410.1; PID:g1766498;
A/Experimental source: strain K-12, substrain MG1655
A/Genetics: 108
A/Genome: 458

C/Superfamily: conserved hypochlorite iron-sulfur protein HP0138, ferredoxin 2 [4e-48] h
C/Keywords: 4e-48; electron transfer; iron-sulfur protein; metalloprotein
P122; 4e-48; 318 372/Binding site: 4e-48 cluster (Cys) (covalent); #status predicted
P122; 4e-48; 369/Binding site: 4e-48 cluster (Cys) (covalent); #status predicted

Query Match 61.1%; Score 44; DB 2; Length 475;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7: Conservative 1: Mismatches 1: Indels 0: Gaps 0;

Matches 7: Conservative 1: Mismatches 2: Indels 0: Gaps 0:

QY 2 GNGYSSFP 10
|||||
DB 329 GNGYSSFP 337

RESULT 5
hypochlorite protein Bce0345 [imported] - *Escherichia coli* (strain O157:H7, sub
C/Spectra: *Escherichia coli*
CDate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C/Accession: A90672
R/Barnett, M.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barto-Whitler, F.; Burt
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A/Title: Nucleotide sequence and predicted functions of the entire *Strombocidium mellicol*
A/Accession: D95384
A/Reference number: AF5262; MIMD:2139509; PMID:11681432
A/Status: preliminary
A/Molecule type: DNA
A/Accession: D95384
A/Cross-references: GB:AB000007; PID:BA83768.1; PID:g13359802; GSP08:GN00154
R/Experimental source: strain O157:H7, substrain RIMD 0509952
A/Genetics: 1475
A/Genome: 458

C/Superfamily: conserved hypochlorite iron-sulfur protein HP0138, ferredoxin 2 [4e-48] h
C/Keywords: 4e-48; electron transfer; iron-sulfur protein; metalloprotein
P122; 4e-48; 318 372/Binding site: 4e-48 cluster (Cys) (covalent); #status predicted
P122; 4e-48; 369/Binding site: 4e-48 cluster (Cys) (covalent); #status predicted

Query Match 61.1%; Score 44; DB 2; Length 475;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7: Conservative 1: Mismatches 1: Indels 0: Gaps 0;

QY 2 GNGYSSFP 10
|||||
DB 329 GNGYSSFP 337

RESULT 6
hypochlorite protein ykgf [imported] - *Escherichia coli* (strain O157:H7, substre
C/Spectra: *Escherichia coli*
CDate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C/Accession: B85522
R/Barnett, M.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barto-Whitler, F.; Burt
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A/Title: Nucleotide sequence and predicted functions of the entire *Strombocidium mellicol*
A/Accession: D95384
A/Reference number: AF5262; MIMD:2139509; PMID:11681432
A/Status: preliminary
A/Molecule type: DNA
A/Accession: D95384
A/Cross-references: GB:AB000174; NID:g12513108; PIRN:JAG54641.1; GSP08:GN00145;
R/Experimental source: strain O157:H7, substrain EDJ933
A/Genetics: 1475
A/Genome: 458

C/Superfamily: conserved hypochlorite iron-sulfur protein HP0138, ferredoxin 2 [4e-48] h
C/Keywords: 4e-48; electron transfer; iron-sulfur protein; metalloprotein
P122; 4e-48; 318 372/Binding site: 4e-48 cluster (Cys) (covalent); #status predicted
P122; 4e-48; 369/Binding site: 4e-48 cluster (Cys) (covalent); #status predicted

Query Match 61.1%; Score 44; DB 2; Length 475;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7: Conservative 1: Mismatches 1: Indels 0: Gaps 0;

QY 329 GNGYSSFP 10
|||||
DB 329 GNGYSSFP 337

RESULT 7
hypochlorite protein BHI397 [imported] - *Bacillus halodurans* (strain C-125)
C/Spectra: *Bacillus halodurans*
CDate: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C/Accession: B83824
R/Takami, H.; Nakano, K.; Takaki, Y.; Mieno, G.; Sasaki, R.; Masui, N.; Fujii,

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

November 7, 2003, 07:21:18 ; Search time 0.865154 Seconds

652.278 Million cell updates/sec

Title:
Page:

US-09-661-992B-6

Sequence

1 DGGHGYGSSFDY 12

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

127863 seqs, 47026705 residues

total number of hits satisfying chosen parameters:

Maximum
Minimum

length: 0

Post-proc

Minimum Match 0%

Listing first 45 summaries

Database

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	Match	DB ID	Description
1	44	61	44	NCBI_S001	P1326 echinocidin
2	43	59	34	NCBI_HUMAN	P27637 baclophen
3	41	56	9	YALD_YABAT	P27637 otycolalque
4	40	56	72	NCBI_HAIT	Q02958 ovis aries
5	40	56	69	NCBI_HUMAN	Q02958 ovis aries
6	40	56	126	YALD_HUMAN	Q02958 ovis aries
7	40	55	6	NCBI_HUMAN	Q02958 ovis aries
8	40	55	139	GRB1_ORSEA	Q02958 ovis aries
9	40	55	6	NCBI_MOUSE	Q02958 ovis aries
10	40	55	6	NCBI_MOUSE	Q02958 ovis aries
11	40	55	6	NCBI_MOUSE	Q02958 ovis aries
12	39	54	213	Y359_TREPA	P08427 homo sapiens
13	39	54	211	Y359_HUMAN	P08427 homo sapiens
14	38	54	2	Y359_PRIVA	P08427 homo sapiens
15	38	54	2	NCBI_MOUSE	P08427 homo sapiens
16	38	54	2	NCBI_MOUSE	P08427 homo sapiens
17	38	54	2	NCBI_MOUSE	P08427 homo sapiens
18	38	54	2	NCBI_MOUSE	P08427 homo sapiens
19	38	54	2	NCBI_MOUSE	P08427 homo sapiens
20	38	54	2	NCBI_MOUSE	P08427 homo sapiens
21	38	54	2	NCBI_MOUSE	P08427 homo sapiens
22	38	54	2	NCBI_MOUSE	P08427 homo sapiens
23	38	54	2	NCBI_MOUSE	P08427 homo sapiens
24	38	54	2	NCBI_MOUSE	P08427 homo sapiens
25	38	54	2	NCBI_MOUSE	P08427 homo sapiens
26	38	54	2	NCBI_MOUSE	P08427 homo sapiens
27	38	54	2	NCBI_MOUSE	P08427 homo sapiens
28	38	54	2	NCBI_MOUSE	P08427 homo sapiens
29	38	54	2	NCBI_MOUSE	P08427 homo sapiens
30	38	54	2	NCBI_MOUSE	P08427 homo sapiens
31	38	54	2	NCBI_MOUSE	P08427 homo sapiens
32	38	54	2	NCBI_MOUSE	P08427 homo sapiens
33	38	54	2	NCBI_MOUSE	P08427 homo sapiens
34	38	54	2	NCBI_MOUSE	P08427 homo sapiens
35	38	54	2	NCBI_MOUSE	P08427 homo sapiens
36	38	54	2	NCBI_MOUSE	P08427 homo sapiens
37	37	53	160	Y359_PRIVA	P08427 homo sapiens
38	37	53	160	Y359_PRIVA	P08427 homo sapiens
39	37	53	160	Y359_PRIVA	P08427 homo sapiens
40	37	53	160	Y359_PRIVA	P08427 homo sapiens
41	37	53	160	Y359_PRIVA	P08427 homo sapiens
42	37	53	160	Y359_PRIVA	P08427 homo sapiens
43	37	53	160	Y359_PRIVA	P08427 homo sapiens
44	37	53	160	Y359_PRIVA	P08427 homo sapiens
45	37	53	160	Y359_PRIVA	P08427 homo sapiens
46	37	53	160	Y359_PRIVA	P08427 homo sapiens
47	37	53	160	Y359_PRIVA	P08427 homo sapiens
48	37	53	160	Y359_PRIVA	P08427 homo sapiens
49	37	53	160	Y359_PRIVA	P08427 homo sapiens
50	37	53	160	Y359_PRIVA	P08427 homo sapiens

[illegible]

Q5	Q6	Q7	Q8	Q9	Q10	Q11	Q12	Q13	Q14	Q15	Q16	Q17	Q18	Q19	Q20	Q21	Q22	Q23	Q24	Q25	Q26	Q27	Q28	Q29	Q30	Q31	Q32	Q33	Q34	Q35	Q36	Q37	Q38	Q39	Q40	Q41	Q42	Q43	Q44	Q45	Q46	Q47	Q48	Q49	Q50	Q51	Q52	Q53	Q54	Q55	Q56	Q57	Q58	Q59	Q60	Q61	Q62	Q63	Q64	Q65	Q66	Q67	Q68	Q69	Q70	Q71	Q72	Q73	Q74	Q75	Q76	Q77	Q78	Q79	Q80	Q81	Q82	Q83	Q84	Q85	Q86	Q87	Q88	Q89	Q90	Q91	Q92	Q93	Q94	Q95	Q96	Q97	Q98	Q99	Q100	Q101	Q102	Q103	Q104	Q105	Q106	Q107	Q108	Q109	Q110	Q111	Q112	Q113	Q114	Q115	Q116	Q117	Q118	Q119	Q120	Q121	Q122	Q123	Q124	Q125	Q126	Q127	Q128	Q129	Q130	Q131	Q132	Q133	Q134	Q135	Q136	Q137	Q138	Q139	Q140	Q141	Q142	Q143	Q144	Q145	Q146	Q147	Q148	Q149	Q150	Q151	Q152	Q153	Q154	Q155	Q156	Q157	Q158	Q159	Q160	Q161	Q162	Q163	Q164	Q165	Q166	Q167	Q168	Q169	Q170	Q171	Q172	Q173	Q174	Q175	Q176	Q177	Q178	Q179	Q180	Q181	Q182	Q183	Q184	Q185	Q186	Q187	Q188	Q189	Q190	Q191	Q192	Q193	Q194	Q195	Q196	Q197	Q198	Q199	Q200	Q201	Q202	Q203	Q204	Q205	Q206	Q207	Q208	Q209	Q210	Q211	Q212	Q213	Q214	Q215	Q216	Q217	Q218	Q219	Q220	Q221	Q222	Q223	Q224	Q225	Q226	Q227	Q228	Q229	Q230	Q231	Q232	Q233	Q234	Q235	Q236	Q237	Q238	Q239	Q240	Q241	Q242	Q243	Q244	Q245	Q246	Q247	Q248	Q249	Q250	Q251	Q252	Q253	Q254	Q255	Q256	Q257	Q258	Q259	Q260	Q261	Q262	Q263	Q264	Q265	Q266	Q267	Q268	Q269	Q270	Q271	Q272	Q273	Q274	Q275	Q276	Q277	Q278	Q279	Q280	Q281	Q282	Q283	Q284	Q285	Q286	Q287	Q288	Q289	Q290	Q291	Q292	Q293	Q294	Q295	Q296	Q297	Q298	Q299	Q300	Q301	Q302	Q303	Q304	Q305	Q306	Q307	Q308	Q309	Q310	Q311	Q312	Q313	Q314	Q315	Q316	Q317	Q318	Q319	Q320	Q321	Q322	Q323	Q324	Q325	Q326	Q327	Q328	Q329	Q330	Q331	Q332	Q333	Q334	Q335	Q336	Q337	Q338	Q339	Q340	Q341	Q342	Q343	Q344	Q345	Q346	Q347	Q348	Q349	Q350	Q351	Q352	Q353	Q354	Q355	Q356	Q357	Q358	Q359	Q360	Q361	Q362	Q363	Q364	Q365	Q366	Q367	Q368	Q369	Q370	Q371	Q372	Q373	Q374	Q375	Q376	Q377	Q378	Q379	Q380	Q381	Q382	Q383	Q384	Q385	Q386	Q387	Q388	Q389	Q390	Q391	Q392	Q393	Q394	Q395	Q396	Q397	Q398	Q399	Q400	Q401	Q402	Q403	Q404	Q405	Q406	Q407	Q408	Q409	Q410	Q411	Q412	Q413	Q414	Q415	Q416	Q417	Q418	Q419	Q420	Q421	Q422	Q423	Q424	Q425	Q426	Q427	Q428	Q429	Q430	Q431	Q432	Q433	Q434	Q435	Q436	Q437	Q438	Q439	Q440	Q441	Q442	Q443	Q444	Q445	Q446	Q447	Q448	Q449	Q450	Q451	Q452	Q453	Q454	Q455	Q456	Q457	Q458	Q459	Q460	Q461	Q462	Q463	Q464	Q465	Q466	Q467	Q468	Q469
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RT      Unaligned length, blood feeding process 7,
RW      PubMed: 7900103; GenBank: EMBL/genbank/DDBJ database.
DR      EMBL: AJ300192; CACC0599.1).
KW      Hypochelal protein.
SQ
Query Match          63.9%   DB 5; Length 381;
Best local similarity 63.6%   Pred. No. 21;
Matches              7; Conservative 2; Mismatches 2; Indels 0; Gaps 0
Qy              |||||
                2 GGGGCGSGY 12
Db              210 GGGYGSGYGV 220

RESULT 7
OxRH19          PRELIMINARY; PRT; 1023 AA.
ID              OxRH19
AC              OXKH19; 2002 (FRESHBCEL_20, Created)
DT              01-JUN-2002 (FRESHBCEL_21, Last annotation update)
DR              01-JUN-2002 (FRESHBCEL_21, Last annotation update)
DE              Probable peritrochial-binding protein 2.
OS              CP2140.
OC              eum peritrogam.
CC              Bacteria; Planctomycetes; Clostridia; Clostridiales; Clostridiaceae;
NCBI_TaxId=1502;
OX              NCBI_STANDPROT FROM N.A.
RN              STPAIN38.1 / Type A;
RX              PUBMED11793842)
RA              Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamauchi A.,
RA              Ohtani T., Ogasawara M., Harachi M., Akutsu S., Hayashi H.,
RA              Ogasawara K. et al. (2002) Complete sequence of Clostridium peritrogam, an anaerobic
FL               flesh-eater".
PR               Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR              EMBL: AF001393; BA81846.1;
DR              Interpro: IPRO0144; PF01466.
DR              Pfam: PF03717; PAP_dimer_1.
DR              Pfam: PF03095; Transpeptidase_1.
KM              complete proteome.
SQ
SeqData        1023 Db; 114912 MW; EMD10298347C2C3 CRCK4;
Query Match    63.9%; Score 46; DB 16; Length 1023;
Best Local Similarity 60.0%; Pred. No. 65;
Matches        1; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy              |||||
                1 DGGNGCSGP 10
Db              912 DGGNGCSGP 921

RESULT 8
OxS651          PRELIMINARY; PRT; 348 AA.
ID              OxS651
AC              OxS651
DT              01-JUN-2002 (FRESHBCEL_21, Created)
DR              01-JUN-2002 (FRESHBCEL_21, Last sequence update)
DE              01-OCT-2002 (FRESHBCEL_22, Last annotation update)
OS              OSRB0000441 Protein.
OS              Oryza sativa (Rice);
OS              Oryza sativa (Rice), and
OS              Oryza sativa [spontaneous cultivar-group].
CC              Bacteria; Verrucomicrobia; Streptophyta; Embryophyta; Tracheophyta;
CC              Charophyceae; Orobanchales; Liliopsida; Poales; Poaceae;
CC              Shariatkoideae; Oxycoryzoideae.
NCBI_TaxId=330. 39947; Cyfra.
(1)            SOURCE FROM N.A.
SR              SPRI000000000;
RC              SPRI000000000;
MC              McCombie W.R.; de la Parilla M.; Sifredo L.; MacCreanor L.; Rajiv v
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RA Zlatavren T., Bell M., Preston R., Kirchoff K., Nait K., Baker J.,
 RA Santos L., Miller R., Cunniff D.M., Kitzberger F., Miller S.,
 RA Shan K., King L., Yang C., Dike S., O'Shaughnessy A., Palmer L.,
 RA "Genomic sequence for Oryza sativa, Nipponbare strain, clone
 RL OSNBA0009410, from chromosome 10, complete sequence."
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 RC STRAIN=CV, Suncress; Tissue=Fruit;
 RP SEQUENCE FROM N.A.
 RA Wang R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Sack C.,
 RA Currie J., Collier K., "
 RL Submitted (Sep-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC098683; AN00113.1;
 DR EMBL: AC131968; AN00952.1;
 DR "Genomic sequence for Oryza sativa, Nipponbare strain, clone
 RL OSNBA0009410, from chromosome 10, complete sequence."
 RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 SQ SEQUENCE 348 AA; 35920 MW; FTERRCE3AB599BFP CRC64;
 Query Match 61.1%; Score 44; DB 10; Length 348;
 Best Local Similarity 77.8%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 DGGGTCG 8
 Db 224 EGGGTCG 231

RESULT 9
 0925H2 PRELIMINARY; PRT; 87 AA.
 ID 0925H2
 AC 0925H2 (TRENBERG, 19, Created)
 DT 01-DEC-2001 (TRENBERG, 19, Last sequence update)
 DT 01-DEC-2002 (TRENBERG, 22, Last annotation update)
 DB Keratin-associated protein 16.9.
 DR KERP16.9 OR KERP16.9.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 NX NCBI_Taxid:10090;
 RP SEQUENCE FROM N.A.
 RF STRAIN=FVB;
 RC MEDLINE:21185977; PubMed:1130294;
 RA Trechenko A.V., Vassonci R.P., Shang L., Papenbrock T., Fretet N.D.,
 RA "Overexpression of a novel hair keratin gene cluster and alopecia,"
 RT "Overexpression of a novel hair keratin gene cluster and alopecia,"
 RL Development 128:1547-1558 (2001).
 DR EMBL: U03164; AA09740.1;
 DR MED: W01217759; Knapic-9.
 SQ SEQUENCE 87 AA; 8449 MW; 3936ADBE617369 CRC64;
 Query Match 51.1%; Score 44; DB 11; Length 87;
 Best Local Similarity 77.8%; Pred. No. 7.9;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 7 GGGYCCSSY 65
 Db 57 GGGYCCSSY 65

RESULT 10
 093W26 PRELIMINARY; PRT; 193 AA.
 ID 093W26
 AC 093W26 (TRENBERG, 19, Created)
 DT 01-DEC-2001 (TRENBERG, 19, Last sequence update)
 DT 01-DEC-2002 (TRENBERG, 22, Last annotation update)
 DB Abiotic stress ripening-like protein.
 DR "Abiotic stress ripening-like protein."
 RL Tissue=peach (fresh).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroids II; Rosales; Rosaceae; Amygdaloideae; Prunus.
 NX NCBI_Taxid:3760;
 RP SEQUENCE FROM N.A.
 RA STRAIN=CV, Suncress; Tissue=Fruit;
 RA Callahan A.M., Meyers E.H., Cohen R.A.;
 RL "Regulation and initial characterization of cDNAs for mRNAs regulated
 RL during ripening of peach (Prunus persica) fruit."
 RL J. Am. Soc. Hort. Sci. 118:531-537 (1993).
 [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=CV, Suncress; Tissue=Fruit;
 RA Callahan A.M., Meyers E.H., Cohen R.A.;
 RL "Regulation of peach gene expression in a peach/almond hybrid."
 RL Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF111900.1; AF2689.1; F04.
 DR EMBL: AF111900.1; AF2689.1; F04.
 RP STRAIN=CV, Suncress; Tissue=Fruit;
 SQ SEQUENCE 193 AA; 20760 MW; D06C2D062D719P CRC64;
 Query Match 61.1%; Score 44; DB 10; Length 193;
 Best Local Similarity 72.7%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 GGGYCCSSY 12
 Db 73 GGGYCCSSY 83

RESULT 11
 050000 PRELIMINARY; PRT; 200 AA.
 ID 050000
 AC 050000 (TRENBERG, 05, Created)
 DT 01-JUN-1998 (TRENBERG, 05, Last sequence update)
 DT 01-OCT-2002 (TRENBERG, 22, Last annotation update)
 DB Abiotic stress ripening protein homolog.
 DR Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC euroids II; Rosales; Rosaceae; Amygdaloideae; Prunus.
 NX NCBI_Taxid:36596;
 RP SEQUENCE FROM N.A.
 RA STRAIN=CV, Suncress; Tissue=Mesocarp; and Exocarp;
 RA Moguel-Gonzalez D., Gomez R.-R., Fila-Lydon B., Jimenez R.,
 RT "Stress-Regulation of a Novel Protein from Apricot Fruit
 RL (Accession No. U93164). Gene Expression During Fruit Ripening." (CR97-
 RL 166). "
 DR EMBL: U93164; AA09740.1; 115:1288-1289 (1997).
 DR EMBL: U93164; AA09740.1; 115:1288-1289 (1997).
 RP STRAIN=CV, Suncress; Tissue=Mesocarp; and Exocarp;
 DR InterPro: IPR001496; AAA_WDS.
 DR Pfam: PF02496; AAA_WDS; I.
 SQ SEQUENCE 200 AA; 21240 MW; C45BAA5534C2D62 CRC64;
 Query Match 61.1%; Score 44; DB 10; Length 200;
 Best Local Similarity 72.7%; Pred. No. 21;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 GGGYCCSSY 12
 Db 80 GGGYCCSSY 90

RESULT 12
 091001 PRELIMINARY; PRT; 357 AA.
 ID 091001
 AC 091001 (TRENBERG, 23, Created)
 DT 01-MAR-2003 (TRENBERG, 23, Last sequence update)


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SQ SEQUENCE: 475 AA: 53000 MW: F81B64DD6A1CB0E CRC64:
Query Match 61.1%; Score 44; DB 16; Length 475;
      Identical 77.8%; Pred. No. 57;
      Matches 1; Mismatches 1; Indels 0; Gaps 0;
Q: 2 GGGGCGGSGF 10
D: 329 GGGGCGGSI 337

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increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis -

Claim 7, Page 74; 13pp; English.

The present sequence is that of complementarily determining region 3 (CDR3) of the heavy chain of an antibody expressed by mouse hybridoma 193/K2. This antibody has anti-factor IX (FIX) or anti-FIX/FIXa antibodies of the invention. Such antibodies and their derivatives (including those that comprise the present CDR3 peptide) have Factor VIIa (FVIIa) cofactor activity or FIXa derivatives leads to an increase in the amidolytic activity of FIXa, even in the presence of FVIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIIa or FVIIa in the case of FVIIa inhibitor patients. The antibodies or their derivatives are used in the treatment of haemorrhagic diathesis for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic diathesis.

Sequence 12 AA;

Query March 100.0%; Score 72; DB 22; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGGHGYSSSPFY 12
DB 1 DGGHGYSSSPFY 12

RESULT 2
AAR70433 100
XX 21-JUN-2001 (first entry)
AC AAR20434;

XX 21-JUN-2001 (first entry)
XX Anti-FIX/FIXa antibody 193/K2 scfv.

XX Factor IX, FIX, Factor VIIa, FIXa, scfv, antibody, procoagulant;
XX Factor VIII cofactor blood coagulation disorders, haemorrhagic diathesis; haemorrhagic diathesis; haemostatic; amyloid; therapy; mouse.

XX Chimeric - Mus musculus.
XX Chimeric - Synthetic.

XX Key Location/Qualifiers
XX Protein 1..121 WH
XX Region 98..110
XX Peptide 122..135
XX 122..135 linker
XX 122..135 linker
XX Protein /label= VU
XX Region 230..238
XX /label= CDR3

W0200119992-A2.

22-MAR-2001.

PF 13-SEP-2000; 2000MO-EP08036.

XX 14-SEP-1999; 99AT-0001576.

XX (BAXT) BAXTER AG.

XX Schellinger F, Kerschbamer R, Falkner F, Dornier F;

NR NPI; 2001-200159/30.
NR N-PDB; AAR70724.

XX New Factor IX/Factor IXa antibodies and their derivatives useful for increasing amidolytic activity of factor IXa, and for treating blood coagulation disorders such as haemophilia A and haemorrhagic diathesis -

Claim 10; Fig 15; 13pp; English.

The present sequence is that of a single chain Fv (scFv) derivative of antibody 193/K2 comprising the heavy (WH) and light (VL) variable regions of 193/K2 joined by an artificial, flexible linker peptide. The scFv was obtained by PCR amplification of CDRs for 193/K2 WH and VL regions and cloning in vector pDR2. 193/K2 is an antibody of the invention. Anti-FIX/FIXa and their derivatives (including scFv and CDR3 fragments) have Factor VIIa (FVIIa) cofactor activity or FIXa activating activity. Administration leads to an increase in the amidolytic activity of FIXa, even in the presence of FVIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIIa or FVIIa in the case of FVIIa inhibitor patients. The antibodies and derivatives are used in a treatment of haemorrhagic diathesis for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic diathesis.

Sequence 249 AA;

Query March 100.0%; Score 72; DB 22; Length 249;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DGGHGYSSSPFY 12
DB 99 DGGHGYSSSPFY 110

RESULT 3
AAR7835 100
XX AAR97935 standard; Protein; 1376 AA.
AC AAR7835;

XX 11-SEP-1996 (first entry)

XX Kaposi's sarcoma associated herpesvirus ORF25 product.

XX Kaposi's sarcoma; gamma-2 herpesvirus; KSHV, therapy; diagnosis;
XX vaccine; diagnosis; AIDS.

XX Kaposi's sarcoma associated herpesvirus.

XX Key Location/Qualifiers
XX Protein 1..121 WH
XX Region /note= "Ig and MHC protein signature"

W0615779-A1.

30-MAY-1996.

PF 21-NOV-1995; 95MO-US15138.

XX 11-APR-1995; 95US-0420235.

XX 21-NOV-1994; 94US-0343101.

XX (OTCO) UNIV COLUMBIA NEW YORK.

XX Chang Y, Moore PS;

NR 1996-268320/27.

XX N-705B; N070057.

XX Herpes virus associated with Kaposi's sarcoma - also definitive DNA

PT sequences, useful for diagnosis of and to develop prods. for
 XX treatment of Kaposi's sarcoma
 SS Claim 17; Page 175-180; 277pp; English.
 CC Lambda clone KS2 (AA170621) is a fragment of a newly identified human
 CC lambda phage genome that encodes a 17 open reading frames (ORFs),
 CC including ORF25 (AA106677). The protein products (AA07930-46,
 CC respectively) of the 17 ORFs can be expressed in eukaryotic or
 CC bacterial host cells for use as vaccines, for KS diagnosis, or for
 CC raising antibodies.
 XX Sequence 1376 AA;
 SQ Query Match 65.3%; Score 47; DB 17; Length 1376;
 Best Local Similarity 65.3%; Posd 99.97; Mismatches 2; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 DB 476 DDB/BLAST/BLAST 486
 OR 1 DDB/BLAST/BLAST 11
 DB 476 DDB/BLAST/BLAST 486
 RESULT 4
 ID AA093601 standard; Protein; 1376 AA.
 XX AA093601;
 XX AA093601;
 DT 25-MAR-2003 (updated)
 DT 13-AUG-1996 (first entry)
 DB 13-AUG-1996
 XX Kaposi's sarcoma associated herpesvirus major capsid protein.
 XX Kaposi's sarcoma; KSHV; lymphoma; AIDS; vaccine; diagnosis; therapy;
 XX capsid protein.
 XX Kaposi's sarcoma associated herpesvirus.
 XX M09606159-A1.
 XX 22-FEB-1996.
 XX 11-NOV-1995; 95NC-US10194.
 PR 18-AUG-1994; 94US-0292365.
 PR 21-NOV-1994; 94US-0343101.
 PR 11-APR-1995; 95US-0420235.
 XX (YVOC) UNIV COLIMBIA NEW YORK.
 XX (GRAN) GRANT D E.
 XX (VIEL) VIELE L.
 XX Chang Y, Moore PS, Grant DB, Viele L,
 XX WPI, 1996-151362/15.
 DR N-PDB; AA176807.
 PT Herpes virus DNA associated with Kaposi's sarcoma - also associated
 PT vectors and proteins, used in detection and vaccination.
 XX Claim 17; Page 188-193; 305pp; English.
 CC Kaposi's sarcoma associated herpes virus (KSHV) clone KS2 (AA168603)
 CC obit. from a KS lesion genomic library, includes 18 complete ORFs and
 CC 2 incomplete ORFs (AA176907-23) named according to their herpesvirus
 CC homologs. The protein products of the major capsid protein (AA093601)
 CC is the product of ORF25 (AA106677). The protein products (AA07930-46,
 CC respectively) of the 17 ORFs can be expressed in eukaryotic or
 CC bacterial host cells for use as vaccines, for KS diagnosis, or for
 CC raising antibodies. They are useful in vaccines or for raising
 CC antibodies of diagnostic or therapeutic value.
 CC (updated on 25-MAR-2003 to correct FR field.)
 XX Sequence 1376 AA;
 SQ Query Match 65.3%; Score 47; DB 17; Length 1376;
 Best Local Similarity 65.3%; Posd 99.97; Mismatches 2; Indels 0; Gaps 0;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 DB 476 DDB/BLAST/BLAST 486
 OR 1 DDB/BLAST/BLAST 11
 DB 476 DDB/BLAST/BLAST 486
 RESULT 5
 ID AA093601 standard; Protein; 475 AA.
 XX AA093601;
 XX AA093601;
 DT 26-SEP-2001 (first entry)
 DT 26-SEP-2001 (first entry)
 DB 26-SEP-2001
 XX E. coli growth and proliferation related protein sequence SEQ ID NO:403.
 XX Escherichia coli; growth; proliferation; microbials; antimicrobial;
 XX bacterial infection; microorganism.
 XX Escherichia coli.
 XX M020013481-02.
 XX 17-MAY-2001.
 PF 09-NOV-2000; 2000NC-US0950.
 XX 09-NOV-1999; 95US-0164415.
 PR 09-NOV-1999; 95US-0164415.
 XX (BLT-) BLTMA PHARM INC.
 XX Forayth PA, Ohlsen K, Zybind J;
 XX WPI, 2001-33693/35.
 DR N-PDB; AA084604.
 PT Novel nucleic acids that inhibit Escherichia coli proliferation, useful
 PT for screening for homologous genes and for designing expression vectors
 XX Claim 19; Page 467-468; 522pp; English.
 CC AA094377 to AA094499 represent Escherichia coli growth and proliferation
 CC related DNA sequences (1) AA094450 to AA094500 and AA094880
 CC growth and proliferation related proteins given in AA094078 and AA094880
 CC to AA094999. (1) can be used as potential targets for the generation of
 CC antimicrobial agents, and for identification of compounds which
 CC interfere with the growth and proliferation of the bacteria. The expression of
 CC (1) and the purification of the proteins. The purified proteins can be
 CC used to generate reagents and screen small molecule libraries or other
 CC candidate compound libraries for compounds that can be further developed
 CC complementary to (1) that are specific for particular microorganism species
 CC in clinical specimens, therefore, providing a rapid and dependable
 CC method for identifying the causative agents of a bacterial
 CC infection. Also antibodies to the proteins can be used to screen for
 CC mAb transcribed from proliferation-required sequences can also be used
 CC to screen for specific microorganisms that produce such proteins in a
 CC primary cell culture. AA094377 and AA094670 represent sequencing
 CC related sequences, which are used in an example from the present
 CC invention.
 XX Sequence 475 AA;
 SQ Query Match 61.1%; Score 44; DB 22; Length 475;

Best Local Similarity 77.8%; Pred. No. 99;
Matches 7; Conservative 1; Mismatches 8;
DB 2 GENE3638P 10
329 GENE3638P 337

RESULT 6
AB27993
ID AB27993 standard: Protein; 81 AA.
AA AB27993.
DT 18-FEB-2002 (first entry)
XX Novel human diagnostic protein #27984.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder.
XX Homo sapiens.
XX WO200175067-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2001; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649457.
XX (HRS-) HRSQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDS; AAB92380.
XX New isolated polynucleotide and encoded polypeptide, useful in
XX diagnostics, forensic, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX Claim 20; SEQ ID NO 58352; 103bp; English.
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences, primers, oligomers, and for chromosome
XX polymerase chain reaction (PCR) primers, oligomers and for chromosome
XX and gene mapping, and also used in diagnostics, as expressed sequence tags
XX and for identifying genetic disorders, and for identifying genetic
XX disorders. The polynucleotides are also used in diagnostics, as expressed sequence tags
XX (II), (II) is useful for generating antibodies against it, detecting or
XX quantifying a polypeptide in tissue, as molecular weight markers and as
XX imaging of sites expressing (II). (II) and (II) are useful in medical
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX responsible for genetic disorders, identification of mutations, diversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABB00010-AB030177 represent novel human
XX polynucleotide sequences of the invention.
XX Non-patent literature sequences of the invention appear in the printed
XX specification, but was obtained in electronic format directly from WFO
XX at ftp.wipo.int/pub/published_pcr_sequences.
XX Sequence 61 Ab;

Query Match 59.7%; Score 43; DB 23; Length 81;
Best Local Similarity 77.8%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 2 GENE3638P 10
42 GENE3638P 50

RESULT 7
AB27993
ID AB27993 standard: Protein; 81 AA.
AA AB27993.
DT 20-JAN-2003 (first entry)
XX Human polypeptide SEQ ID NO 1665.
XX Human; genome mapping; gene therapy, food supplement, virus; fungus;
XX cell-proliferative disorder; neurodegenerative disease; bacterial;
XX multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
XX arthritis; cysticercosis; immunomodulator; neoplastic; neuroprotective;
XX antiparkinsonian; antidepressant; immunosuppressive; dermatological;
XX antidiabetic; antihypertensive; fungicide; antibacterial; vitinoid; proteaseinhibitor;
XX antitubercular.
XX Homo sapiens.
XX WO200270539-A2.
XX 12-SEP-2002.
XX 05-MAR-2002; 2002NO-US05095.
XX 05-MAR-2001; 2001US-0799451.
XX (HRS-) HRSQ INC.
XX Tang YT, Zhou P, Goodrich RM, Anundi V, Zhang J, Zhao QK, Fan F;
XX Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghoosh M;
XX Weinman T, Wang D, Drmanac RT;
XX WPI; 2002-759812/82.
XX N-PSDS; AAB21855.
XX New polynucleotides comprising sequences assembled from expressed
XX sequence tags (ESTs), useful for treating cell-proliferative
XX neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or
XX platelet or coagulation disorders -
XX Claim 9; SEQ ID NO 1665; 102bp + sequence listing; English.
XX The invention relates to an isolated polynucleotide (I) comprising a
XX sequence selected from any of the sequences of the invention, active domain
XX (AB21119-AB21065) or complementary sequences. The polynucleotides are useful
XX for identifying expressed genes or for physical mapping of human genome.
XX The polynucleotides are also used in diagnostics, as expressed sequence tags
XX and for identifying genetic disorders, and for identifying genetic
XX disorders. The polynucleotides are also used in diagnostics, as expressed sequence tags
XX (II), (II) is useful for generating antibodies against it, detecting or
XX quantifying a polypeptide in tissue, as molecular weight markers and as
XX imaging of sites expressing (II). (II) and (II) are useful in medical
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX responsible for genetic disorders, identification of mutations, diversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABB00010-AB030177 represent novel human
XX polynucleotide sequences of the invention.
XX Non-patent literature sequences of the invention appear in the printed
XX specification, but was obtained in electronic format directly from WFO
XX at ftp.wipo.int/pub/published_pcr_sequences.
XX Sequence 81 Ab;

Query Match 59.7%; Score 43; DB 23; Length 81;
Best Local Similarity 77.8%; Pred. No. 24;

10

100

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CC The present amino acid sequence is the human RNA-associated protein-3
CC (RNPAP-3), identified in hyove clone 2243514, derived from U738N0702
CC library. RNPAP-3 is a 285 amino acid protein that is expressed in
CC immune tissues. It has cytotoxic, immunosuppressive, keratinolytic,
CC antiinflammatory, antileukotrienic, hepatotropic, virocidic,
CC neuroprotective, antipapillat, anti-HIV antiallergic, antipneumatic,
CC and antiparasitic activities. RNPAP-3 is a diacyl glycerol-activated
CC RMAP antibodies are useful for diagnosis of diacyl glycerol-activated
CC altered expression or activity of RMAP. It is used to treat call
CC and to produce other types of data and products dependent on DNA and
CC protein. RNPAP-3 is a protein that is involved in the regulation of
CC circadian rhythm, primary thrombocythemia and cancer. HIV, allergies,
CC rheumatoid arthritis, urethritis, Crohn's disease, and bacterial, viral and
CC parasitic infections.

Sequence 285 AA;
Query Match 59.7%; Score 43; DB 21; Length 285;
Best Local 59.0%; 17ed. No. 83;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 GGGGYSRSP 11
DB 116 GGGGYSRSP 125

Residue 15

ID ABG02073 standard; Protein; 354 AA.

AC ABG02073;

DT 11-FEB-2002 (first entry)

DE Novel human diagnostic protein #2064.

KE Human; chromosome mapping; gene mapping; gene therapy; forensic;
KE food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX NC020175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001MC-US00651.

XX 31-MAR-2000; 2000QS-0540217.

XX 23-AUG-2000; 2000QS-0649167.

PA (HRSB-) HYSD INC.

PI Dmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR N-FSDB; PA866260.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostic and therapeutic applications, and in the treatment of
PT disorders responsible for genetic disorders of other traits and to assess
PT biodiversity -

Claim 20; SEQ ID No 32432; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences, (I) is useful as hybridization probes,
CC and (II) is useful as primer, oligomer, and for chromosome
CC mapping and in recombinant DNA technology. (I) and (II)
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC (II), (III) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC and assaying protein expression or biological activity.
CC The polypeptide and mutant protein expression or biological activity.
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC protein. RNPAP-3 is a protein that is involved in the regulation of
CC circadian rhythm, primary thrombocythemia and cancer. HIV, allergies,
CC rheumatoid arthritis, urethritis, Crohn's disease, and bacterial, viral and
CC parasitic infections.

Sequence 354 AA;
Query Match 59.7%; Score 43; DB 22; Length 354;
Best Local 59.0%; 17ed. No. 83;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 GGGGYSRSP 11
DB 185 GGGGYSRSP 194

Search completed: November 7, 2003, 07:26:58
Job time 7:1749 secs

GenScan version 3.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:30:19 / Search time 10.536 seconds

(without alignments)
195,799 Million cell updates/sec

Title: US-09-661-992b-6

Perfect score: 72

Sequence: 1 DOHGVSSSFY 12

Scoring table: BLOSUM62

Gap: 10.0, Gap: 0.5

Searched: 644079 seqs, 17174292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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18. /cgn2_6/prodata2/pubmap/US10_PUBCOMB.pep.*

Prod. No. is the number of results predicted by chance to have a
sequence identical to the one reported by the database.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	1	12	US-10-029-386-28297	Sequence 28297, A
2	44	61	1	US-10-029-386-28297	Sequence 103, App
3	44	59	7	US-09-852-659-116	Sequence 116, App
4	43	59	7	US-09-852-659-116	Sequence 116, App
5	43	57	223	US-09-852-659-116	Sequence 116, App
6	43	57	223	US-09-852-659-116	Sequence 116, App
7	40	55	6	US-09-253-791-7	Sequence 2, App1
8	40	55	6	US-09-253-791-7	Sequence 2, App1
9	40	55	6	US-09-253-791-7	Sequence 2, App1
10	40	55	6	US-09-253-791-7	Sequence 2, App1
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26	40	55	6	US-09-253-791-7	Sequence 2, App1
27	40	55	6	US-09-253-791-7	Sequence 2, App1
28	40	55	6	US-09-253-791-7	Sequence 2, App1
29	40	55	6	US-09-253-791-7	Sequence 2, App1
30	40	55	6	US-09-253-791-7	Sequence 2, App1
31	40	55	6	US-09-253-791-7	Sequence 2, App1
32	40	55	6	US-09-253-791-7	Sequence 2, App1
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ALIGNMENTS

RESULT 1
US-10-029-386-28297
Sequence 28297, Application US/1002386
GENERAL INFORMATION
APPLICANT: Penn, Sharon G.
APPLICANT: Penn, David K.
APPLICANT: Penn, David K.
FILE REFERENCES: ABOVICA-X-2
CURRENT APPLICATION NUMBER: US/10/029.386
NUMBER OF SEQ ID: 102
SOFTWARE: Anomax Sequence Mapping Engine vers. 1.1
SEQ ID NO: 28297
LENGTH: 102
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CH21.50.0
US-10-029-386-28297
Query Match Similarity: 61.1%, Score 44, DB 12, Length 102;
Matches 0, Mismatches 2, Indels 0, Gaps 0;
DB 91, Gaps 100
RESULT 2
US-10-029-386-28297
Sequence 403, Application US/1002386
GENERAL INFORMATION:
Publication No. US200181408A1


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1 PRIOR APPLICATION NUMBER: 60/040,762
2 PRIOR FILING DATE: 1997-03-14
3 PRIOR APPLICATION NUMBER: 60/040,710
4 PRIOR FILING DATE: 1997-03-14
5 PRIOR FILING DATE: 1997-03-14
6 PRIOR FILING DATE: 1997-03-14
7 PRIOR FILING DATE: 1997-03-14
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98 PRIOR FILING DATE: 1997-03-14
99 PRIOR FILING DATE: 1997-03-14
100 PRIOR FILING DATE: 1997-03-14

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Query Match 59.74; Score 43; DB 10; Length 223;
Best Local Similarity 70.04; Pred. No. 54;
Matches 1; Mismatches 2; Indels 0; Gaps 0;
2 GARGOYLED 11
162 GARGOYLED 171

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RESULT 6
US-10-240-819-2
Sequence 7: Application US/02923794
GENERAL INFORMATION:
APPLICANT: HENSEN, JAMES PETER
TITLE OF INVENTION: TREATMENT OF FUNGAL INFECTIONS WITH POLYMER OR BETA GLUCAN
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 050885/0232613
CURRENT APPLICATION NUMBER: US/10/240,819
PRIOR APPLICATION NUMBER: PCT/GB01/01195
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: GB 0008305-5
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 2
TYPE: PAT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic modified
US-10-240-819-2

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Query Match 59.74; Score 43; DB 12; Length 248;
Best Local Similarity 67.44; Pred. No. 40;
Matches 7; Mismatches 1; Indels 3; Gaps 0;
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102 GARGOYLED 112

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RESULT 7
US-09-253-794-7

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Sequence 7: Application US/02923794
Patent No. US02020018750A1
GENERAL INFORMATION:
APPLICANT: HENSEN, JAMES PETER
TITLE OF INVENTION: TREATMENT OF FUNGAL INFECTIONS WITH POLYMER OR BETA GLUCAN
TITLE OF INVENTION: ANTIBODIES
FILE REFERENCE: 050885/0232613
CURRENT APPLICATION NUMBER: US/09/253,794
PRIOR APPLICATION NUMBER: PCT/GB01/01195
PRIOR FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: GB 0008305-5
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 2
TYPE: PAT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic modified
US-09-253-794-7

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Query Match 55.64; Score 40; DB 9; Length 126;
Best Local Similarity 67.44; Pred. No. 40;
Matches 7; Mismatches 1; Indels 3; Gaps 0;
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99 DEXAGYLED 107

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SOFTWARE: unknown
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/229,200A
  FILING DATE: 11-Jan-1999
  CLASSIFICATION: US-DOA
  ATTORNEY/AGENT INFORMATION:
    NAME: John W. Wallen, III
    REGISTRATION NUMBER: 35,403
    ADDRESS: 10000 Wilshire Blvd., Suite 1000
    TELEPHONE: (858) 784-3239
    TELEFAX: (858) 524-2808
  INFORMATION OR SEQ ID NO: 8
  SEQUENCE CHARACTERISTICS:
    LENGTH: 126
    TYPE: amino acid
    TOPOLOGY: linear
  SOURCE OR DISCONTINUITY: SEQ ID NO: 8

US-09-229-200A-8

Query Match
  Score Similarity: 55.64; Score 40; DB 9; Length 126;
  Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 99 DCDHFFCS 107

RESULT 9
US-09-229-200A-18
  Sequence 18: Application US/09229200A
  Patent No. US20020099179A1
  GENERAL INFORMATION: fcs, cf, a1
  TITLE OF INVENTION: CD4 Specific Recombinant Antibody
  NUMBER OF SEQUENCES: 28
  CORRESPONDENCE ADDRESS:
    STREET ONE: Johnson & Johnson
    STREET TWO: One Johnson & Johnson Plaza
    CITY: New Brunswick
    STATE: NJ USA
    ZIP: 08933-7003
  COMPUTER READABLE FORM:
    MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
    COMPUTER: IBM
    SOFTWARE: PC-DOS
    APPLICATION DATA:
      APPLICATION NUMBER: US/09/229,200A
      FILING DATE: 11-Jan-1999
      CLASSIFICATION: US-DOA
  ATTORNEY/AGENT INFORMATION:
    NAME: John W. Wallen, III
    REGISTRATION NUMBER: 35,403
    ADDRESS: 10000 Wilshire Blvd., Suite 1000
    TELEPHONE: (858) 784-3239
    TELEFAX: (858) 524-2808
  INFORMATION OR SEQ ID NO: 8
  SEQUENCE CHARACTERISTICS:
    LENGTH: 126
    TYPE: amino acid
    TOPOLOGY: linear
  SOURCE OR DISCONTINUITY: SEQ ID NO: 18

US-09-229-200A-18

Query Match
  Score Similarity: 55.64; Score 40; DB 9; Length 126;
  Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 99 DCDHFFCS 9

```

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DB 99 DCDHFFCS 107

RESULT 10
US-09-78-515-10
  Sequence 10: Application US/0979515
  Publication No. US2003003645A1
  GENERAL INFORMATION:
    NAME: Mark R.
    REGISTRATION NUMBER: 35,403
    ADDRESS: 10000 Wilshire Blvd., Suite 1000
    TELEPHONE: (858) 784-3239
    TELEFAX: (858) 524-2808
  INFORMATION OR SEQ ID NO: 8
  SEQUENCE CHARACTERISTICS:
    LENGTH: 126
    TYPE: amino acid
    TOPOLOGY: linear
  SOURCE OR DISCONTINUITY: SEQ ID NO: 10

US-09-78-515-10

Query Match
  Score Similarity: 55.64; Score 40; DB 11; Length 126;
  Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 99 DCDHFFCS 9

RESULT 11
US-10-422-049-10
  Sequence 10: Application US/10422049
  Publication No. US2003019679A1
  GENERAL INFORMATION:
    NAME: John R.
    REGISTRATION NUMBER: 35,403
    ADDRESS: 10000 Wilshire Blvd., Suite 1000
    TELEPHONE: (858) 784-3239
    TELEFAX: (858) 524-2808
  INFORMATION OR SEQ ID NO: 8
  SEQUENCE CHARACTERISTICS:
    LENGTH: 126
    TYPE: amino acid
    TOPOLOGY: linear
  SOURCE OR DISCONTINUITY: SEQ ID NO: 10

US-10-422-049-10

Query Match
  Score Similarity: 55.64; Score 40; DB 11; Length 126;
  Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 99 DCDHFFCS 9

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PRIOR FILING DATE: 1995-06-01
 PRIOR APPLICATION NUMBER: 08/373,882
 PRIOR FILING DATE: 1995-01-17
 PRIOR APPLICATION NUMBER: 07/920,378
 PRIOR FILING DATE: 1992-09-28
 PRIOR APPLICATION NUMBER: 08/018,520
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 10
 LENGTH: 126
 ORGANISM: Homo sapiens
 US-10-422-049-10

Query Match 55.6%; Score 40; DB 12; Length 126;
 Best Local Similarity 70.0%; Pctd No. 66
 Matches 7; Conservative 1; Mismatches 0; Gaps 0;

Cy 1 DGGHGYGSS 9
 Db 99 DGGHGYGSS 107

RESULT 12
 US-10-267-286A-11
 Sequence 11, Application US/10267286A
 Publication No. US2003010849A1
 INVENTOR: BLUESSTONE, JEFFREY A.
 APPLICANT: BLUESSTONE, JEFFREY A.
 APPLICANT: ZIVIN, ROBERT A.
 APPLICANT: DOLLEFF, LINDA K.
 TITLE OF INVENTION: IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
 ANTIBODIES
 FILE REFERENCES: POLY 00485C3, US/10/267,286A
 CURRENT FILING DATE: 2003-01-28
 PRIOR APPLICATION NUMBER: 08/557,050
 PRIOR FILING DATE: 1998-10-09 US94/06138
 PRIOR APPLICATION NUMBER: 08/557,050
 PRIOR FILING DATE: 1994-06-01
 PRIOR APPLICATION NUMBER: 08/070,116
 PRIOR FILING DATE: 1993-06-01
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: PatentIn ver. 2.1
 SEQ ID NO 11
 LENGTH: 126
 TYPE: PRT Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-10-267-286A-11

Query Match 55.6%; Score 40; DB 15; Length 126;
 Best Local Similarity 77.8%; Pctd No. 66;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 DGGHGYGSS 9
 Db 99 DGGHGYGSS 107

RESULT 13
 US-09-661-992b-1
 Sequence 630, Application US/09295302
 Patent No. US2002004494A1
 GENERAL INFORMATION: A1
 TITLE OF INVENTION: Nucleic Acids, Proteins and Antihodies
 FILE REFERENCE: P404
 CURRENT APPLICATION NUMBER: US/09/925,302
 PRIOR FILING DATE: 2001-09-10
 PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 60/124,270
 PRIOR FILING DATE: 1999-03-12
 NUMBER OF SEQ ID NOS: 896
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 10
 LENGTH: 159
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-925-301-630

Query Match 55.6%; Score 40; DB 3; Length 159;
 Best Local Similarity 70.0%; Pctd No. 1,1e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 3 DGGHGYGSS 12
 Db 128 DGGHGYGSS 137

RESULT 14
 US-09-738-626-6160
 Sequence 11, Application US/09738626
 Publication No. US20030137605A1
 GENERAL INFORMATION: A1
 APPLICANT: MAKAMURA, SATOSHI
 APPLICANT: MAKAMURA, SATOSHI
 APPLICANT: ANDO, SEIRO
 APPLICANT: ANDO, SEIRO
 APPLICANT: HAYASHI, MITSUO
 APPLICANT: OCHIAI, KENICHI
 APPLICANT: OCHIAI, KENICHI
 APPLICANT: IWATISHI, MAKIKO
 APPLICANT: SENOH, AKIHIRO
 APPLICANT: IYEDA, MASATO
 TITLE OF INVENTION: MODEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-125
 CURRENT APPLICATION NUMBER: US/09/738,626
 PRIOR FILING DATE: 2000-03-08
 PRIOR APPLICATION NUMBER: 09/077,884
 PRIOR FILING DATE: 1999-12-16
 PRIOR APPLICATION NUMBER: JP 00/159162
 PRIOR FILING DATE: 2000-04-07 00/280986
 PRIOR FILING DATE: 2000-08-03
 NUMBER OF SEQ ID NOS: 7059
 SOFTWARE: PatentIn ver. 3.0
 SEQ ID NO 10
 LENGTH: 295
 TYPE: PRT
 ORGANISM: Corynebacterium glutamicum
 US-09-738-626-6160

Query Match 54.2%; Score 39; DB 10; Length 295;
 Best Local Similarity 56.3%; Pctd No. 2,8e+02;
 Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Cy 1 DGGHGYGSS 12
 Db 282 DGGHGYGSS 293

RESULT 15
 US-09-661-992b-1
 Sequence 630, Application US/0950368
 Patent No. US20020061560A1
 GENERAL INFORMATION: A1
 TITLE OF INVENTION: Interactinal, Inc.
 FILE REFERENCE: C551-1C7
 CURRENT APPLICATION NUMBER: US/09/503,68
 PRIOR FILING DATE: 2001-09-10
 PRIOR APPLICATION NUMBER: 09/355,166

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; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NOS: 1
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Bacillus
US-09-950-368-1
Query Match          54.2%; Score 39; DB 9; Length 657;
Best Local Similarity 66.7%; Pred. No. 6a+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Ox 2 GCGGTGSSF 10
Db 469 GSHGYCEEF 477

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Search completed: November 7, 2003, 08:16:50
 Job time : 11.526 secs

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DECRYPTED 11
 Db 468 DGHGTYGLAYE 478

RESULT 2

US-09-183-688-18

/ Sequence 18, Application US/09183688

/ Patent No. 6093350

/ APPLICANT: Chans, Yvan

/ TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma

/ TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma

/ NUMBER OF SEQUENCES: 22

/ CORRESPONDENCE ADDRESS:

/ ADDRESS: Cooper & Dunham

/ STREET: 1185 Avenue of the Americas

/ CITY: New York

/ STATE: New York

/ COUNTRY: U.S.A.

/ ZIP: 10036

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent Release #1.24

/ TELEPHONE: 212-278-0400

/ FAX: 212-278-0400

/ TELEFAX: 212-391-0526

/ INVESTIGATOR: PCR SEQ ID NO: 18

/ SECURITY CLASSIFICATION: 18

/ LENGTH: 861 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: single

/ MOLECULE TYPE: peptide

/ ANTI-SENSE: N

/ NAME/KEY: Peptide

/ LOCATION: 1..861

/ OTHER INFORMATION:

/ US-09-519-489-18

Query Match 65.3%; Score 47; DB 3; Length 861;

Best Local Similarity 63.6%; Prd. No. 32;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DECRYPTED 11
 Db 468 DGHGTYGLAYE 478

RESULT 3

US-09-519-489-18

/ Sequence 18, Application US/09519489

/ Patent No. 6500663

/ APPLICANT: Chans, Yvan

/ TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma

/ TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma

/ NUMBER OF SEQUENCES: 22

/ CORRESPONDENCE ADDRESS:

/ ADDRESS: Cooper & Dunham

/ STREET: 1185 Avenue of the Americas

/ CITY: New York

/ STATE: New York

/ COUNTRY: U.S.A.

/ ZIP: 10036

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patent Release #1.24

/ TELEPHONE: 212-278-0400

/ FAX: 212-278-0400

/ TELEFAX: 212-391-0526

/ INVESTIGATOR: PCR SEQ ID NO: 18

/ SECURITY CLASSIFICATION: 18

/ LENGTH: 861 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: single

/ MOLECULE TYPE: peptide

/ ANTI-SENSE: N

/ NAME/KEY: Peptide

/ LOCATION: 1..861

/ OTHER INFORMATION:

/ US-09-519-489-18

Query Match 65.3%; Score 47; DB 3; Length 861;

Best Local Similarity 63.6%; Prd. No. 32;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DECRYPTED 11
 Db 468 DGHGTYGLAYE 478

RESULT 4

US-08-420-335B-3

/ Sequence 3, Application US/08420335B

/ Patent No. 6500663

/ APPLICANT: Chans, Yvan

/ TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma

/ TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma

/ NUMBER OF SEQUENCES: 22

/ CORRESPONDENCE ADDRESS:

/ ADDRESS: Cooper & Dunham

/ STREET: 1185 Avenue of the Americas

/ CITY: New York

/ STATE: New York

/ COUNTRY: U.S.A.

/ ZIP: 10036

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE RELEASE: 41.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/420,235B
/ FILING DATE:
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ TELEPHONE: (212) 278-0400
/ TELEFAX: (212) 391-0525
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1376 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-420,235B-3

Query Match 65.3%; Score 47; DB 1; Length 1376;
Best Local Similarity 63.6%; Pred. No. 50;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DQSHGYSSGFP 11
DB 476 DQSHGYSLATYE 486

RESULT 5
US-09-624-3
/ Sequence 3; Application US/08793624C
/ Patent No. 6150093
/ GENERAL INFORMATION:
/ APPLICANT: Chang, Yuan
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ TELEPHONE: (212) 278-0400
/ TELEFAX: (212) 391-0525
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1376 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-793,624-3

Query Match 65.3%; Score 47; DB 3; Length 1376;
Best Local Similarity 63.6%; Pred. No. 50;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DQSHGYSSGFP 11
DB 476 DQSHGYSLATYE 486

RESULT 6
PCT-US95-10194-3
/ Sequence 3; Application PC/US9510194
/ Patent No. 5,449,923
/ APPLICANT: The Trustees of Columbia University in the City of New York
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ TELEPHONE: (212) 278-0400
/ TELEFAX: (212) 391-0525
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1376 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-152,060-116

Query Match 65.3%; Score 47; DB 5; Length 1376;
Best Local Similarity 63.6%; Pred. No. 50;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DQSHGYSSGFP 11
DB 476 DQSHGYSLATYE 486

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/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10016
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE RELEASE: 41.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/10194
/ FILING DATE:
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ TELEPHONE: (212) 278-0400
/ TELEFAX: (212) 391-0525
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1376 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ PCT-US95-10194-3

Query Match 65.3%; Score 47; DB 5; Length 1376;
Best Local Similarity 63.6%; Pred. No. 50;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DQSHGYSSGFP 11
DB 476 DQSHGYSLATYE 486

RESULT 7
US-09-152-060-116
/ Sequence 3; Application US/09152060
/ Patent No. 6,144,923
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: 28 Human Secreted Proteins
/ CURRENT APPLICATION NUMBER: US/09/152,060
/ FILING DATE: 1998-09-11
/ EARLIER APPLICATION NUMBER: PCT/US98/04858
/ EARLIER APPLICATION NUMBER: 03-07040,762
/ EARLIER FILING DATE: 1997-03-14
/ EARLIER APPLICATION NUMBER: 60/040,710
/ EARLIER FILING DATE: 1997-03-14
/ EARLIER FILING DATE: 1997-05-30,934
/ EARLIER FILING DATE: 1997-05-30
/ EARLIER APPLICATION NUMBER: 60/048,100
/ EARLIER FILING DATE: 1997-05-30
/ EARLIER FILING DATE: 1997-05-30,048,357
/ EARLIER FILING DATE: 1997-05-30
/ EARLIER APPLICATION NUMBER: 60/048,189
/ EARLIER FILING DATE: 1997-05-30,048,765
/ EARLIER FILING DATE: 1997-05-30
/ EARLIER APPLICATION NUMBER: 60/048,970
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/068,168
/ EARLIER FILING DATE: 1997-12-19
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO: 116
/ LENGTH: 215
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-152-060-116

```



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/ APPLICANT: Studnicka, Gary M.
/ TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
/ NUMBER OF CLAIMS: 1
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Sterna, Keasler, Goldstein and Fox P.L.L.C.
/ STREET: 1100 New York Ave., N.W., Suite 600
/ STATE: D. C.
/ COUNTRY: United States of America
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ APPLICATION NUMBER: US/08/107,669D
/ FILING DATE: 13-AUG-1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/10906
/ FILING DATE: 14-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/808,464
/ NAME: Michele A. Ciaballa
/ REGISTERATION NUMBER: 33,851
/ ATTORNEY/AGENT INFORMATION:
/ ADDRESSER: Sterna, Keasler, Goldstein and Fox P.L.L.C.
/ TELEPHONE: 202/371-2600
/ TELEFAX: 202/371-2540
/ INVENTOR FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 126 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-107-669D-8
/
/ Query Match 55.6%; Score 40; DB 1; Length 126;
/ US Local Similarity 2.0%; Pct 49;
/ Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
/
/ Db 1 DGEHNGSS 9
/ 99 DGEHNGSS 107
/
/ RESULT 13
/ US-08-172-788A-9
/ Sequence 8, Application US/08472788A
/ Patent No. 5770196
/ GENERAL INFORMATION:
/ ADDRESSER: Sterna, Keasler, Goldstein and Fox P.L.L.C.
/ TITLE OF INVENTION: Modified Antibody Variable Domains
/ NUMBER OF SEQUENCES: 89
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Sterna, Keasler, Goldstein and Fox P.L.L.C.
/ STREET: 1100 New York Ave., N.W., Suite 600
/ STATE: D. C.
/ COUNTRY: United States of America
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ APPLICATION NUMBER: US/08/472,788A
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 424

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/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/082,842
/ FILING DATE: 23-JUN-1993
/ PRIOR APPLICATION DATA: PCT/US92/10906
/ FILING DATE: 14-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/808,464
/ NAME: Michele A. Ciaballa
/ REGISTERATION NUMBER: 33,851
/ ATTORNEY/AGENT INFORMATION:
/ ADDRESSER: Sterna, Keasler, Goldstein and Fox P.L.L.C.
/ TELEPHONE: 202/371-2600
/ TELEFAX: 202/371-2540
/ INVENTOR FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 126 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-472-788A-8
/
/ Query Match 55.6%; Score 40; DB 1; Length 126;
/ US Local Similarity 2.0%; Pct 49;
/ Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
/
/ Db 1 DGEHNGSS 9
/ 99 DGEHNGSS 107
/
/ RESULT 13
/ US-08-472-531B-8
/ Sequence 8, Application US/08477531B
/ Patent No. 5821123
/ GENERAL INFORMATION:
/ ADDRESSER: Sterna, Keasler, Goldstein and Fox P.L.L.C.
/ TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)
/ NUMBER OF SEQUENCES: 67
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Sterna, Keasler, Goldstein and Fox P.L.L.C.
/ STREET: 1100 New York Ave., N.W., Suite 600
/ STATE: D. C.
/ COUNTRY: United States of America
/ ZIP: 20005-3934
/ COMPUTER READABLE FORM:
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ APPLICATION NUMBER: US/08/477,531B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/107,669
/ FILING DATE: 13-AUG-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/10906
/ FILING DATE: 14-DEC-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/808,464
/ NAME: Michele A. Ciaballa
/ REGISTERATION NUMBER: 33,851
/ ATTORNEY/AGENT INFORMATION:
/ ADDRESSER: Sterna, Keasler, Goldstein and Fox P.L.L.C.
/ TELEPHONE: 202/371-2600

```

TELEFAX: 202/371-2540
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 126 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-477-5318-8

Query Match 55.6%; Score 40; DB 2; Length 126;
 Best Local Similarity 77.8%; Pred. No. 49;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGRGVSS 9
 |||||
 DB 99 DGGRGVSS 107

RESULT 14
 US-08-303-5698-10
 Sequence 10; Application US/08/03/5698

GENERAL INFORMATION:
 REGISTRATION NUMBER: 33,851
 APPLICANT: Abnair, John R.
 INVENTOR: Abnair, John R.
 TITLE OF INVENTION: Humanized Antibodies
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESS: Woodcock, Washburn Kurtz MacLewitz & No. 5859205-16
 CITY: Philadelphia
 STATE: PA

COUNTRY: USA
 FILING DATE: 07-SEP-1994
 PCT APPLICATION NO:
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 SOFTWARE: GENES, GENES, GENES, GENES
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/303,5698
 FILING DATE: 07-SEP-1994
 PCT APPLICATION NO:
 ATTORNEY/AGENT INFORMATION:
 NAME: Trujillo, Doreen Yalko
 REGISTRATION NUMBER: 33,851
 TELEPHONE: (215) 568-3100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 INVENTOR: Abnair, John R.
 SEQUENCE CHARACTERISTICS:
 LENGTH: 126 amino acids
 TYPE: amino acid
 MOLECULE TYPE: peptide
 US-08-303-5698-10

Query Match 55.6%; Score 40; DB 2; Length 126;
 Best Local Similarity 77.8%; Pred. No. 49;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGRGVSS 9
 |||||
 DB 99 DGGRGVSS 107

RESULT 15
 US-08-082-842A-8
 Sequence 8; Application US/08082842A
 Patent No. 5869619
 GENERAL INFORMATION:

APPLICANT: SmithKline, Gary M.
 TITLE OF INVENTION: Modified Antibody Variable Domains
 NUMBER OF SEQUENCES: 89
 CORRESPONDENCE ADDRESS:
 ADDRESS: SmithKline Beecham, Goldstein and Box P.L.L.C.
 STREET: 1100 Market Ave., N.W., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 FILING DATE: 07-DEC-1992
 PCT APPLICATION NO:
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 SOFTWARE: GENES, GENES, GENES, GENES
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/082,842A
 FILING DATE: 07-DEC-1992
 PCT APPLICATION NO:
 ATTORNEY/AGENT INFORMATION:
 NAME: Trujillo, Doreen Yalko
 REGISTRATION NUMBER: 33,851
 TELEPHONE: (215) 568-3100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: 202/371-2540

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 126 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-082-842A-8
 Query Match 55.6%; Score 40; DB 2; Length 126;
 Best Local Similarity 77.8%; Pred. No. 49;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DGGRGVSS 9
 |||||
 DB 99 DGGRGVSS 107

Search completed: November 7, 2003, 07:30:06
 Job time : 2.7623 secs

A: Molecule type: mAb

A: Residues: 1-146 <ID>

A: Cross-references: EMBL: M16072; NID: g195270; PDB: 1AA3829; 1; PDB: g195271

Query Match

Best Local Similarity 84.1%; Score 543.5; DB 4; Length 146;

Best Local Similarity 84.3%; Pred. No. 2, 3e-40;

Matches 102; Conservative 8; Mismatches 8; Indels 3; Gaps 2;

DB 1 EVLVSGPELKKGGYVISCASGYITFGNGWVWQAPKQKLMKMGNTNTTGGPT 60

DB 20 QIQVSGPELKKGGYVISCASGYITFGNGWVWQAPKQKLMKMGNTNTTGGPT 79

DB 61 ADFFKGRFASLSTASNYIQLNKLNEEDATYFCALAMWTTFCARPSYONS-FEYDVGQITLVTS 118

DB 80 ADFFKGRFASLSTASNYIQLNKLNEEDATYFCALAMWTTFCARPSYONS-FEYDVGQITLVTS 138

DB 119 A 119

DB 139 S 139

RESULT 3

19 heavy chain V and J region, monoclonal antibody 5CCT 48.1 - mouse (fragment)

A: Residues: 1-119 <ID>

A: Cross-references: EMBL: M16072; NID: g195270; PDB: 1AA3829; 1; PDB: g195271

A: Sequence: 18-Nov-1994 Hteck_change 20-Jun-2000

A: Accession: A53285

A: Molecule type: mAb

A: Residues: 1-119 <ID>

A: Cross-references: GB: D12166; NID: g220595; PDB: 1BA0228; 1; PDB: g220596

A: Note: sequence extracted from NCB1 backbone (NCBI: 63271, NCBI: 63293)

A: Keywords: heterocytamer; immunoglobulin

A: Reference number: A53285; MID: 9201897; MID: 1922102

A: Accession: A53285

A: Status: preliminary

A: Molecule type: mAb

A: Residues: 1-119 <ID>

A: Cross-references: GB: D12166; NID: g220595; PDB: 1BA0228; 1; PDB: g220596

A: Note: sequence extracted from NCB1 backbone (NCBI: 63271, NCBI: 63293)

A: Keywords: heterocytamer; immunoglobulin

A: Reference number: A53285; MID: 9201897; MID: 1922102

A: Accession: A53285

A: Status: preliminary

A: Molecule type: mAb

A: Residues: 1-119 <ID>

A: Cross-references: GB: D12166; NID: g220595; PDB: 1BA0228; 1; PDB: g220596

A: Note: sequence extracted from NCB1 backbone (NCBI: 63271, NCBI: 63293)

A: Keywords: heterocytamer; immunoglobulin

A: Reference number: A53285; MID: 9201897; MID: 1922102

A: Accession: A53285

A: Status: preliminary

A: Molecule type: mAb

A: Residues: 1-119 <ID>

A: Cross-references: GB: D12166; NID: g220595; PDB: 1BA0228; 1; PDB: g220596

A: Note: sequence extracted from NCB1 backbone (NCBI: 63271, NCBI: 63293)

A: Keywords: heterocytamer; immunoglobulin

A: Reference number: A53285; MID: 9201897; MID: 1922102

A: Accession: A53285

A: Status: preliminary

A: Molecule type: mAb

A: Residues: 1-119 <ID>

A: Cross-references: EMBL: M16072; NID: g195270; PDB: 1AA3829; 1; PDB: g195271

A: Sequence: 18-Nov-1994 Hteck_change 20-Jun-2000

A: Accession: A53285

A: Molecule type: mAb

Query Match

Best Local Similarity 84.7%; Pred. No. 1, 5e-39;

Matches 100; Conservative 4; Mismatches 12; Indels 2; Gaps 1;

DB 4 INVEGSGPELKKGGYVISCASGYITFGNGWVWQAPKQKLMKMGNTNTTGGPT 63

DB 1 LVGSGPELKKGGYVISCASGYITFGNGWVWQAPKQKLMKMGNTNTTGGPT 60

DB 61 ADFFKGRFASLSTASNYIQLNKLNEEDATYFCALAMWTTFCARPSYONS-FEYDVGQITLVTS 119

DB 61 ADFFKGRFASLSTASNYIQLNKLNEEDATYFCALAMWTTFCARPSYONS-FEYDVGQITLVTS 118

DB 81 A 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

DB 81 S 81

Db 61 ADPFKRFASLETSASVYLQINLNKNDPATFCAQNGMS-AMPEWQGITLVSS 118

RESULT 7

S26325

1g heavy chain V region - mouse

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000

C/Species: Mus musculus (house mouse)

C/Accession: S26325

R/Stack: S.F. Caton, A.J.

J. Exp. Med. 174: 613-624, 1991

A/Description: Amino acid specific for a single amino acid interchange in a protein

A/Accession: S26325

A/Status: preliminary

A/Residues: 1-109 <EFL>

A/Cross-references: EMBL:X72910; MID:952080; PDB:Q1334043

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heteroreceptor; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IM>

Query Match 81.0%; Score 523.5; DB 2; Length 109;

Best Local Similarity 88.5%; Pred. No. 9-2e-39;

Matches 100; Conservative 0; Mismatches 4; Indels 9; Gaps 2;

QY 11 LKREGEVYVSCASGYFTFYGNWYVQAQKGLANMGNINVTGEPYADDEKRRAN 70

Db 1 LKREGEVYVSCASGYFTFYGNWYVQAQKGLANMGNINVTGEPYADDEKRRAN 60

71 SLETSASVYLQINLNKNDPATFCAQNGMS-AMPEWQGITLVSS 118

Db 61 SLETSASVYLQINLNKNDPATFCAQNGMS-AMPEWQGITLVSS 109

RESULT 8

S26325

1g heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C/Accession: S26325

submitted to the EMBL Data Library, May 1993

A/Reference number: S26325

A/Accession: S26325

A/Status: preliminary

A/Residues: 1-136 <EFL>

A/Cross-references: EMBL:X72910; MID:9312496; PDB:1CMA5116.1; PDB:9312497

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

F:15-117/Domain: immunoglobulin homology <IM>

Query Match 80.4%; Score 532; DB 2; Length 136;

Best Local Similarity 80.3%; Pred. No. 1.6e-38;

Matches 98; Conservative 8; Mismatches 8; Indels 8; Gaps 2;

QY 1 EVLVESGSELEKKGQVTKSCASGYFTFYGNWYVQAQKGLANMGNINVTGEPY 60

Db 20 QIDLVSGSELEKKGQVTKSCASGYFTFYGNWYVQAQKGLANMGNINVTGEPY 79

64 ADPFKRFASLETSASVYLQINLNKNDPATFCAQNGMS-AMPEWQGITLV 117

Db 80 VDFKRFASLETSASVYLQINLNKNDPATFCAQNGMS-AMPEWQGITLV 134

QY 116 SA 119

Db 135 SS 136

RESULT 9

S26325

1g heavy chain V region T33 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 18-Jan-1991 #sequence_revision 13-Jan-1993 #text_change 21-Jan-2000

C/Accession: B5659

R/Stack: B. J. Scher, T. J. Levitt, M. J. Angillet, J.

Art. Rev. 2, 10572-10581, 1990

A/Description: Amino acid specific for a single amino acid interchange in a protein

A/Reference number: A56259; MID:91104915; PMID:2271636

A/Accession: B5659

A/Status: preliminary

A/Residues: 1-113 <EFL>

A/Cross-references: GB:M0481; GB:M0489; GB:M0480; GB:M0481; GB:M0482; GB:M0483

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

F:15-98/Domain: immunoglobulin homology <IM>

Query Match 79.4%; Score 514; DB 2; Length 113;

Best Local Similarity 79.4%; Pred. No. 6.4e-38;

Matches 93; Conservative 11; Mismatches 9; Indels 6; Gaps 1;

QY 1 EVLVESGSELEKKGQVTKSCASGYFTFYGNWYVQAQKGLANMGNINVTGEPY 60

Db 1 QIDLVSGSELEKKGQVTKSCASGYFTFYGNWYVQAQKGLANMGNINVTGEPY 60

64 ADPFKRFASLETSASVYLQINLNKNDPATFCAQNGMS-AMPEWQGITLVSS 119

Db 64 VDFKRFASLETSASVYLQINLNKNDPATFCAQNGMS-AMPEWQGITLVSS 113

RESULT 10

S26325

1g heavy chain V region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

C/Accession: S32187

submitted to the EMBL Data Library, February 1993

A/Reference number: S32185

A/Accession: S32187

A/Status: preliminary

A/Residues: 1-117 <EFL>

A/Cross-references: EMBL:470091; MID:9288251; PDB:1CMA4566.1; PDB:9288252

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

F:15-98/Domain: immunoglobulin homology <IM>

Query Match 79.1%; Score 511; DB 2; Length 117;

Best Local Similarity 79.8%; Pred. No. 1.2e-37;

Matches 95; Conservative 10; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVLVESGSELEKKGQVTKSCASGYFTFYGNWYVQAQKGLANMGNINVTGEPY 60

Db 1 QIDLVSGSELEKKGQVTKSCASGYFTFYGNWYVQAQKGLANMGNINVTGEPY 60

64 ADPFKRFASLETSASVYLQINLNKNDPATFCAQNGMS-AMPEWQGITLVSS 119

Db 64 VDFKRFASLETSASVYLQINLNKNDPATFCAQNGMS-AMPEWQGITLVSS 117

RESULT 11

S26325

1g heavy chain V region (M-7408) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000

C/Accession: S19963

submitted to the EMBL Data Library, March 1992

A/Description: Structural characterization of CD4 mb.

A/Reference number: S19963

A/Status: preliminary

A/Molecule type: RNA

A/Residues: 1-115 <EFL>


```

Qy      1 EVLWESGRLKXKGTWVKSQASGTLFTYGGNWTQAPKGLNWKH-INTTGEPT 59
Db      1 CIGLVSGTBLKKTGTVLSCHASGTLFTYGGNWTQAPKGLNWKH-INTTGEPT 60
Qy      60 YADDFKRRASLTSTASTAYLQIWNKNEEDVATYFOLYGNSPKPA--YMGQTLVT 116
Db      61 YVDFKRRASLTSTASTAYLQIWNKNEEDVATYFOLYGNSPKPA--YMGQTLVT 116
Qy      117 VSA 119
Db      117 VSA 119

```

Search completed: November 7, 2003, 07:36:18
 Job time : 15:5112 secs

GenCore version 5.1.6
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MW protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 8.57944 Seconds
(without alignments)
632,276 Million cell updates/sec

US-09-661-992b-82_COPY_1_119

Perfect score: 646

Sequence: 1 EVLVSEPPKPEVTSKASGVTKI.....GNSPKGFAYGGQGLTVTUSA 119

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 127863 sequ, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Maximum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: SwissProt_41.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	348	53.9	1	HV02 MOUSE
2	344	53.3	1	HV03 MOUSE
3	343	53.2	1	HV04 MOUSE
4	330.5	51.2	1	HV01 MOUSE
5	330.5	51.1	1	HV05 MOUSE
6	325.5	50.4	1	HV02 MOUSE
7	325.5	50.4	1	HV03 MOUSE
8	325.5	50.4	1	HV04 MOUSE
9	324	50.2	1	HV05 MOUSE
10	324	50.2	1	HV01 MOUSE
11	321	49.7	1	HV02 MOUSE
12	321	49.7	1	HV03 MOUSE
13	321	49.7	1	HV04 MOUSE
14	320.5	49.6	1	HV05 MOUSE
15	319.2	49.4	1	HV01 MOUSE
16	319.2	49.4	1	HV02 MOUSE
17	318	49.2	1	HV03 MOUSE
18	316.5	49.0	1	HV04 MOUSE
19	316.5	49.0	1	HV05 MOUSE
20	316	48.9	1	HV01 MOUSE
21	316	48.9	1	HV02 MOUSE
22	315.5	48.8	1	HV03 MOUSE
23	314	48.6	1	HV04 MOUSE
24	314	48.6	1	HV05 MOUSE
25	313	48.1	1	HV01 MOUSE
26	313	48.1	1	HV02 MOUSE
27	310	48.0	1	HV03 MOUSE
28	309.5	47.9	1	HV04 MOUSE
29	309.5	47.9	1	HV05 MOUSE
30	309	47.8	1	HV01 MOUSE
31	309	47.8	1	HV02 MOUSE
32	307	47.2	1	HV03 MOUSE
33	305	47.2	1	HV04 MOUSE

P0421 homo sapien
P01741 mus muscu
P01763 mus sapie
P01772 homo sapie
P01773 mus muscu
P01803 mus muscu
P01742 homo sapie
P01811 mus muscu
P01774 mus muscu
P01758 mus muscu
P01763 homo sapie
P01808 mus muscu

ALIGNMENTS

RESULT 1
HV02 MOUSE
ID HV02 MOUSE STANDARD; PRET: 140 AA.
AC P01746; 198 (Rel. 01, Created)
AC P01746; 198 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DR Ig heavy chain V region 9307 precursor.
DR Ig heavy chain V region 9307 precursor.
OC Mus musculus (mouse)
OC Rukamalia; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Rukamalia; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
PC SEQUENCE FROM N.A.
PC STRAIN:AJ;
RA MEDLINE=9252818; PubMed=6801765;
RA Sine J.; Rabbits T.H.; Ereses P.; Slaughter C.; Tucker P.M.;
RA Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.
RT Science 216:309-311(1982).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; J06493; AAA36128.1; -;
DR PIR; A94264; HWS07.
DR RSCD; A94264; HWS07.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003066; IG-MEC.
DR InterPro; IPR003586; IG-V.
DR SMART; SM00476; IG-V.
DR PROSITE; PSS0835; IG-LIKE; 1.
DR Immunoglobulin V region; Hybridsoma; Signal.
FT SIGNAL 1 19
FT DOMAIN 20 139 IG HEAVY CHAIN V REGION 9307.
FT NON TER 140 140
FT SEQUENCE 140 AA; 15514 MW; 25A4CB8E1D8C8 CRC64;
Query Match 53.9%; Score 348; DB 1; Length 140;
Best Local Similarity 54.1%; Pred. No. 1.3e-28;
Matches 66; Conservative 24; Mismatches 4; Gaps 2;
Oy 1 EVLVSEPPKPEVTSKASGVTKI.....GNSPKGFAYGGQGLTVTUSPT 60
DB 20 EVLVSEPPKPEVTSKASGVTKI.....GNSPKGFAYGGQGLTVTUSPT 79
Oy 61 AUDFGKPRPSLTSTAVLQINLQNEITATVFCN---LYNSHKSPAYGGQGLTVT 117


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FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 D SEGMENT.
FT DOMAIN 118 128 BY SIMILARITY.
FT NON TER 129 139
FT SC SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 51 24; Score 330.5; DB 1; Length 118;
Best Local Similarity 51.5%; Pref. No. 7.3e-27;
Matches 64; Conservative 32; Mismatches 3; Gaps 2;

Qy 1 EVLVSGDEPLKKEGTGVTYVGNWVQAPGKLGWGNINVTGEPY 60
1 EVLVSGDEPLKKEGTGVTYVGNWVQAPGKLGWGNINVTGEPY 60
Db 1 EVLVSGDEPLKKEGTGVTYVGNWVQAPGKLGWGNINVTGEPY 60
61 ADYKGFAPFSEFSAATATQINLNEDATYFCW-LYGSFPGFAPWGGTLVNSA 119
1 EVLVSGDEPLKKEGTGVTYVGNWVQAPGKLGWGNINVTGEPY 60
61 NQFKKATVTVQSSNTATWELGSLSDGATVYVGNWVQAPGKLGWGNINVTGEPY 118
1 EVLVSGDEPLKKEGTGVTYVGNWVQAPGKLGWGNINVTGEPY 60

RESULT 6
HV32 MOUSE STANDARD; PRT; 115 AA.
ID HV32_MOUSE
AC P01602;
DT 21-JUL-1986 (Rel. 01. Created)
DT 15-SEP-2003 (Rel. 42. Last annotation update)
DB Ig heavy chain V-III region J606.
OS Mus musculus (Mouse).
OC Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CC NCBI_TaxID:10090;
LN SEQUENCE FROM M.A.
RA MEDLINE=81234548; PubMed=6788176;
RA Rothwell A.L.M., Paskind M., Beth M., Imanishi-Kari T., Rajewsky K.,
RT "The complete V domain amino acid sequences of two myeloma immunoglobulin proteins";
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RT Cell 24:628-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MY CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
CC (NPB ANTIBODIES);
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CC ENBL; J00529; AA38170.1;
DR FR; A90809; MMS18.
DR PUB; 1466; 15-JUL-98.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR PIR; P003596; Ig_v.
DR PIR; P003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR IMMUNOGLOBULIN V region; Signal; 3D-structure.
DR CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT CHAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 58 FRAMEWORK-2.
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 118 124 FRAMEWORK-3.
FT DOMAIN 125 139 D SEGMENT.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 115 115
SQ SEQUENCE 115 AA; 12810 MW; B67AD638A121A5F CRC64;

Query Match 51.5%; Score 330.5; DB 1; Length 115;
Best Local Similarity 51.5%; Pref. No. 7.3e-27;
Matches 67; Conservative 16; Mismatches 28; Indels 12; Gaps 3;

2y 1 EVLVSGDEPLKKEGTGVTYVGNWVQAPGKLGWGNINVTGEPY 56
1 EVLVSGDEPLKKEGTGVTYVGNWVQAPGKLGWGNINVTGEPY 56
Db 1 EVLVSGDEPLKKEGTGVTYVGNWVQAPGKLGWGNINVTGEPY 56
2y 57 ETTADYKGFAPFSEFSAATATQINLNEDATYFCW-LYGSFPGFAPWGGTLVNSA 116
1 EVLVSGDEPLKKEGTGVTYVGNWVQAPGKLGWGNINVTGEPY 56
61 H-H-VASVQKRTITSDKSSVLYQNNLRADDTGYCT-----TGFAPWGGTLV 112
117 VSA 119
113 VSA 115

```

```

RESULT 6
HV07 MOUSE STANDARD; PRT; 139 AA.
ID HV07_MOUSE
AC P01751; P01752; 01. Created)
DT 21-JUL-1986 (Rel. 01. Last sequence update)
DT 15-SEP-2003 (Rel. 42. Last annotation update)
DB Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
CC NCBI_TaxID:10090;
LN SEQUENCE FROM M.A.
RA MEDLINE=81234548; PubMed=6788176;
RA Rothwell A.L.M., Paskind M., Beth M., Imanishi-Kari T., Rajewsky K.,
RT "The complete V domain amino acid sequences of two myeloma immunoglobulin proteins";
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RT Cell 24:628-637(1981).
CC -1- MISCELLANEOUS: THE B1-8 MY CHAIN mRNA WAS CLONED FROM A HYBRIDOMA
CC (NPB ANTIBODIES);
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CC ENBL; J00529; AA38170.1;
DR FR; A90809; MMS18.
DR PUB; 1466; 15-JUL-98.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR PIR; P003596; Ig_v.
DR PIR; P003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR IMMUNOGLOBULIN V region; Signal; 3D-structure.
DR CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
FT CHAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 58 FRAMEWORK-2.
FT DOMAIN 86 117 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 118 124 FRAMEWORK-3.
FT DOMAIN 125 139 D SEGMENT.
FT DISULFID 22 98 BY SIMILARITY.
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC0CF465 CRC64;

Query Match 50.4%; Score 325.5; DB 1; Length 139;
Best Local Similarity 50.4%; Pref. No. 7.3e-26;
Matches 61; Conservative 28; Mismatches 5; Gaps 2;

Qy 1 EVLVSGDEPLKKEGTGVTYVGNWVQAPGKLGWGNINVTGEPY 60
1 EVLVSGDEPLKKEGTGVTYVGNWVQAPGKLGWGNINVTGEPY 60
Db 20 QVQLQPGELAVFASVLSKCSQITFTSWHWVQKQKGLKRIQDPNSSEK 79
61 ADYKGFAPFSEFSAATATQINLNEDATYFCW-LYGSFPGFAPWGGTLV 117
1 EVLVSGDEPLKKEGTGVTYVGNWVQAPGKLGWGNINVTGEPY 60
80 NQFKKATVTVQSSNTATWELGSLSDGATVYVGNWVQAPGKLGWGNINVTGEPY 137
118 SA 119
138 SA 139

```



```

RESULT 7
H12 MOUSE STANDARD; PRT; 117 AA.
ID P01537
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-SEP-2003 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
OS Mus musculus (Mouse) NCBI taxon 10090.
OC Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
SF SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RA MEDLINE=83073344; PubMed=6816276;
RA Kohn Y.R., Putman J.S., Schilling J.W., Rogers J., Shiley C.H.,
RT "Complete amino acid sequence of a mouse m chain: homology among
RT heavy chain constant region domains."
CC 1- PROTEIN HAS ALSO BEEN DESCRIBED AS
CC Biochemistry 21:5415-5424(1982) OR THE LIGHT CHAIN OF THIS IGH MYELOMA
CC 1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC 1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSBP_000047; 197.1.
DR InterPro: IPR003396; 19.v.
DR InterPro: IPR003396; 19.v.
DR SMART: SM00406; 10v; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
FM Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12993 MW; 3CFBACB4B8447B41 CRC64;

Query Match 50.3%; Score 325; DB 1; Length 117;
Seed Local Similarity 52.0%; Pred. No. 2,4e-26;
Matches 64; Conservative 21; Mismatches 28; Indels 10; Gaps 2;

OY 1 EVLVESGPELKEKPEVYVLCASGVPTFNQNMVYQVQKQKAMGNINLTTEPT 60
DB 1 EVQVQSGPELVKQVAVKQVSCASGVPTFDYNNKQVQKQKAMGNINLTTEPT 60
OY 61 ADDKGRFAVSLSTAVYQVNNLNIAEETVTPQA---LYQSKKQPVWQGLTAY 116
DB 61 NQKFKKATLVQSSVHNMVQNLISDSVYLCIDRQVY-----EDWASGIVTV 114
OY 117 VSA 119
DB 115 VSS 117

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*amino acid sequence of human-gene antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments."
BL Nature 283:35-40(1980).
CC 1- MISCELLANEOUS: THE SEQUENCES OF 10 MYELOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH ARE IN THE C-TERMINAL REGION.
CC 1- SIMILARITY: THIS PROTEIN BINDS DEXTRAN.
CC PIR_A8624; MMS835.
DR HSBP_000047; 197.1.
DR InterPro: IPR003396; 19.v.
DR InterPro: IPR003396; 19.v.
DR SMART: SM00406; 10v; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
FM Immunoglobulin V region.
FT DISULFID 22 116
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 23282AF4B8447B41 CRC64;

Query Match 50.3%; Score 325; DB 1; Length 117;
Seed Local Similarity 52.0%; Pred. No. 2,4e-26;
Matches 64; Conservative 21; Mismatches 28; Indels 10; Gaps 2;

OY 1 EVLVESGPELKEKPEVYVLCASGVPTFNQNMVYQVQKQKAMGNINLTTEPT 60
DB 1 EVQVQSGPELVKQVAVKQVSCASGVPTFDYNNKQVQKQKAMGNINLTTEPT 60
OY 61 ADDKGRFAVSLSTAVYQVNNLNIAEETVTPQA---LYQSKKQPVWQGLTAY 116
DB 61 NQKFKKATLVQSSVHNMVQNLISDSVYLCIDRQVY-----EDWASGIVTV 114
OY 117 VSA 119
DB 115 VSS 117

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RESULT 8
H13 MOUSE STANDARD; PRT; 117 AA.
ID P01537
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-SEP-2003 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
OS Mus musculus (Mouse) NCBI taxon 10090.
OC Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
SF SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RA MEDLINE=83073344; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood T.,
RT "Complete amino acid sequence of a mouse m chain: homology among
RT heavy chain constant region domains."
CC 1- PROTEIN HAS ALSO BEEN DESCRIBED AS
CC Biochemistry 21:5415-5424(1982) OR THE LIGHT CHAIN OF THIS IGH MYELOMA
CC 1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC 1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSBP_000047; 197.1.
DR InterPro: IPR003396; 19.v.
DR InterPro: IPR003396; 19.v.
DR SMART: SM00406; 10v; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
FM Immunoglobulin V region.
FT DISULFID 22 96
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (COMPLEX).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12993 MW; 3CFBACB4B8447B41 CRC64;

Query Match 50.3%; Score 325; DB 1; Length 117;
Seed Local Similarity 52.0%; Pred. No. 2,4e-26;
Matches 64; Conservative 21; Mismatches 28; Indels 10; Gaps 2;

OY 1 EVLVESGPELKEKPEVYVLCASGVPTFNQNMVYQVQKQKAMGNINLTTEPT 60
DB 1 EVQVQSGPELVKQVAVKQVSCASGVPTFDYNNKQVQKQKAMGNINLTTEPT 60
OY 61 ADDKGRFAVSLSTAVYQVNNLNIAEETVTPQA---LYQSKKQPVWQGLTAY 116
DB 61 NQKFKKATLVQSSVHNMVQNLISDSVYLCIDRQVY-----EDWASGIVTV 114
OY 117 VSA 119
DB 115 VSS 117

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RESULT 9
H13 MOUSE STANDARD; PRT; 113 AA.
ID P01799;
DT 21-JUL-1986 (Rel. 01, Created)
DT 15-SEP-2003 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
OS Mus musculus (Mouse) NCBI taxon 10090.
OC Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
SF SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
RA Vrana W., Rudikoff S., Porter W.,
RT "Heavy-chain variable-region sequence from an insulin-binding myeloma
RT protein."
CC 1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INSULIN.
CC 1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSBP_000047; 197.1.
DR InterPro: IPR003396; 19.v.
DR InterPro: IPR003396; 19.v.
DR SMART: SM00406; 10v; 1.
DR PROSITE: PS00835; IG_LIKE; 1.
FM Immunoglobulin V region.
FT DISULFID 22 113
FT NON_TER 113 113

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SQ SEQUENCE 113 AA; 12675 MW; 76658C16C7798458 CRC64;
 Query Match 50.2% Score 324; DB 1; Length 113;
 Beat Local Similarity 53.0% Pct. No. 3.4e-26;
 Matches 64; Conservative 19; Mismatches 28; Indels 8; Gaps 2;
 QY 1 EVKLVSSEGLKRPETVYISCKASGYIFNNGWVKAQKGLKMGKMT--NTTGEPT 58
 DB 1 EVKLVSSEGLKRPETVYISCKASGYIFNNGWVKAQKGLKMGKMT--NTTGEPT 58
 DB 1 EVKLVSSEGLKRPETVYISCKASGYIFNNGWVKAQKGLKMGKMT--NTTGEPT 58
 DB 59 TADDFKRPASLETSASZAYLQINLAKEDYATFALYANSPEFVWQGGTLVTV 117
 QY 61 HVAESVWRTITLSDKSSVYLQNNLQNDLADLYTCS-----RQFVWQGGTLVTV 113
 RESULT 12
 ID HV33 MOUSE STANDARD; PRT; 115 AA.
 AC P01802;
 DT 21-JUL-1986 (rel. 01, Created)
 DR InterPro: IP8003106; 19-MHC.
 DT 15-SEP-2003 (rel. 42, Last annotation update)
 DR 19 heavy chain V-II region W3082.
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Castoridae; Vertebrata; Eucleostomi;
 OC Nemata; Insecta; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI TaxId:10090;
 RN MOUSE
 RX Mus musculus:209361; PubMed:679811;
 RZ Johnson J., Stankard V., Paul L.;
 RT "The complete V domain amino acid sequences of two myeloma immunoglobulin proteins."
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN HEAT
 CC -1- BINDS INULIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DC HSBP: P03810; 1982.
 DR InterPro: IP8003110; 19-like.
 DR InterPro: IP8003106; 19-MHC.
 DR 19 heavy chain V region W3082.
 DR 19 heavy chain V region W3082.
 DR SMART: SM00406; 19-V.
 DR PROSITE: PS50835; 19-Like; 1.
 PM Immunoglobulin V region.
 FT DISULFID 23 18
 FT NON_TER 115 115
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12887 MW; 984517648C121C5A CRC64;
 Query Match 50.0% Score 323; DB 1; Length 115;
 Beat Local Similarity 52.9% Pct. No. 3.4e-26;
 Matches 64; Conservative 19; Mismatches 30; Indels 8; Gaps 2;
 QY 1 EVKLVSSEGLKRPETVYISCKASGYIFNNGWVKAQKGLKMGKMT--NTTGEPT 58
 DB 1 EVKLVSSEGLKRPETVYISCKASGYIFNNGWVKAQKGLKMGKMT--NTTGEPT 58
 DB 1 EVKLVSSEGLKRPETVYISCKASGYIFNNGWVKAQKGLKMGKMT--NTTGEPT 58
 DB 59 TADDFKRPASLETSASZAYLQINLAKEDYATFALYANSPEFVWQGGTLVTV 117
 QY 61 HVAESVWRTITLSDKSSVYLQNNLQNDLADLYTCS-----RQFVWQGGTLVTV 114
 QY 119 A 119
 DB 115 A 115

DT 21-JUL-1986 (rel. 01, Last annotation update)
 DT 15-SEP-2003 (rel. 42, Last annotation update)
 DR 19 heavy chain V region MHC 11.
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Castoridae; Vertebrata; Eucleostomi;
 OC Nemata; Insecta; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI TaxId:10090;
 RN SEQUENCE FROM N.A.
 RX Mus musculus:6253904; PubMed:6253904;
 RZ Zuker R., Cohen J., Givol D.;
 RT "Cloning and sequence of the cDNA corresponding to the variable
 RT region of immunoglobulin heavy chain MC11."
 CC -1- From a myeloma that secretes IgG2b.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DC HSBP: A03708; GWS11.
 DR InterPro: IP8003110; 19-like.
 DR InterPro: IP8003106; 19-MHC.
 DR 19 heavy chain V region W3082.
 DR SMART: SM00406; 19-V.
 DR PROSITE: PS50835; 19-Like; 1.
 PM Immunoglobulin V region.
 FT DISULFID 121 112
 FT NON_TER 111 112
 FT NON_TER 111 112
 SQ SEQUENCE 121 AA; 13135 MW; 227AFB3C5E809F CRC64;
 Query Match 49.7% Score 321; DB 1; Length 121;
 Beat Local Similarity 52.2% Pct. No. 6.4e-26;
 Matches 62; Conservative 22; Mismatches 34; Indels 2; Gaps 1;
 QY 1 EVKLVSSEGLKRPETVYISCKASGYIFNNGWVKAQKGLKMGKMT--NTTGEPT 60
 DB 1 EVKLVSSEGLKRPETVYISCKASGYIFNNGWVKAQKGLKMGKMT--NTTGEPT 60
 DB 1 EVKLVSSEGLKRPETVYISCKASGYIFNNGWVKAQKGLKMGKMT--NTTGEPT 60
 QY 61 ADYFKEPFLSLETSASZAYLQINLAKEDYATFALYANSPEFVWQGGTLVTV 118
 DB 61 HVAESVWRTITLSDKSSVYLQNNLQNDLADLYTCS-----RQFVWQGGTLVTV 120
 QY 119 A 119
 DB 121 A 121
 RESULT 12
 ID HV33 MOUSE STANDARD; PRT; 136 AA.
 AC P01759;
 DT 21-JUL-1986 (rel. 01, Created)
 DT 12-JUL-1986 (rel. 01, Last annotation update)
 DR 19 heavy chain V region W3082.
 DR 19 heavy chain V region W3082.
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Castoridae; Vertebrata; Eucleostomi;
 OC Nemata; Insecta; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI TaxId:10090;
 RN SEQUENCE FROM N.A.
 RX Mus musculus:622262; PubMed:606821;
 RZ Zuker R., Cohen J., Givol D.;
 RT "Cloning and sequence of the cDNA corresponding to the variable
 RT region of immunoglobulin heavy chain MC11."
 CC -1- From a myeloma that secretes IgG2b.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DC HSBP: A03708; GWS11.
 DR InterPro: IP8003110; 19-like.
 DR InterPro: IP8003106; 19-MHC.
 DR 19 heavy chain V region W3082.
 DR SMART: SM00406; 19-V.
 DR PROSITE: PS50835; 19-Like; 1.
 PM Immunoglobulin V region.
 FT DISULFID 121 112
 FT NON_TER 111 112
 FT NON_TER 111 112
 SQ SEQUENCE 121 AA; 13135 MW; 227AFB3C5E809F CRC64;
 Query Match 49.7% Score 321; DB 1; Length 121;
 Beat Local Similarity 52.2% Pct. No. 6.4e-26;
 Matches 62; Conservative 22; Mismatches 34; Indels 2; Gaps 1;
 QY 1 EVKLVSSEGLKRPETVYISCKASGYIFNNGWVKAQKGLKMGKMT--NTTGEPT 60
 DB 1 EVKLVSSEGLKRPETVYISCKASGYIFNNGWVKAQKGLKMGKMT--NTTGEPT 60
 DB 1 EVKLVSSEGLKRPETVYISCKASGYIFNNGWVKAQKGLKMGKMT--NTTGEPT 60
 QY 61 ADYFKEPFLSLETSASZAYLQINLAKEDYATFALYANSPEFVWQGGTLVTV 118
 DB 61 HVAESVWRTITLSDKSSVYLQNNLQNDLADLYTCS-----RQFVWQGGTLVTV 120
 QY 119 A 119
 DB 121 A 121

FT CONFLICT 115 115 W -> H (IN REF. 2).
 FT CONFLICT 120 120 Y -> W (IN REF. 2).
 FT CONFLICT 131 131
 SEQUENCE 136 AA; 15071 MW; 2276A9DEDBP7016 CMC64;

Query Match 49.6%; Score 320.5; DB 1; Length 136;
 Species: Local Similarity 33.0%; Pred. No. 8, 2e-26;
 Matches 60; Conservative 27; Mismatches 32; Indels 1; Gaps 1;

Oy 1 EVLVSEPELKKFETWIKSCASGYITFNQGMWVQAPQKILNMGCHINTYTGEPY 60
 Db 17 EVLVSEPELKKFETWIKSCASGYITFNQGMWVQAPQKILNMGCHINTYTGEPY 76
 Oy 61 ADFKESFAFSLSEASVYQIINLKNEDATYFCALYGNAP-KGRVWQGGTLVYSA 119
 Db 77 ADFKESFAFSLSEASVYQIINLKNEDATYFCALYGNAP-KGRVWQGGTLVYSA 136

RESULT 15

ID 2727 MOUSE STANDARD; PRT, 113 AA.
 AC P01796;
 DT 21-JUL-1986 (rel. 01, Created)
 DE 21-JUL-1986 (rel. 01, Last sequence update)
 DE 12-SEP-1993 (rel. 02, Last sequence update)
 DE Ig heavy chain V-II region AA.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eumammalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxId:10990;
 RN [1]

RP SEQUENCE.
 RA Vrain W/Indel 83, 93, 94;
 RT "sequence variation among heavy chains from immun-binding myeloma proteins";
 CC "-. NRESL. NRESL: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC CONTAINS AN IMMUNOGLOBULIN-LIKE DOMAIN."
 CC PRT: A3918; AWMAB.

DR Interpro: IPR007110; IG-1Lk.
 DR Interpro: IPR003066; IG-MHC.
 DR Interpro: IPR003596; IG-V.
 DR SMART: PF00040; Ig_1.
 DR SMART: PF00040; Ig_1.
 DR PROSITE: PS00315; IG_LIKE; 1.
 KM Immunoglobulin V region.
 FT DOMAIN 21 >113 IG-LIKE.
 FT PROSITE 21 >113 BY SIMILARITY.
 FT NON THR 113 113
 SO SEQUENCE 113 AA; 12675 MW; 76658C12C59285 CRC64;

Query Match 49.4%; Score 319; DB 1; Length 113;
 Best Local Similarity 52.9%; Pred. No. 9, 2e-30; Indels 8; Gaps 2;
 Matches 63; Conservative 18; Mismatches

Oy 1 EVLVSEPELKKFETWIKSCASGYITFNQGMWVQAPQKILNMGCHINTYTGEP 58
 Db 1 EVLVSEPELKKFETWIKSCASGYITFNQGMWVQAPQKILNMGCHINTYTGEP 60
 Oy 59 TADDKERFAFSLSEASVYQIINLKNEDATYFCALYGNAPKGRVWQGGTLVY 117
 Db 61 HLFESKFAFSLSEASVYQIINLKNEDATYFCALYGNAPKGRVWQGGTLVY 113

Search completed: November 7, 2003, 07:28:07
 Job time: 2:57:44 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 10.243 seconds

Without alignment 782.516 Million cell updates/sec

US-09-661-992b-82_COPY_1_119

Sequence: 1 EKVYSGEELKKRREIVYI.....NSRPFAYWGQITATVA 119

Scoring table: Gapex 10.0, Gapex 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: 1: sp.archaea:*

2: sp.bacteria:*

3: sp.fungi:*

4: sp.invertebrates:*

5: sp.mammal:*

6: sp.plant:*

7: sp.virus:*

8: sp.unclassified:*

9: sp.yeast:*

10: sp.yeast:*

11: sp.yeast:*

12: sp.yeast:*

13: sp.yeast:*

14: sp.yeast:*

15: sp.yeast:*

16: sp.yeast:*

17: sp.yeast:*

18: sp.yeast:*

19: sp.yeast:*

20: sp.yeast:*

21: sp.yeast:*

22: sp.yeast:*

23: sp.yeast:*

24: sp.yeast:*

25: sp.yeast:*

ALIGNMENTS

RESULTS

ID

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PRELIMINARY: BPT, 241 AA.

01-DEC-2001 (TRENCH, 18, Created)

01-DEC-2001 (TRENCH, 18, Last sequence update)

01-DEC-2001 (TRENCH, 18, Last sequence update)

Anti-CEA 79 single chain Fv fragment (fragment).

MS Musculus (Mouse).

Shayyeda; Metacore; Chordata; Vertebrata; Euteleostomi;

OC Metazoa; Chordata; Rodentia; Sciurognathi; Muridae; Mus;

NCBI_Taxid-10990;

[1]

SEQUENCE FROM N.A. Rahmeh-990406;

Chung J.H. Choi S.H., Kim H.J. Kim I.J., Choi I.H., Lee S.D.,

Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;

"Cloning and characterization of cDNAs encoding VH and VL of a

monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and

CEA 79 antibody in the Fv molecule (accy)."

EMBL, U88067, AB84804.1;

InterPro: IPR007110, IPR0118E.

InterPro: IPR003596, IPR0118E.

InterPro: IPR003596, IPR0118E.

InterPro: IPR003596, IPR0118E.

InterPro: IPR003596, IPR0118E.

092422 mus musculus

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092422 mus musculus

092422 mus musculus

092422 mus musculus

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092422 mus musculus

Db 61 ASFAFGQINTLNEDVYFCVEMAS--NFANQGGTLYVNA 120

RESULT 5

Q92088 PRELIMINARY; PRT; 120 AA.

DR 01-DEC-2001 (TRIMBACel. 19, Created)
 DT 01-DEC-2001 (TRIMBACel. 19, Last sequence update)
 DE 01-MAR-2003 (TRIMBACel. 23, Last annotation update)
 DB Protein-antibody anti-idiotope heavy chain variable region
 OS Mus musculus (Mouse)
 OC Birkycota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 MM Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCBI_TaxID=10090.

SEQUENCE FROM N.A.
 RA Aikin J.D., Iape A., Jennings I.G., Horvath O., Cotton R.G.H.;
 RL In: Immunology of the Idiotope of Protein-Matching Antibodies Expressed
 in Transgenic Mice, pp. 1-10, 1999, to the EMBL/Genbank/DBD databases.
 DR EMBL; AF079365; Akl09420.1; -
 DR EMBL; AF079365; Akl09420.1; -
 DR InterPro; IPR003596; 19_1-11ke.
 DR InterPro; IPR003596; 19_1-11ke.
 DR Pfam; PF00047; 19_1-11ke.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LINE; 1.
 FT NON-TER

SEQUENCE 120 AA; 1200 MW; DC4834BIDE563C CRC64;
 Query Match 61.1%; Score 395; DB 11; Length 120;
 Best Local Similarity 60.8%; Pred. No. 6.9e-32;
 Matches 73; Conservative 21; Mismatches 24; Indels 2; Gaps 1;

Qy 1 EVKVGSGEKKKRRVYICGASCTFFNYGNGWYKQAGKAGKMGNTVTEERT 60
 Db 1 EVQVSGEKKKRRVYICGASCTFFNYGNGWYKQAGKAGKMGNTVTEERT 60
 61 ADDGKFAFSLSTANVYQINNNANEDVYFCV--YVNSPKPFA--VWGGTLYV 118
 61 NQKFKKATLVKSSSTVWQKSLTSHSNVYVYVYVYVYVYVYVYVYVYVYV 120

RESULT 6
 Q92084 PRELIMINARY; PRT; 119 AA.

DR 01-MAY-2000 (TRIMBACel. 13, Created)
 DT 01-MAY-2000 (TRIMBACel. 13, Last sequence update)
 DE 01-MAR-2003 (TRIMBACel. 23, Last annotation update)
 DB Myosin-reactive immunoglobulin heavy chain variable region
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 MM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NC NCBI_TaxID=9606.

SEQUENCE FROM N.A.
 RA MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Werf P.L., Kalis N.M., Bernay S.M.,
 RT Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus; -

CLIN. Immunol. Immunopathol. 87:184-192(1998).
 DR HSBP; P01772; 28k.
 DR InterPro; IPR003596; 19_1-11ke.
 DR InterPro; IPR003596; 19_1-11ke.
 DR InterPro; IPR003596; 19_1-11ke.

DR Pfam; PF00047; 19_1-11ke.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LINE; 1.
 FT NON-TER

SEQUENCE 119 AA; 1200 MW; 13B6F545FPA168 CRC64;
 Query Match 58.4%; Score 377; DB 4; Length 119;
 Best Local Similarity 57.3%; Pred. No. 4.3e-30;
 Matches 69; Conservative 22; Mismatches 29; Indels 0; Gaps 0;

Qy 1 EVKVGSGEKKKRRVYICGASCTFFNYGNGWYKQAGKAGKMGNTVTEERT 60
 Db 1 EVQVSGEKKKRRVYICGASCTFFNYGNGWYKQAGKAGKMGNTVTEERT 60
 61 ADDGKFAFSLSTANVYQINNNANEDVYFCV--YVNSPKPFA--VWGGTLYV 118
 61 NQKFKKATLVKSSSTVWQKSLTSHSNVYVYVYVYVYVYVYVYVYVYVYV 119
 61 NQKFKKATLVKSSSTVWQKSLTSHSNVYVYVYVYVYVYVYVYVYVYVYV 119

RESULT 7
 Q92092 PRELIMINARY; PRT; 124 AA.

DR 01-MAY-2000 (TRIMBACel. 13, Created)
 DT 01-MAY-2000 (TRIMBACel. 13, Last sequence update)
 DE 01-MAR-2003 (TRIMBACel. 23, Last annotation update)
 DB Myosin-reactive immunoglobulin heavy chain variable region
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 MM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NC NCBI_TaxID=9606;

SEQUENCE FROM N.A.
 RA MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Werf P.L., Kalis N.M., Bernay S.M.,
 RT Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus; -

CLIN. Immunol. Immunopathol. 87:184-192(1998).
 DR HSBP; P01772; 28k.
 DR InterPro; IPR003596; 19_1-11ke.
 DR InterPro; IPR003596; 19_1-11ke.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LINE; 1.
 FT NON-TER

SEQUENCE 124 AA; 1580 MW; 1BAACED96ACD2A2 CRC64;
 Query Match 58.3%; Score 376.5; DB 4; Length 124;
 Best Local Similarity 57.3%; Pred. No. 5.1e-33;
 Matches 71; Conservative 24; Mismatches 24; Indels 5; Gaps 2;

Qy 1 EVKVGSGEKKKRRVYICGASCTFFNYGNGWYKQAGKAGKMGNTVTEERT 60
 Db 1 EVQVSGEKKKRRVYICGASCTFFNYGNGWYKQAGKAGKMGNTVTEERT 60
 61 ADDGKFAFSLSTANVYQINNNANEDVYFCV--YVNSPKPFA--VWGGTLYV 118
 61 NQKFKKATLVKSSSTVWQKSLTSHSNVYVYVYVYVYVYVYVYVYVYVYV 120
 121 TVSS 124

RESULT 8
 Q92095 PRELIMINARY; PRT; 125 AA.

Db 80 SCKFGR/MTWDTSTVYNDVSLSDSTDAVFCAREMEITFGVANGKPYTGMDV 139
 Qy 110 GQGVLYTSS 119
 Db 140 GQGVLYTSS 149
 RESULT 11
 QGVYJ1 PRELIMINARY; PRT: 123 AA.
 AC QGVYJ1; 20
 DT 01-MAR-2002 (TRIMBREL: 20, Created)
 DT 01-MAR-2002 (TRIMBREL: 20, Last sequence update)
 DT 01-MAR-2003 (TRIMBREL: 23, Last annotation update)
 DE Anti-DNA heavy chain (fragment).
 NR 3559.
 CC Buleyeta; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID:10090;
 CC NCBI_SEQ: PRCA N.A.
 RC STRAHC-CH/Hu/1pr/1pr;
 RA MEDLINE:36409289; PubMed:8814271;
 RX Wloch M.K., Alexander A.L., Pigen A.W., Piatetsky D.S., Gilkeson G.S.;
 RT anti-DNA from C3H/10Pr.D.Sj and immunization and YH CD3 sequence among
 RL Bur. J. Immunol. 26:2225-2233(1996). Note with significance.
 DR EMBL: U59154; AL002916.1;
 DR InterPro: IPR003106; 15.MC.
 DR InterPro: IPR003596; 15.V.
 DR Pfam: PF00047; 19.1.
 DR PROSITE: PS00645; 10V; 1.
 FT NON_TER 123
 SQ SEQUENCE 123 AA; 13806 MW; CC0037A80E93911E CRC64;
 Query Match 55.4%; Score 355; DB 11; Length 123;
 Best Local Similarity 54.6%; Pred. No. 76-28;
 Matches 69; Conservative 20; Mismatches 30; Indels 4; Gaps 2;
 Qy 1 EVKLVSGLKKEKRYVISCASGYFTFNQGMWYKACGCLVWNGVYTGCTY 60
 Db 1 EIQAGSGLVLRKASVAVISCASGYFTFNQGMWYKACGCLVWNGVYTGCTY 60
 Qy 61 ADPQKGRASLFLATAYVYQNNKMEQVYTCG--LQNSDPC FVNGGTYT 116
 Db 61 SCKFGR/MTWDTSTVYNDVSLSDSTDAVFCAREMEITFGVANGKPYTGMDV 120
 Qy 117 VSA 119
 Db 121 VSA 123
 RESULT 12
 QGVYJ1 PRELIMINARY; PRT: 497 AA.
 AC QGVYJ1; 20
 DT 01-MAR-2002 (TRIMBREL: 20, Created)
 DT 01-MAR-2002 (TRIMBREL: 20, Last sequence update)
 DT 01-MAR-2003 (TRIMBREL: 23, Last annotation update)
 DE SMC6 protein.
 NR 3559.
 CC Buleyeta; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Cetermnia; Homidae; Homo.
 NCBI_TaxID:9606;
 CC NCBI_SEQ: PRCA N.A.
 RC STRAHC-CH/Hu/1pr/1pr;
 RA Zhang S., Shao X., Cao J., Geng L., Pang Y., Dong Q.;
 RT Identification and characterization of SMC6, a 19.1-kb gene which is
 RT down-regulated in colorectal cancer.
 RT

RL Submitted (JUN-2000) to the EMBL/Genbank/DDBJ databases.
 DR EMBL: AF26566; AL05697.1;
 DR InterPro: IPR007110; 19-11k.
 DR InterPro: IPR003006; 19.MC.
 DR Pfam: PF00047; 19.1.
 DR Pfam: PF00047; 19.1.
 DR SMART: SM00405; 10V; 1.
 DR PROSITE: PS00645; 10V; 1.
 DR PROSITE: PS00645; 10V; 1.
 DR PROSITE: PS00645; 10V; 1.
 FT NON_TER 119
 SQ SEQUENCE 119 AA; 13025 MW; F6B9044381C7C CRC64;
 Query Match 54.6%; Score 353; DB 11; Length 119;
 Best Local Similarity 54.6%; Pred. No. 11e-27;
 Matches 65; Conservative 24; Mismatches 30; Indels 0; Gaps 0;
 Qy 1 EVKLVSGLKKEKRYVISCASGYFTFNQGMWYKACGCLVWNGVYTGCTY 60
 Db 1 EVKLVSGLKKEKRYVISCASGYFTFNQGMWYKACGCLVWNGVYTGCTY 60
 Qy 61 ADPQKGRASLFLATAYVYQNNKMEQVYTCG--LQNSDPC FVNGGTYT 116
 Db 61 PDSVGR/FTSRDAKRLVYLNSSLSKSEDFVWYTCARHDDVDVFAVWQGVLYTSS 119
 Db 141 TVSS 144
 RESULT 13
 QGVYJ1 PRELIMINARY; PRT: 119 AA.
 AC QGVYJ1; 20
 DT 01-DEC-2001 (TRIMBREL: 19, Created)
 DT 01-DEC-2001 (TRIMBREL: 19, Last sequence update)
 DT 01-MAR-2003 (TRIMBREL: 23, Last annotation update)
 DE 63 DKPGRASLFLATAYVYQNNKMEQVYTCG--LQNSDPC FVNGGTYT 115
 Db 82 KFCGR/FTSRDAKRLVYLNSSLSKSEDFVWYTCARHDDVDVFAVWQGVLYTSS 140
 Qy 116 TVSS 119
 Db 141 TVSS 144
 RESULT 14
 QGVYJ1 PRELIMINARY; PRT: 119 AA.
 AC QGVYJ1; 20
 DT 01-DEC-2001 (TRIMBREL: 19, Created)
 DT 01-DEC-2001 (TRIMBREL: 19, Last sequence update)
 DT 01-MAR-2003 (TRIMBREL: 23, Last annotation update)
 DE 63 DKPGRASLFLATAYVYQNNKMEQVYTCG--LQNSDPC FVNGGTYT 115
 Db 82 KFCGR/FTSRDAKRLVYLNSSLSKSEDFVWYTCARHDDVDVFAVWQGVLYTSS 140
 Qy 116 TVSS 119
 Db 141 TVSS 144

```

ID C91WR1 PRELIMINARY; PRT; 488 AA.
AC C91WR1;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DR 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DS 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE Hypothetical 53.0 kDa protein.
GN IGH-V1558 OR A1893585.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Cetacea; Ursidae; Eulacostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId:10090;
RN (1)
RS SOURCE FROM N.A.
RA STRAUSBERG R.;
RC STRAUSBERG R.;
RL EMBL; BC013592; A01359.1; -.
RL NCBI; BC013592; A01359.1; -.
DR Interpro; IPRO03596; I4_V.
DR Interpro; IPRO03596; I4_V.
DR Interpro; IPRO03596; I4_V.
DR SMART; SM00406; I4_V.1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_YMC; 2.
DR PROSITE; PS00290; IG_YMC; 2.
DE PROSITE local protein.
SO SEQUENCE 488 AA; 5264 MW; F1206460840DBD CRC64;

Query Match 53.8%; Score 347.5; DB 11; Length 488;
Best Local Similarity 53.8%; Pred. No. 2.1e-26;
Matches 67; Conservative 23; Mismatches 28; Indels 7; Gaps 2;

Qy 1 EYLVESGPELKPQETVYKSCKASGYIFETNGMWYQAPQKGLKMWGMINTTGEPT 60
Db 20 EYVQDSSPELVFQALVYKSCKASGYIFETNGMWYQAPQKGLKMWGMINTTGEPT 79
Qy 61 ADDPKGFAPSLFETASTAYLQINNLKAEPTATYFCALGKMSKGFPAWQGLTVTVA 114
Db 80 ADDPKGFAPSLFETASTAYLQINNLKAEPTATYFCALGKMSKGFPAWQGLTVTVA 138
Qy 115 VTVA 119
Db 139 VTVA 143

RESULT 15
Q98Q24 PRELIMINARY; PRT; 480 AA.
AC Q98Q24;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DR 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DS 01-OCT-2002 (TEMBLrel. 22, Last annotation update)
DE Similar to expressed sequence A193385.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Cephalata; Vertebrata; Eulacostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId:10090;
RN (1)
RS SEQUENCE FROM N.A.
RA STRAUSBERG R.;
RC STRAUSBERG R.;
RL Submitted (May 2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029188; A029188.1; -.
DR Interpro; IPRO03599; I9_1like.
DR Interpro; IPRO03599; I9_1like.
DR Interpro; IPRO03599; I9_1like.
DR Interpro; IPRO03599; I9_1like.
DR Interpro; IPRO03599; I9_1like.
DR SMART; SM00406; I9_1.
DR SMART; SM00407; I9_1.3.
DR SMART; SM00406; I9_1.
DR PROSITE; PS00835; IG_LIKE; 4.

```

```

DR PROSITE; PS00290; IG_YMC; 2.
DE PROSITE local protein.
SO SEQUENCE 480 AA; 5169 MW; 8690A63C69C8BD CRC64;

Query Match 53.7%; Score 347; DB 11; Length 480;
Best Local Similarity 52.9%; Pred. No. 2.3e-26;
Matches 63; Conservative 26; Mismatches 28; Indels 7; Gaps 1;

Qy 1 EYLVESGPELKPQETVYKSCKASGYIFETNGMWYQAPQKGLKMWGMINTTGEPT 60
Db 20 EYVQDSSPELVFQALVYKSCKASGYIFETNGMWYQAPQKGLKMWGMINTTGEPT 79
Qy 61 ADDPKGFAPSLFETASTAYLQINNLKAEPTATYFCALGKMSKGFPAWQGLTVTVA 119
Db 80 ADDPKGFAPSLFETASTAYLQINNLKAEPTATYFCALGKMSKGFPAWQGLTVTVA 136

Search completed: November 7, 2003, 07:34:32
Job time : 42.343 secs

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XX PF 13-SEP-2000; 2000MO-BP08936.
 XX XX
 XX PF 14-SEP-1993; 99AT-0001576.
 XX XX
 XX (BAXT) BAXTER AG.
 XX PF
 XX Scheflinger F, Kerschbaurer R, Falkner F, Dornier F,
 DE MPI. 2001-290358/30.
 DE N-PDB: AAF30723.
 XX PF
 XX New factor IX/factor IXa antibodies and their derivatives useful for
 XX increasing haemostatic activity in haemophilic patients with
 XX congenital disorders such as haemophilia A and haemorrhagic diathesis -
 XX Claim 8; Fig 14; 13pp; English.
 XX XX
 XX The present sequence is that of a single chain Fv (scFv) derivative
 XX of antibody 133/AD3, comprising the heavy (VH) and light (VL) chain
 XX variable regions of 133/AD3 joined by an artificial, flexible linker
 XX region. The scFv is suitable for the production of chimeric for
 XX 133/AD3 VH and VL regions and chimeric antibodies for the treatment
 XX of anti-haemophilic Factor IX (FIX) antibodies of the invention. Anti-FIX/FIXa and their derivatives,
 XX including scFv and CDR3 fragments, have Factor VIIa (FVIIa) cofactor
 XX activity and are useful for the treatment of haemophilic patients
 XX CC increase in the procoagulant activity of FIXa, even in the presence
 XX of FVIIa inhibitors. This allows for rapid blood coagulation even
 XX in the absence of FVIII or FVIIa, and in the case of FVIII
 XX deficiency. The antibodies are useful for treating liver disease, a
 XX claimed pharmaceutical composition for treating liver disease, a
 XX coagulation disorders, especially haemophilia A and haemorrhagic
 XX diathesis.
 XX
 XX Sequence 242 Aa:
 XX
 XX Query Match 100.0%; Score 646; DB 22; Length 242;
 XX Local Similarity 100.0%; Pct. No. 2, Aa: 46;
 XX Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 EVLVYSGPELKKPEKPEVYKSCASGYFTNNGMNYKAKNGKAWQANINTYSEPT 60
 XX Db 1 EVLVYSGPELKKPEKPEVYKSCASGYFTNNGMNYKAKNGKAWQANINTYSEPT 60
 XX QY 61 ADDFGKRPASPLTSASPTVYQINNNANREPTATPCALYSPKGPAYWQGGTLVTS 119
 XX Db 61 ADDFGKRPASPLTSASPTVYQINNNANREPTATPCALYSPKGPAYWQGGTLVTS 119
 XX
 XX RESULT 2
 XX ID AAE29156 standard; Protein; 137 Aa.
 XX AC AAE29156;
 XX DX 27-JAN-2003 (first entry)
 XX DB Chimeric 31.1 antibody heavy chain variable region.
 XX XX
 XX 31.1 antibody; pancreatic cancer; pancreatic carcinoma; antibody therapy;
 XX heavy chain variable region
 XX XX
 XX Undeidentified.
 XX OS
 XX MO200274251-A2.
 XX PN
 XX 26-SEP-2002.
 XX PD
 XX 15-MAR-2002; 2002MO-US09193.
 XX PF
 XX 15-MAR-2001; 2001US-27684P.
 XX PR
 XX

BA (TIB-1) INT BIOMKING SYSTEMS INC.
 XX PF Aileen M, Tsang KY;
 XX PF
 XX MPI. 2002-759857/82.
 XX N-75091 AAD46728.
 XX PF
 XX New nucleic acid encoding light and heavy chain variable regions of the
 XX antibody 31.1, useful for expressing chimerized 31.1 antibodies for
 XX treating pancreatic cancer or for diagnosing pancreatic carcinoma -
 XX Claim 5; Fig 4; 40pp; English.
 XX XX
 XX The present invention relates to novel nucleic acid sequences encoding
 XX the heavy chain variable region of antibody 31.1, and to chimeric
 XX CC of the invention are useful in expressing chimerized 31.1 antibodies
 XX which can be used for treating pancreatic cancer or for diagnosing
 XX pancreatic carcinoma. They are also used in antibody therapy. The present
 XX sequence is chimeric 31.1 antibody heavy chain variable region.
 XX
 XX Sequence 137 Aa:
 XX
 XX Query Match 86.6%; Score 559.5; DB 23; Length 137;
 XX Local Similarity 86.6%; Pct. No. 2, Aa: 37; 5; Indels 5; Gaps 2;
 XX Matches 105; Conservative 6; Mismatches 10;
 XX
 XX QY 1 EVLVYSGPELKKPEKPEVYKSCASGYFTNNGMNYKAKNGKAWQANINTYSEPT 60
 XX Db 20 QGLVDSPELKKPEKPEVYKSCASGYFTNNGMNYKAKNGKAWQANINTYSEPT 79
 XX QY 61 ADDFGKRPASPLTSASPTVYQINNNANREPTATPCALYSPKGPAYWQGGTLVTS 119
 XX Db 61 ADDFGKRPASPLTSASPTVYQINNNANREPTATPCALYSPKGPAYWQGGTLVTS 136
 XX
 XX QY 119 A 119
 XX Db 137 8 137
 XX
 XX RESULT 2
 XX ID AAM02278 standard; Protein; 250 Aa.
 XX AC AAM02278;
 XX DX 25-MAR-2003 (updated)
 XX DT 29-OCT-1996 (first entry)
 XX XX
 XX 741F8 anti-c-erbB-2 two single chain Fv construct.
 XX XX
 XX 741F8; anti-c-erbB-2; monoclonal antibody; single chain Fv; scFv;
 XX construct; polypeptide linker; C-terminal amino acid sequence;
 XX in vivo imaging; drug targeting experiment; homodimer;
 XX increased; binding avidity; tissue retention time.
 XX Homo sapiens.
 XX OS
 XX Key
 XX Localizer/Qualifiers
 XX FT 132..135
 XX FT /label= linker
 XX FT Peptide
 XX FT 246..250
 XX /note= "Chimeric C-terminal tail to facilitate
 XX crosslinking of two scFv polypeptides"
 XX
 XX US5534254-A.
 XX PN
 XX 09-JUL-1996.
 XX PD
 XX 07-OCT-1993; 93US-0133804.
 XX PF
 XX 07-OCT-1993; 93US-0133804.
 XX PR 06-FEB-1992; 92US-0831967.
 XX

PA (CHIR) CHIRON CORP.
 XX (CRA-) CREATIVE BIOMOLECULES INC.
 XX Houston Lt., Houston J5, Oppermann H, Ring DB;
 PT WPI, 1996-131194/33.
 DR H-PDBJ, AAT9369/8.
 XX

PT Compans, cong. antigen-targeting antibody fragment constructs -
 comprising dimer of single-chain Fv fragments
 Claim 25, Columns 27-28, 30pg. English.

XX The variable heavy (VH) and variable light (VL) genes of the 7419
 CC anti-c-erbB-2 monoclonal antibody (9Nb), were isolated from the
 CC hybridoma cell line 9Nb. A two single chain Fv
 CC (scFv) gene was constructed by connecting the variable
 CC DNA sequence encoding a polypeptide linker. A synthetic DNA duplex
 CC encoding the C-terminal amino acid sequence, (Gly)4-Cys was
 CC inserted into the resulting 7419 anti-c-erbB-2 two svf inserted
 CC linker. The resulting scFv gene was transformed into E. coli, and protein
 CC expression sequence, was transformed into E. coli, and protein
 CC expression induced by the addn. of IPTG to the culture medium.
 CC A compn. comprising a carrier and the 2 svf protein prod. can be
 CC used for immunizing a subject with the antigen. The
 CC 2 svf protein prod. is a homodimer in which both fragments
 CC the same antigen, therefore giving greater binding avidity and
 CC longer tissue retention times, compared to individual svf protein
 CC (updated on 25-MAR-2003 to correct PF field.)
 XX

SQ Sequence 250 AA;
 XX

Query Match 85.4%; Score 552, DB 17, Length 250;
 Best Local Similarity 85.4%; Pred. No. 2, 3e-38;
 Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;

QY 1 PPKVYSGEHLKXGKGGYKSCVAGSITFFNCGNNYKQAPKFGKAMGNNITTTGGY 60
 Db 3 EIQLVQSGEHLKXGKGGYKSCVAGSITFFNCGNNYKQAPKFGKAMGNNITTTGGY 62
 QY 61 ADPPKGPSPKSLFSAFNQINNNKREGTATYCA---LXGSPKGFANWQDGLTY 116
 Db 63 AEEFGKGFPSLSTASVYQLNNKNDSDYITFCORPTTGG---GFMNWDGDIY 118

QY 117 VSA 119
 Db 119 VSA 121

RESULT 4
 AAW23261
 ID AAW23261 standard: Protein; 250 AA.
 XX
 XX AAW23261;
 XX
 XX 25-MAR-2003 (updated)
 DT 07-JAN-1998 (first entry)
 XX
 XX Anti-c-erbB-2 single chain antibody 7419.
 XX
 XX Adenovirus, E1A; transactivator; transcription activator; stimulate;
 XX expression vector; single-chain binding protein; VAI; enhancer; PCR;
 XX single-chain antibody fragment; transfection; imaging
 XX ovarian cancer; c-erbB-2 antigen; digoxin intoxication.
 XX
 XX Synthetic.
 XX
 XX US668763-A.
 XX
 XX 19-NOV-1997.

PF 05-JUN-1995; 9505-0463675.
 XX
 XX 25-OCT-1993; 93US-0143498.
 PR 05-JUN-1995; 9505-0463675.
 XX
 PA (CRA-) CREATIVE BIOMOLECULES INC.
 XX
 XX Doral H, Oppermann H;
 XX WPI, 1997-42425/39.
 DR H-PDBJ, AAT91837.
 XX

XX Producing single chain binding protein in immortalized eukaryotic
 PT cells and antibodies for immunization of cells and tissue
 PT activator and translation promotion sequences, provides high
 XX expression at low copy number
 XX

XX Example 2, column 29-32, 24pg. English.

XX This sequence is a single chain anti-c-erbB-2 antibody (scFv)
 CC derived from hybridoma 7419. The protein product includes a C-terminal
 CC derived using a novel construction. Single-chain antibodies can be raised
 CC eukaryotic cell having transfected DNA sequences (encoding the protein
 CC of interest), integrated into its genome. In particular expression
 CC of vector vectors containing a non-active reporter DNA (encoding the scFv)
 CC adenovirus E1A and VAI genes as shown in AAT91831 and AAT91843
 CC respectively) are used. The scFv that is produced, when properly folded,
 CC has a structure with mono- or bi-functional binding activity. The method
 CC e.g. for imaging tumor localization.
 CC particularly breast and ovarian cancers that express the c-erbB-2
 CC antigen. Other scFv are used in model studies and for treating digoxin
 CC (updated on 25-MAR-2003 to correct PF field.)
 XX

SQ Sequence 250 AA;
 XX

Query Match 85.4%; Score 552, DB 18, Length 250;
 Best Local Similarity 85.4%; Pred. No. 3e-38;
 Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;

QY 1 PPKVYSGEHLKXGKGGYKSCVAGSITFFNCGNNYKQAPKFGKAMGNNITTTGGY 60
 Db 3 EIQLVQSGEHLKXGKGGYKSCVAGSITFFNCGNNYKQAPKFGKAMGNNITTTGGY 62
 QY 61 ADPPKGPSPKSLFSAFNQINNNKREGTATYCA---LXGSPKGFANWQDGLTY 116
 Db 63 AEEFGKGFPSLSTASVYQLNNKNDSDYITFCORPTTGG---GFMNWDGDIY 118

QY 117 VSA 119
 Db 119 VSA 121

RESULT 5
 AAW22400
 ID AAW22400 standard: Protein; 250 AA.
 XX
 XX AAW22400;
 XX
 XX 25-MAR-2003 (updated)
 DT 09-OCT-1997 (first entry)
 XX
 XX Single chain antibody 7419 protein sequence.
 XX
 XX Production; single-chain binding protein; antibody; eukaryotic; virus;
 XX transcription activator; promoter; expression; adenovirus; E1A; PCR;
 XX transmembrane chain reaction; amplification; primer; herpes simplex virus;
 XX thymidine kinase; vector; enhancer; translation; heterologous.
 XX
 XX Synthetic.

XX US631158-A.
 FN 20-MAY-1997.
 XX
 XX 05-JUN-1995; 95US-0461184.
 PP
 XX 25-OCT-1993; 93US-0143498.
 RR
 XX 05-JUN-1995; 95US-0461184.
 RR
 XX (CREA-) CREATIVE BIOMOLECULES INC.
 PA
 XX Dorei H, Oppermann H;
 XX NPI, 1997-288577/26.
 DR
 XX N-P8DB; AAT78879.
 PT
 XX Production of cell line for producing single-chain binding protein -
 XX using construct containing DNA encoding viral transcription
 XX activator protein
 XX
 XX Example 2; Column 29-32; 24pp; English.
 XX
 XX The invention relates to methods of increasing production of a
 XX single-chain binding protein, especially a single chain antibody,
 XX by using a transcription activator protein (TAP) encoding either
 XX a viral transcription activator protein, such as the adenovirus Ad5
 XX single-chain binding protein, such as the adenovirus Ad5 E1A protein
 XX encoded by the sequence AAT7878, or an RNA sequence able to promote
 XX the transcription of the gene encoding the heterologous gene, such as
 XX the adenoviral Val gene (AAT78876).
 XX
 XX The sequence presented here is the amino acid sequence of the
 XX anti-c-erbB2 single chain antibody 7419. The coding sequence was
 XX synthesized by using a TAP expression vector for secretion from mammalian
 XX cells, the sequence is preceded by the signal peptide sequence from
 XX the monoclonal antibody 520C9 (AAT78880) or from Pac1 (AAT78881).
 XX
 XX (updated on 25-MAY-2003 to correct PF field.)
 XX
 XX Sequence 250 AA;
 XX
 XX Query Match 85.4%; Score 552; DB 19; Length 250;
 XX Best Local Similarity 85.4%; Pred NO.2; 2e-35;
 XX Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;
 XX
 XX 1 EVLVSSPEFLKREFVYVSKSGSGTFFNGGVWVQVQKGLKMGVQINNTTDEPT 60
 XX 3 EIOVSGPEFLKREFVYVSKSGSGTFFNGGVWVQVQKGLKMGVQINNTTDEPT 62
 XX 61 AADKREKNSLETSASTNYQINNLNEDNTTPCA---LVGNSKGFKNVQGGTLYV 116
 XX 63 AAEIKRNFSLTSASTNYQINNLNEDNTTPCA---LVGNSKGFKNVQGGTLYV 118
 XX
 XX 117 VSA 119
 XX 119 VSA 121
 XX
 XX Db
 XX
 XX RESULT 5
 XX AAM53168
 XX ID AAM53168 standard; Protein; 250 AA.
 XX
 XX AAM53168;
 XX
 XX 16-JUL-1998 (first entry)
 XX
 XX 741P8 anti-c-erbB-2 sFv dimeric construct protein sequence.
 XX Antigen imaging; single chain Fv; sFv; linker; dimeric; cancer;
 XX c-erbB-2; tumour; diagnosis.
 XX
 XX Synthetic.

XX NUS DP.
 XX Key Location/Qualifiers
 XX Peptide 122..135 linker peptide*
 XX Peptide 206..250 /note="Gly4-Cys C-terminal tail"
 XX
 XX US9733204-A.
 XX
 XX 19-MAY-1998.
 XX
 XX 05-JUN-1995; 95US-0461838.
 XX
 XX 07-OCT-1993; 93US-0138804.
 XX 06-FEB-1992; 92US-0831987.
 XX 05-JUN-1995; 95US-0461838.
 XX
 XX (CHIT) CHIRON CORP.
 XX (CREA-) CREATIVE BIOMOLECULES INC.
 XX
 XX Houston LT, Oppermann H, Ring DB,
 XX NPI, 1998-311316/27.
 XX N-P8DB; AAM71796.
 XX
 XX Imaging of antigens in vivo - using dimeric of single-chain antibody
 XX Fv fragments
 XX
 XX Example 1; Column 25-28; 30pp; English.
 XX
 XX This represents the protein sequence of a 7419 sFv* (single chain Fv)
 XX C-terminal Gly4-Cys construct. This was constructed by connecting the Vh
 XX and Vl genes with a DNA sequence encoding a 14 residue polypeptide-2
 XX linker. 7419 is a monoclonal antibody useful in targeting C-erbB-2
 XX in vivo targeting of an epitope on an antigen with greater apparent
 XX avidity, including greater tumour specificity, tumour localization and
 XX tumour retention properties than that of the Fab fragment having the same
 XX C-ends as the construct.
 XX
 XX Sequence 250 AA;
 XX
 XX Query Match 85.4%; Score 552; DB 19; Length 250;
 XX Best Local Similarity 85.4%; Pred NO.2; 2e-35;
 XX Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;
 XX
 XX 1 EVLVSSPEFLKREFVYVSKSGSGTFFNGGVWVQVQKGLKMGVQINNTTDEPT 60
 XX 3 EIOVSGPEFLKREFVYVSKSGSGTFFNGGVWVQVQKGLKMGVQINNTTDEPT 62
 XX 61 AADKREKNSLETSASTNYQINNLNEDNTTPCA---LVGNSKGFKNVQGGTLYV 116
 XX 63 AAEIKRNFSLTSASTNYQINNLNEDNTTPCA---LVGNSKGFKNVQGGTLYV 118
 XX
 XX 117 VSA 119
 XX 119 VSA 121
 XX
 XX Db
 XX
 XX RESULT 7
 XX AAM47012
 XX ID AAM47012 standard; Protein; 250 AA.
 XX
 XX AAM47012;
 XX
 XX 13-JUL-1998 (first entry)

ID AAR6432 standard; Protein; 140 AA.
 XX AAR6432;
 AC AAR6432;
 DT 25-MAR-2003 (updated)
 DT 31-0UL-1995 (first entry)
 DE MAb 1243 VH region.
 DE MAb 1243 VH region.
 DE Unlabeled antibody; antibody engineering; MHC class II;
 DE major histocompatibility region; HLA; monoclinal antibody; MAb;
 DE 1243; immunological disease; transplantation; light chain;
 DE heavy chain; variable region; complementarity determining region;
 DE CDR.
 OS Mus sp.
 PN MO9429451-A2.
 XX MO9429451-A2.
 PD 22-DEC-1994.
 XX 15-JUN-1994; 94MO-GB01291.
 XX 16-JUN-1993; 93GB-0012415.
 PR 27-JUN-1994; 94GB-0001597.
 PR 09-FEB-1994; 94GB-0002439.
 PR 29-MAR-1994; 94GB-0002422.
 XX (CLUT) CELTECH LTD.
 FA Atrial DS, Bodmer WM, Emeage JS, Morgan SA;
 DR WFI; 1995-036409/05.
 DR N-PSDB; AA080360.
 PT New humanised anti-HLA DR antibodies - used for diagnosis and
 PT treatment of immunological diseases and transplantation related
 PT conditions
 XX Disclosure; Fig. 2; 66pp; English.
 CC 1243 is a mouse MAb raised against human MHC class II. The
 CC nucleotide and amino acid sequences of 1243 VL and VH regions are
 CC given in AA080357/64321 and AA080358/64322, respectively.
 CC 1243 is a murine monoclonal antibody based on these sequences have
 CC been constructed.
 CC (Updated on 25-MAR-2003 to correct FN field.)
 XX Sequence 140 AA:
 SQ
 Query Match 84.5%; Score 546; DB 16; Length 140;
 Best Local Similarity 83.5%; Pred. No. 4,1e-38;
 Matches 10; Conservative 6; Mismatches 10; Indels 2; Gaps 1;
 Db 1 EYKLVESGPELKEKGFVAKISCSAGYIFPNNGWVQAQKRGKLMWQMIINTTGEPT 60
 QY 20 QQLQVQSGPELKEKGFVAKISCSAGYIFPNNGWVQAQKRGKLMWQMIINTTGEPT 79
 DB 61 ADDKGRFAFSLETSASVAYIQINNLKEDTATFCA--LVGNSPKGFANWQCGITLVYS 118
 QY 80 ADDKGRFAFSLETSASVAYIQINNLKEDTATFCA--LVGNSPKGFANWQCGITLVYS 139
 DB 119 A 119
 QY 140 S 140
 DB 140 S 140
 RESULT 14
 AA664257 standard; Protein; 140 AA.
 XX AA664257;
 AC AA664257;
 DT 25-MAR-2003 (updated)
 DT 31-0UL-1995 (first entry)

DT 25-MAR-2003 (updated)
 DT 31-0UL-1995 (first entry)
 DE MHC-II MAb 1243 heavy chain.
 DE MHC-II MAb 1243 heavy chain.
 DE 1243; heavy chain; VH; monoclonal antibody; MAb; MHC-II;
 DE major histocompatibility complex class II; immunosuppressive;
 DE variable region; FC receptor 1; FcRI; antibody engineering;
 DE cancer; immunotherapy.
 OS Mus sp.
 PN MO9429451-A2.
 XX MO9429451-A2.
 PD 22-DEC-1994.
 XX 15-JUN-1994; 94MO-GB01290.
 XX 16-JUN-1993; 93GB-0012415.
 PR 27-JUN-1994; 94GB-0001597.
 PR 09-FEB-1994; 94GB-0002439.
 PR 29-MAR-1994; 94GB-0002424.
 PR 29-MAR-1994; 94GB-0002422.
 XX (CLUT) CELTECH LTD.
 FA Atrial DS, Bodmer WM, Emeage JS, Morgan SA;
 DR WFI; 1995-036409/05.
 DR N-PSDB; AA080426.
 PT New antibodies with altered ability to fix complement - having
 PT one or more amino acid residues in the N-terminal region of the
 PT constant chain heavy domain altered
 XX Disclosure; Fig. 3; 91pp; English.
 CC cDNA for mouse anti-human MHC-II MAb 1243 (ATCC HB 55) heavy chain
 CC variable region was cloned by PCR. Clone p1702 was obtained that
 CC contained a VH insert having the sequence given in AA080426; the
 CC amino acid sequence of the heavy chain variable region of the
 CC antibodies has been prepared that retain immunosuppressive
 CC properties but show reduced binding to FcRI.
 CC (Updated on 25-MAR-2003 to correct FN field.)
 XX Sequence 140 AA:
 SQ
 Query Match 84.5%; Score 546; DB 16; Length 140;
 Best Local Similarity 83.5%; Pred. No. 4,1e-38;
 Matches 10; Conservative 6; Mismatches 10; Indels 2; Gaps 1;
 Db 1 EYKLVESGPELKEKGFVAKISCSAGYIFPNNGWVQAQKRGKLMWQMIINTTGEPT 60
 QY 20 QQLQVQSGPELKEKGFVAKISCSAGYIFPNNGWVQAQKRGKLMWQMIINTTGEPT 79
 DB 61 ADDKGRFAFSLETSASVAYIQINNLKEDTATFCA--LVGNSPKGFANWQCGITLVYS 118
 QY 80 ADDKGRFAFSLETSASVAYIQINNLKEDTATFCA--LVGNSPKGFANWQCGITLVYS 139
 DB 119 A 119
 QY 140 S 140
 DB 140 S 140
 RESULT 15
 AA637717 standard; Protein; 138 AA.
 XX AA637717;
 AC AA637717;
 DT 25-MAR-2003 (updated)
 DT 30-SEP-1993 (first entry)

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DE Mouse 4C10 anti-idiotypic Ab heavy chain V region.
XX
XX MA1A; monoclonal antibody; hybridoma; organ transplant rejection;
KM immuno-modulator; cancer; treatment; diagnosis; melanoma;
KM anti-cancer immunity; enhancement; suppression.
OS Mus musculus.
XX
XX WC0310221-A1.
XX
XX 27-MAY-1993.
XX
XX 12-NOV-1992; 92MO-US10166.
XX
XX 13-NOV-1991; 91US-0791934.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Hastings A. Irie RP. Morrison SL;
XX WPI, 1993-182538/22.
XX
XX Chimeric murine-human anti-idiotypic monoclonal antibodies -
XX useful as immuno-modulators for treating and diagnosing cancers,
XX and for suppressing organ transplant rejection and autoimmune
XX diseases.
XX
XX Disclosure; Page 33; 46DP; English.
XX
XX The sequence is that of the 4C10 anti-idiotypic Ab heavy chain V region
XX of mouse. This sequence is a complement of a murine anti-idiotypic V
XX anti-idiotypic antibody (MA1A). The MA1A elicits an anti-ganglioside
XX response and produces antibodies which induce cytotoxic destruction
XX of cancer cells bearing the gangliosides. It can be used for treating
XX of cancer cells bearing the gangliosides. This sequence is a complement
XX to enhance anti-cancer immunity/ suppress organ transplant rejection and
XX suppress autoimmune disease. The MA1A can also be used in the diagnosis
XX of cancers.
XX (updated on 15-MAR-2003 to correct PN field.)
XX
XX Sequence 138 AA;
XX
XX Query Match      84.2%; Score 544; E 14; Length 138;
XX Best Local Similarity 84.0%; Pred. No. 5.9e-38;
XX Matches 100; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
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XX 11111111111111111111111111111111111111111111111111111
XX Db 80 TEFKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 138
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Search completed: November 7, 2003, 07:26:59
 Job time : 55.3178 secs

GenCore version 5.1.6
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OW protein - protein search, using SW method

Run on: November 7, 2003, 07:30:19 / Search time 104.383 seconds

(without alignments)
195.799 Million cell updates/sec

Title: US-09-661-992b-82_COPY_1_119

Perfect score: 646
Sequence: 1 EVKLIVSGEHLKKKRGKRWKLT.....GNSPGFAVWGQGLVATSA 119

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 644079 seqs, 17174922 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Copy Length	DB ID	Description
1	552	85.4	250	10	US-09-887-853-2
2	552	85.4	138	12	US-10-142-744-35
3	532.5	82.4	116	12	US-10-138-727A-18
4	532.5	82.4	116	12	US-10-268-883-9
5	532.5	82.4	117	12	US-10-268-883-8
6	532.5	82.4	117	12	US-09-887-853-6
7	532.5	82.4	117	12	US-09-887-853-6
8	528.5	82.0	253	10	US-09-971-843-2
9	528.5	81.8	118	12	US-10-127-990-124
10	528.5	81.5	116	12	US-10-138-727A-2
11	526	81.4	119	12	US-10-268-883A-26
12	526	81.4	119	12	US-10-268-883A-26
13	526	81.4	119	12	US-10-268-883A-26
14	526	81.4	119	12	US-10-268-883A-26
15	525	81.3	138	11	US-09-977-883A-13

16	522.5	80.9	116	12	US-10-138-727A-25	Sequence 25, Appl
17	522	80.8	123	9	US-09-056-1608-9	Sequence 9, Appl1
18	522	80.8	113	12	US-10-234-671-9	Sequence 9, Appl1
19	520.5	80.6	118	12	US-09-949-553-106	Sequence 106, Appl
20	520.5	80.6	118	12	US-09-949-553-106	Sequence 106, Appl
21	520	80.5	138	11	US-09-977-883A-156	Sequence 156, Appl
22	516.5	80.0	116	12	US-10-138-727A-18	Sequence 18, Appl
23	516.5	80.0	116	12	US-10-310-713-20	Sequence 20, Appl
24	516.5	80.0	116	12	US-10-310-713-20	Sequence 20, Appl
25	515	79.9	123	10	US-09-948-059-41	Sequence 41, Appl
26	515	79.7	121	10	US-09-965-099-111	Sequence 11, Appl
27	515	79.7	121	10	US-10-051-852-7	Sequence 7, Appl1
28	515	79.7	121	14	US-10-051-852-111	Sequence 11, Appl
29	515	79.7	123	14	US-10-051-852-111	Sequence 11, Appl
30	515	79.7	123	14	US-10-051-852-111	Sequence 11, Appl
31	513	79.4	138	11	US-09-977-883A-21	Sequence 21, Appl
32	512.5	79.3	116	12	US-10-138-727A-24	Sequence 24, Appl
33	512.5	79.3	116	12	US-10-138-727A-24	Sequence 24, Appl
34	510.5	79.0	116	12	US-09-867-719C-8	Sequence 8, Appl1
35	509.5	78.9	116	12	US-10-138-727A-23	Sequence 23, Appl
36	507	78.5	135	11	US-09-967-719C-8	Sequence 8, Appl1
37	506.5	78.4	116	12	US-10-138-727A-20	Sequence 20, Appl
38	500	77.4	119	11	US-09-977-883A-80	Sequence 80, Appl
39	499.5	77.3	116	12	US-10-138-727A-22	Sequence 22, Appl
40	499.5	77.3	116	12	US-10-138-727A-22	Sequence 22, Appl
41	499.5	77.3	116	12	US-10-138-727A-22	Sequence 22, Appl
42	499.5	77.3	116	12	US-10-138-727A-22	Sequence 22, Appl
43	494.5	76.5	122	11	US-09-862-745-32	Sequence 32, Appl
44	493.5	76.4	116	12	US-10-138-727A-19	Sequence 19, Appl
45	491	76.0	117	12	US-10-138-727A-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-887-853-2
Sequence 2, Application US/09887853
Patent No. US2002016875A1
GENSEC: R08CON: R08CON
APPLICANT: R08CON, James S.
Houston, L. L.
R08CON, David B.
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
STREET: R08CON, Place, 55 State Street
CITY: Boston
COUNTY: Massachusetts
COUNTRY: USA
COMPUTER RESOLVED FOR:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887,853
FILING DATE: 11-Jun-2001
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/133,804
FILING DATE: Unknown
ATTORNEY: Unknown
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELEPHONE: 617-248-7277
TELEFAX: 617-248-7100

QY 61 ADDRESS: PATENT & TRADEMARK OFFICE, WASHINGTON, DC 20503-1400
 DB 61 ADDRESS: PATENT & TRADEMARK OFFICE, WASHINGTON, DC 20503-1400
 QY 118 SA 119
 DB 117 SA 118
 RESULT 5
 US-10-266-883-8
 Sequence 8, Application US/10268833
 Publication No. US2003013862A1
 Applicant: Tso, J
 Applicant: Green, Jennifer Macphace
 TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
 CURRENT FILING DATE: 2003-03-26 US/0266,883
 PRIOR APPLICATION NUMBER: US/00/266,883
 PRIOR APPLICATION NUMBER: US/98/60/329,178
 PRIOR APPLICATION NUMBER: US/96/60/331,965
 PRIOR FILING DATE: 2001-11-21
 NUMBER OF SEQ ID NOS: 16
 SEQUENCE CHARACTERISTICS: SEQ ID NOS: 1-16
 LENGTH: 137
 TYPE: PRT
 US-10-266-883-8
 ORIGINATOR: Mause
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 Matches 100; Conservative 6; Mismatches 3; Indels 7; Gaps 2
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 QY 61 ADDRESS: PATENT & TRADEMARK OFFICE, WASHINGTON, DC 20503-1400
 DB 80 ADDRESS: PATENT & TRADEMARK OFFICE, WASHINGTON, DC 20503-1400
 QY 118 SA 119
 DB 116 SA 137
 RESULT 6
 US-09-887-863-6
 Sequence 6, Application US/0987863
 Patent No. US20020168175A1
 GENERAL INFORMATION:
 APPLICANT: Huseon, James S.
 Huseon, L. L.
 Huseon, L. L.
 TITLE OF INVENTION: Biosynthetic Binding Proteins For
 Ring David B.
 ADDRESS: Tasea, Hurwitz & Traheault/Patent Department
 CORRESPONDENCE ADDRESSES:
 ADDRESS: Tasea, Hurwitz & Traheault/Patent Department
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 SOFTWARE: Patent Release #1.0, Version #1.25
 SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA
 APPLICATION NUMBER: US/09/887,863
 FILING DATE: 21-Jun-2001
 CLASSIFICATION: (unknown)
 PRIOR APPLICATION DATA: US/08/133,804
 FILING DATE: (unknown)
 ATTORNEY/AGENT INFORMATION:
 NAME: Kaley, Robin D.
 TELEPHONE: 617-248-1477
 TELEPHONE: 617-248-1477
 TELEPHONE: 617-248-1477
 INFORMATION FOR SEQ ID NOS: 1-16
 SEQUENCE CHARACTERISTICS:
 LENGTH: 243 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-887-863-6
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 Best Local Similarity 82.4%; Score 530; DB 10; Length 243;
 Matches 98; Conservative 10; Mismatches 7; Indels 4; Gaps 1
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 DB 1 EVLTVEGSPRLKSGEYVYKSCAGSYIFNTGNNWYKQAKPKQKLNKNNWNTYTGPT 60
 QY 61 ADDRESS: PATENT & TRADEMARK OFFICE, WASHINGTON, DC 20503-1400
 DB 61 ADDRESS: PATENT & TRADEMARK OFFICE, WASHINGTON, DC 20503-1400
 RESULT 7
 US-09-971-543-8
 Sequence 8, Application US/09971543
 Patent No. US2001014544A1
 GENERAL INFORMATION:
 APPLICANT: FUCHTNER, ANDREAS
 APPLICANT: HUSEON, JAMES S.
 TITLE OF INVENTION: NOVEL METHOD FOR THE STABILIZATION OF CHEMIC
 TITLE OF INVENTION: STABILIZED ANTI-B2M-2 B-CELL FRAGMENT
 CURRENT FILING DATE: 2001-10-04
 PRIOR APPLICATION NUMBER: PCT/EP00/03176
 PRIOR APPLICATION NUMBER: US/99/10/7030.1
 PRIOR FILING DATE: 1999-04-09
 NUMBER OF SEQ ID NOS: 12
 SEQUENCE CHARACTERISTICS: SEQ ID NOS: 1-12
 LENGTH: 116
 TYPE: PRT
 US-09-971-543-8
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 Matches 100; Conservative 6; Mismatches 3; Indels 3; Gaps 2
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 QY 61 ADDRESS: PATENT & TRADEMARK OFFICE, WASHINGTON, DC 20503-1400
 DB 61 ADDRESS: PATENT & TRADEMARK OFFICE, WASHINGTON, DC 20503-1400

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RESULT 8
US-09-971-843-2
Sequence 2, Application US/09971543
GENERAL INFORMATION
APPLICANT: PLUCKTHIN, ANDREAS
APPLICANT: KROEMER, ANDREAS
TITLE OF INVENTION: NOVEL METHOD FOR THE STABILIZATION OF CHEMIC
TITLE OF INVENTION: IMMUNOGLOBULIN OR IMMUNOGLOBULIN FRAGMENTS, AND
CURRENT APPLICATION NUMBER: US/09/971,543
CURRENT FILING DATE: 2001-10-04
PRIOR FILING DATE: 2000-04-10
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 253
TYPE: PRT
ORGANISM: Mus sp.
US-09-971-843-2
Query Match
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Matches 100; Conservative 8; Mismatches 8; Indels 3; Gaps 2;
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RESULT 9
US-10-127-890-124
Sequence 2, Application US/10127890
GENERAL INFORMATION
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
CURRENT APPLICATION NUMBER: 173
CURRENT FILING DATE: 2001-05-03
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 116
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: KS VH mouse
US-10-138-727A-2
Query Match
Best Local Similarity 81.5%; Pred. No. 2.5e-39;
Matches 97; Conservative 11; Mismatches 8; Indels 3; Gaps 2;
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RESULT 11
US-10-138-727A-26
Sequence 2, Application US/0108727A
Publication No. US20030127054A1
GENERAL INFORMATION:
APPLICANT: Gilles, Stephen
INVENTOR: Gilles, Stephen
TITLE OF INVENTION: Recombinant Tumor Specific Antibody and Use Thereof
FILE REFERENCE: Lex-019
CURRENT FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 60/280,564
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 26: cdc25m version 3.0
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: KS VR mouse
US-10-138-727A-26

Query Match
Best Local Similarity 81.5%; Score 526.5; DB 12; Length 116;
Best Local Similarity 81.5%; Pred. No. 2.5e-39;
Matches 97; Conservative 11; Mismatches 8; Indels 3; Gaps 2;
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RESULT 12
US-10-268-883-3
Sequence 2, Application US/1026883
Publication No. US2003013862A1
GENERAL INFORMATION:
APPLICANT: Teo, J. Yun
INVENTOR: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
FILE REFERENCE: 05882,0062,JP2001,US/10/268,883
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US60/331,965
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 119
TYPE: PRT
ORGANISM: Mouse
US-10-268-883-3

Query Match
Best Local Similarity 81.4%; Score 526; DB 12; Length 119;
Best Local Similarity 81.4%; Pred. No. 3.2e-39;
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RESULT 13
US-10-269-010-1
Sequence 2, Application US/10269010
Publication No. US20030096285A1
GENERAL INFORMATION:
APPLICANT: Teo, J.
INVENTOR: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HLA-DR ANTIBODIES AND THE METHODS OF USE THEREOF
FILE REFERENCE: 05882,0062,JP2001,US/10/269,010
CURRENT APPLICATION NUMBER: US/10/269,010
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US60/331,965
PRIOR FILING DATE: 2001-10-11
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 119
TYPE: PRT
ORGANISM: Mouse
US-10-269-010-1

Query Match
Best Local Similarity 82.4%; Score 526; DB 15; Length 119;
Best Local Similarity 82.4%; Pred. No. 2.8e-39;
Matches 98; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
QY 1 EVYLVSQPELKKSGEYVISCASGIFPTNIGMNVQVQKGLKMGWIMINTTGGPT 60
1 QIQLVSGPELKKSGEYVISCASGIFPTNIGMNVQVQKGLKMGWIMINTTGGPT 60
QY 61 ADPDKRPAEISLTSASVYIOLINLNKEDMTATFCALYKNSPGKAYWGOQTLYTSA 119
61 ADPDKRPAEISLTSASVYIOLINLNKEDMTATFCATLTTITTYFWOOGTTLTWS 119

RESULT 14
US-10-268-883-2
Sequence 2, Application US/1026883
Publication No. US2003013862A1
GENERAL INFORMATION:
APPLICANT: Teo, J. Yun
INVENTOR: Green, Jennifer Macphate
TITLE OF INVENTION: Anti-HLA-DR Antibodies and the Methods of Using Thereof
FILE REFERENCE: 05882,0062,JP2001,US/10/268,883
CURRENT APPLICATION NUMBER: US/10/268,883
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: US60/331,965
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-21
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 138
TYPE: PRT
ORGANISM: Mouse
US-10-268-883-2

Query Match
Best Local Similarity 81.4%; Score 526; DB 12; Length 138;
Best Local Similarity 82.4%; Pred. No. 3.2e-39;
Matches 98; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
QY 1 EVYLVSQPELKKSGEYVISCASGIFPTNIGMNVQVQKGLKMGWIMINTTGGPT 60
1 EVYLVSQPELKKSGEYVISCASGIFPTNIGMNVQVQKGLKMGWIMINTTGGPT 60
Db 20 QIQLVSGPELKKSGEYVISCASGIFPTNIGMNVQVQKGLKMGWIMINTTGGPT 79
QY 61 ADPDKRPAEISLTSASVYIOLINLNKEDMTATFCALYKNSPGKAYWGOQTLYTSA 119
80 ADPDKRPAEISLTSASVYIOLINLNKEDMTATFCATLTTITTYFWOOGTTLTWS 128


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BSSOUR 15
US-09-977-283A-13
; Sequence 13: Application us/09/977283A
; Publication No. US20030031664A1
; GENERAL INFORMATION:
; INVENTOR: "US-09-977-283A"
; FILE REFERENCE: 0609.4320003
; TITLE OF INVENTION: Composition and Method for Enhancing Fibrinolysis
; CURRENT APPLICATION NUMBER: US/09/977,283A
; PRIORITY DATE: 2001-06-16
; PRIORITY NUMBER: 06/536,000
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/926,356
; INVENTOR: "US-09-977-283A"
; PRIOR FILING DATE: 1996-09-20
; INVENTOR: "US-09-977-283A"
; SOFTWARE: Patent version 3.1
; SEQ ID NO 13
; LENGTH: 138
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (138)
; OTHER INFORMATION: Alpha-2 Antiplasmin Antibody
; NAME/KEY: MISC_FEATURE
; LOCATION: (138)
; OTHER INFORMATION: May be either Asp or Ala
; NAME/KEY: MISC_FEATURE
; LOCATION: (141) - (14)
; OTHER INFORMATION: May be either Asn or Thr
; US-09-977-283A-13

Query Match 81.34; Score 525; DB 11; Length 138;
Similarity 89.78; Pos. 46-59;13;
Matches 96; Conservative 10; Mismatches 13; Indels 0; Gaps 0,

QY 1 EVKLVESPEELKFGQGVYISCKASGYIFNYGSMWKAPOKGLKMWGMIYTTGSEFY 60
DB 20 QKQVQSSSHAKGSEYVMSCKASGYIFKIGSMWKAPOKGLKMWGMIYNTSSSEFY 79
QY 61 ADPKGEFAFSEFTSASTVYIQNNLKNEDTATFCGLVGSFKGFAPWQGGTLYTGA 119
DB 80 AEFKNGKNSGLSISGNTVQINLKAGSESNITFCGLVWYGGTAMDWQGGTLYTGS 138

Search completed: November 7, 2003, 08:16:50
Job time : 104.383 secs

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Qy 61 AADPGKFAFSLFSAFSAFVQINNLNEDATFYFCA---LYGNSPKGFAGVAGQGLVLT 116
 Db 63 AEFKNGKFAFSLFSAFSAFVQINNLNEDATFYFCA---GFANMGQGLVLT 118
 Qy 117 VSA 119
 Db 119 VSA 121

RESULT 2

US-08-461-184-8 Application US/08/461184
 Patent No. 5631158

GENERAL INFORMATION:
 APPLICANT: DDBAI, HAWAII
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
 TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 STREET: 45 SOUTH STREET
 CITY: HOPEKINTON
 STATE: MA
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC/DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 05/08/461,184
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/143,498
 ATTORNEY/AGENT INFORMATION:
 NAME: KELLEY, ROBIN D
 REGISTRATION NUMBER: 34,637
 TELEPHONE: 617/248-7000
 TELEFAX: 617/248-7100
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 250 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match 85.4%; Score 552; DB 1; Length 250;
 Best Local Similarity: 85.4%; Pcd No. 2,2e-43;
 Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;

Qy 1 EVLVDSGELKPKKGVYVSKASGVTFYNNQVWQAPKGLKMMGNINVTGGPT 60
 Db 3 EICLVDSGELKPKKGVYVSKASGVTFYNNQVWQAPKGLKMMGNINVTGGPT 62
 Qy 61 AADPGKFAFSLFSAFSAFVQINNLNEDATFYFCA---LYGNSPKGFAGVAGQGLVLT 116
 Db 63 AEFKNGKFAFSLFSAFSAFVQINNLNEDATFYFCA---GFANMGQGLVLT 118
 Qy 117 VSA 119
 Db 119 VSA 121

RESULT 3
 US-08-463-674-8

Sequence 8, Application US/08/463675
 Patent No. 5658723
 GENERAL INFORMATION:
 APPLICANT: DDBAI, HAWAII
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
 TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 STREET: 45 SOUTH STREET
 CITY: HOPEKINTON
 STATE: MA
 COUNTRY: USA

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/463,675
 FILING DATE: 05-08-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/143,498
 ATTORNEY/AGENT INFORMATION:
 NAME: KELLEY, ROBIN D
 REGISTRATION NUMBER: 34,637
 TELEPHONE: 617/248-7000
 TELEFAX: 617/248-7100
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 250 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match 85.4%; Score 552; DB 1; Length 250;
 Best Local Similarity: 85.4%; Pcd No. 2,2e-43;
 Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;

Qy 1 EVLVDSGELKPKKGVYVSKASGVTFYNNQVWQAPKGLKMMGNINVTGGPT 60
 Db 3 EICLVDSGELKPKKGVYVSKASGVTFYNNQVWQAPKGLKMMGNINVTGGPT 62
 Qy 61 AADPGKFAFSLFSAFSAFVQINNLNEDATFYFCA---LYGNSPKGFAGVAGQGLVLT 116
 Db 63 AEFKNGKFAFSLFSAFSAFVQINNLNEDATFYFCA---GFANMGQGLVLT 118
 Qy 117 VSA 119
 Db 119 VSA 121

RESULT 4
 US-08-464-589-8 Application US/08/464589
 Patent No. 5707262
 GENERAL INFORMATION:
 APPLICANT: DDBAI, HAWAII
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
 TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 STREET: 45 SOUTH STREET
 CITY: HOPEKINTON

```

COUNTRY: USA
ZIP: 07148
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/461/838
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA: US 69/143-498
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
TELEPHONE: 617-248-7477
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7100
FAX: 617-248-7100
INSTRUMENT FOR SERIAL FILING: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-08-461-838-2
Query Match 85.4%; Score 552; DB 1; Length 250;
Best Local Similarity 85.4%; Pred. No. 2,28-43;
Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;
CY 1 EVYLVSSGRLVKEKPKVYKICQAGTFFNFGMMWYONRQKGLMGMINTTGGPT 60
DB 3 EYLVSSGRLVKEKPKVYKICQAGTFFNFGMMWYONRQKGLMGMINTTGGPT 62
CY 61 ADPRGFAVLSLTSATVYVQNNLNLEDTVPCA---LVGNSRPPVYVQQTIVT 116
DB 63 AERKGRFAVLSLTSATVYVQNNLNLEDTVPCA---LVGNSRPPVYVQQTIVT 118
CY 117 VSA 119
DB 119 VSA 121
DB
RESULT 5
US-08-461-838-2
Sequence 2, Application US/08461838
Patent No. 5837846
GENERAL INFORMATION:
APPLICANT: Opesman, James S.
APPLICANT: Houston, L. L.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA: US/08/461/838
ADDRESSER: Teets, Burwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/461/838
FILING DATE:
CLASSIFICATION: 434
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
TELEPHONE: 617-248-7477
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7100
FAX: 617-248-7100
INSTRUMENT FOR SERIAL FILING: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-08-461-838-2
Query Match 85.4%; Score 552; DB 1; Length 250;
Best Local Similarity 85.4%; Pred. No. 2,28-43;
Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;
CY 1 EVYLVSSGRLVKEKPKVYKICQAGTFFNFGMMWYONRQKGLMGMINTTGGPT 60
DB 3 EYLVSSGRLVKEKPKVYKICQAGTFFNFGMMWYONRQKGLMGMINTTGGPT 62
CY 61 ADPRGFAVLSLTSATVYVQNNLNLEDTVPCA---LVGNSRPPVYVQQTIVT 116
DB 63 AERKGRFAVLSLTSATVYVQNNLNLEDTVPCA---LVGNSRPPVYVQQTIVT 118
CY 117 VSA 119
DB 119 VSA 121
DB

```

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FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
TELEPHONE: 617-248-7477
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7100
FAX: 617-248-7100
INSTRUMENT FOR SERIAL FILING: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-08-461-838-2
Query Match 85.4%; Score 552; DB 1; Length 250;
Best Local Similarity 85.4%; Pred. No. 2,28-43;
Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;
CY 1 EVYLVSSGRLVKEKPKVYKICQAGTFFNFGMMWYONRQKGLMGMINTTGGPT 60
DB 3 EYLVSSGRLVKEKPKVYKICQAGTFFNFGMMWYONRQKGLMGMINTTGGPT 62
CY 61 ADPRGFAVLSLTSATVYVQNNLNLEDTVPCA---LVGNSRPPVYVQQTIVT 116
DB 63 AERKGRFAVLSLTSATVYVQNNLNLEDTVPCA---LVGNSRPPVYVQQTIVT 118
CY 117 VSA 119
DB 119 VSA 121
DB
RESULT 5
US-08-461-386-2
Sequence 2, Application US/0846386
Patent No. 5837846
GENERAL INFORMATION:
APPLICANT: Opesman, James S.
APPLICANT: Houston, L. L.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA: US/08/461/386
ADDRESSER: Teets, Burwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/461/386
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
TELEPHONE: 617-248-7477
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7100
FAX: 617-248-7100
INSTRUMENT FOR SERIAL FILING: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
US-08-461-386-2
Query Match 85.4%; Score 552; DB 1; Length 250;
Best Local Similarity 85.4%; Pred. No. 2,28-43;
Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;
CY 1 EVYLVSSGRLVKEKPKVYKICQAGTFFNFGMMWYONRQKGLMGMINTTGGPT 60
DB 3 EYLVSSGRLVKEKPKVYKICQAGTFFNFGMMWYONRQKGLMGMINTTGGPT 62
CY 61 ADPRGFAVLSLTSATVYVQNNLNLEDTVPCA---LVGNSRPPVYVQQTIVT 116
DB 63 AERKGRFAVLSLTSATVYVQNNLNLEDTVPCA---LVGNSRPPVYVQQTIVT 118
CY 117 VSA 119
DB 119 VSA 121
DB

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TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-461-386-2

Query Match 85.4%; Score 552; DB 2; Length 250;

Best Local Similarity 85.4%; Pred. No. 2,26-43;

Matches 105; Conservative 5; Mismatches 5; Indels 8; Gaps 2;

1 EVKLVESGPELKKRPTVYKSCAGYFFNYGMMVYKQAKGKLMGKINNTTGEPT 60
119 VSA 119

3 EIQVQSGPELKKRPTVYKSCAGYFFNYGMMVYKQAKGKLMGKINNTTGEPT 62
119 VSA 119

61 ADDPKKFPFELTSTASPAVLIQINLIMEDTATFCQKPTTVG---LQNSKSPKAVWQGLTV 116
119 VSA 119

63 ABEKQKFNFLSTASPAVLIQINLIMEDTATFCQKPTTVG---GFANWQGLTV 118
119 VSA 121

US-08-356-786-16
Sequence 16, Application US/08356786

Patient No. 587705
INVENTOR: Hutton, James S.
APPLICANT: Hutton, James S.
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,923
TELEPHONE: (617) 248-7000

REFERENCE/ACCESSION NUMBER: CDP-053
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE: 16
LENGTH: 622 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-356-786-16
Sequence 16, Application US/08356786

Patient No. 587705
INVENTOR: Hutton, James S.
APPLICANT: Hutton, James S.
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,923
TELEPHONE: (617) 248-7000

REFERENCE/ACCESSION NUMBER: CDP-053
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE: 16
LENGTH: 622 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-356-786-16
Sequence 16, Application US/08356786

Patient No. 587705
INVENTOR: Hutton, James S.
APPLICANT: Hutton, James S.
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,923
TELEPHONE: (617) 248-7000

REFERENCE/ACCESSION NUMBER: CDP-053
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE: 16
LENGTH: 622 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-356-786-16
Sequence 16, Application US/08356786

Patient No. 587705
INVENTOR: Hutton, James S.
APPLICANT: Hutton, James S.
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,923
TELEPHONE: (617) 248-7000

REFERENCE/ACCESSION NUMBER: CDP-053
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE: 16
LENGTH: 622 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-356-786-16
Sequence 16, Application US/08356786

DB 3 EIQVQSGPELKKRPTVYKSCAGYFFNYGMMVYKQAKGKLMGKINNTTGEPT 62
QY 61 ADDPKKFPFELTSTASPAVLIQINLIMEDTATFCQKPTTVG---LQNSKSPKAVWQGLTV 116
DB 63 ABEKQKFNFLSTASPAVLIQINLIMEDTATFCQKPTTVG---GFANWQGLTV 118
QY 117 VSA 119
DB 119 VSA 121

US-08-569-147-76
Sequence 8, Application US/08569147

Patient No. 6180377
INVENTOR: HUMANISED ANTIBODIES
APPLICANT: HUMANISED ANTIBODIES
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,923
TELEPHONE: (617) 248-7000

REFERENCE/ACCESSION NUMBER: CDP-053
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE: 8
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-569-147-76
Sequence 8, Application US/08569147

Patient No. 6180377
INVENTOR: HUMANISED ANTIBODIES
APPLICANT: HUMANISED ANTIBODIES
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,923
TELEPHONE: (617) 248-7000

REFERENCE/ACCESSION NUMBER: CDP-053
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE: 8
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-569-147-76
Sequence 8, Application US/08569147

Patient No. 6180377
INVENTOR: HUMANISED ANTIBODIES
APPLICANT: HUMANISED ANTIBODIES
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,923
TELEPHONE: (617) 248-7000

REFERENCE/ACCESSION NUMBER: CDP-053
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE: 8
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-569-147-76
Sequence 8, Application US/08569147

Patient No. 6180377
INVENTOR: HUMANISED ANTIBODIES
APPLICANT: HUMANISED ANTIBODIES
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,923
TELEPHONE: (617) 248-7000

REFERENCE/ACCESSION NUMBER: CDP-053
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE: 8
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-569-147-76
Sequence 8, Application US/08569147

Patient No. 6180377
INVENTOR: HUMANISED ANTIBODIES
APPLICANT: HUMANISED ANTIBODIES
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,923
TELEPHONE: (617) 248-7000

REFERENCE/ACCESSION NUMBER: CDP-053
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE: 8
LENGTH: 140 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-569-147-76
Sequence 8, Application US/08569147

Patient No. 6180377
INVENTOR: HUMANISED ANTIBODIES
APPLICANT: HUMANISED ANTIBODIES
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,923
TELEPHONE: (617) 248-7000

APPLICANT: Russell, David R
 TITLE OF INVENTION: Method for Producing Antibodies in Plant
 NUMBER OF SEQUENCES: 9
 ADDRESSER: Quarles and Brady
 STREET: PO Box 2113
 CITY: Madison
 COUNTRY: United States of America
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIAN TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: US/08/279,772A
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 11,229-9097-1
 TELEPHONE/DOCKET INFORMATION:
 TELEPHONE: 608-251-9166
 INFORMATION FOR SEQ ID NO: 6:
 SOURCE CHARACTERISTICS:
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-279-772A-6
 Query Match 84.1%; Score 543.5; DB 3; Length 252;
 Best Local Similarity 84.3%; Pred. No. 1.3e-42;
 Matches 102; Conservative 6; Mismatches 8; Indels 3; Gaps 2;
 QY 1 EVLVESPEELKATGVETVLSCKAGSYFTNGMNTWQAEKGLMNGMINTTGEPT 60
 DB 131 QIQVSGPELKEPEETVLSCKAGSYFTNGMNTWQAEKGLMNGMINTTGEPT 190
 QY 61 ADDPKRPAFLSTASTVYLNINLMDNATFPC-LYNSPSPKPAWGGCTLVTS 118
 DB 191 ADDPKRPAFLSTASTVYLNINLMDNATFPCSTYNS-KADYWGCTLVTS 249
 QY 119 A 119
 DB 250 S 250
 RESULT 10
 US-08-902-486-9
 Patent No. 6140075
 GENERAL INFORMATION:
 APPLICANT: Russell, David R
 TITLE OF INVENTION: METHOD FOR PRODUCING ANTIBODIES AND
 TITLE OF INVENTION: PROTEIN TOXINS IN PLANT CELLS
 NUMBER OF SEQUENCES: 15
 ADDRESSER: Quarles & Brady
 STREET: 1 South Pinchney Street
 CITY: Madison
 COUNTRY: WI
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIAN TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 FILING DATE: US/08/902,486
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27386
 TELEPHONE/DOCKET INFORMATION:
 TELEPHONE: 608-251-5000
 INFORMATION FOR SEQ ID NO: 9:
 SOURCE CHARACTERISTICS:
 LENGTH: 252 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-902-486-9
 Query Match 84.1%; Score 543.5; DB 3; Length 252;
 Best Local Similarity 84.3%; Pred. No. 1.3e-42;
 Matches 102; Conservative 6; Mismatches 8; Indels 3; Gaps 2;
 QY 1 EVLVESPEELKATGVETVLSCKAGSYFTNGMNTWQAEKGLMNGMINTTGEPT 60
 DB 131 QIQVSGPELKEPEETVLSCKAGSYFTNGMNTWQAEKGLMNGMINTTGEPT 190
 QY 61 ADDPKRPAFLSTASTVYLNINLMDNATFPC-LYNSPSPKPAWGGCTLVTS 118
 DB 191 ADDPKRPAFLSTASTVYLNINLMDNATFPCSTYNS-KADYWGCTLVTS 249
 QY 119 A 119
 DB 250 S 250
 RESULT 11
 US-08-975-011-53
 Patent No. 6045793
 GENERAL INFORMATION:
 APPLICANT: Neeson, Diana L.
 ADDRESSER: Neeson, Diana L.
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESSES:
 ADDRESSER: Townsend and Townsend and Crew LLP
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIAN TYPE: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: US/08/975,811
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend and Townsend and Crew LLP
 REGISTRATION NUMBER: NO ECT/US97/02388
 FILING DATE: 19-FEB-1997
 APPLICATION NUMBER: US 60/011,800
 FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Paris, Susan K.

REGISTRATION NUMBER: 41,739
 REFERENCE/DOCKET NUMBER: 015280-244100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0100
 TELEFAX: (415) 576-0100
 INFORMATION FOR SEQ ID NO: 53:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 365 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-875-811-53

Query Match 83.5%; Score 539.5; DB 3; Length 365;
 Best Local Similarity 86.6%; Pred. No. 4,5e-42;
 Matches 103; Conservative 5; Mismatches 8; Indels 3; Gaps 2;

1 EVLVESGPEKPKETVYKSKASGYTFYNGMMVKQAKGKGLKMGKINVTGERTY 60
 DB 119 QVLSQSGPEKPKETVYKSKASGYTFYNGMMVKQAKGKGLKMGKINVTGERTY 178
 QY 61 ADGKGRPSFELTSSAAYLQINLNKEDRTYFCARF-AIKG-DVWQGITVYSS 119
 DB 179 ADGKGRPSFELTSSAAYLQINLNKEDRTYFCARF-AIKG-DVWQGITVYSS 234

RESULT 12
 US-08-875-811-55
 Sequence 55; Application US/08875811
 Patent No. 6831217
 INVENTOR: Janda, Ralf
 APPLICANT: Rybak, Susanna M.
 APPLICANT: Newton, Diane L.
 APPLICANT: Roque, Luis
 APPLICANT: Roque, Luis
 TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS: 44 Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPILER: IBM PC compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Patent Release #1.0 Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/875,811
 PRIORITY: 1999-05-25
 CLASSIFICATION: 435-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/US97/02588
 PRIORITY: 1997-05-25
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/111,800
 FILING DATE: 21-FEB-1996
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 41,739
 REFERENCE/DOCKET NUMBER: 015280-244100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0100
 TELEFAX: (415) 576-0100
 INFORMATION FOR SEQ ID NO: 55:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 365 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-875-811-55

Query Match 83.5%; Score 539.5; DB 3; Length 366;
 Best Local Similarity 86.6%; Pred. No. 4,5e-42;
 Matches 103; Conservative 5; Mismatches 8; Indels 3; Gaps 2;
 QY 1 EVLVESGPEKPKETVYKSKASGYTFYNGMMVKQAKGKGLKMGKINVTGERTY 60
 DB 2 QVLSQSGPEKPKETVYKSKASGYTFYNGMMVKQAKGKGLKMGKINVTGERTY 61
 QY 61 ADGKGRPSFELTSSAAYLQINLNKEDRTYFCARF-AIKG-DVWQGITVYSS 119
 DB 62 ADGKGRPSFELTSSAAYLQINLNKEDRTYFCARF-AIKG-DVWQGITVYSS 117

RESULT 13
 US-09-318-786-35
 Sequence 35; Application US/09318786
 Patent No. 6842147
 INVENTOR: Janda, Ralf
 APPLICANT: Janda, Ralf
 APPLICANT: Janda, Ralf
 APPLICANT: Janda, Ralf
 APPLICANT: Janda, Ralf
 TITLE OF INVENTION: METHODS FOR DISPLAY OF HETEROLOGIC PROTEINS ON
 TITLE OF INVENTION: FILAMENTOUS PHAGE USING PVI AND PIX, COMPOSITIONS,
 TITLE OF INVENTION: VECTORS AND COMBINATORIAL LIBRARIES
 CURRENT APPLICATION NUMBER: US/09/318,786
 NUMBER OF SEQ ID NOS: 39
 FILING DATE: 1999-05-25
 SOFTWARE: Patent Ver. 2.1
 TYPE: PAT
 LENGTH: 160
 OTHER INFORMATION: Description of Artificial Sequence: fusion
 US-09-318-786-35

Query Match 83.0%; Score 535; DB 4; Length 160;
 Best Local Similarity 85.7%; Pred. No. 3,9e-42;
 Matches 102; Conservative 5; Mismatches 10; Indels 2; Gaps 2;
 QY 1 EVLVESGPEKPKETVYKSKASGYTFYNGMMVKQAKGKGLKMGKINVTGERTY 60
 DB 3 EVLSQSGPEKPKETVYKSKASGYTFYNGMMVKQAKGKGLKMGKINVTGERTY 62
 QY 61 ADGKGRPSFELTSSAAYLQINLNKEDRTYFCARF-AIKG-DVWQGITVYSS 119
 DB 63 ADGKGRPSFELTSSAAYLQINLNKEDRTYFCARF-AIKG-DVWQGITVYSS 119

RESULT 14
 US-08-483-7496-24
 Sequence 24; Application US/08483749A
 Patent No. 6035451
 INVENTOR: King, David B.
 APPLICANT: King, David B.
 TITLE OF INVENTION: MOLECULE-BINDING SITES OF ANTIBODY
 TITLE OF INVENTION: ANTIBODY SPECIFIC FOR CANCER ANTIGENS
 CORRESPONDENCE ADDRESS:
 ADDRESS: CHIRON CORPORATION
 STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
 STATE: CA
 COUNTRY: USA
 ZIP: 94662-8097
 COMPUTER READABLE FORM: disk
 OPERATING SYSTEM: IBM PC compatible
 US-08-483-7496-24

SOFTWARE: PatentIn Release #1.0, Version #1.10
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,749A
 PUBLICATION NUMBER: 2003/012,295
 CLASSIFICATION: 53c-2595
 ATTORNEY/AGENT INFORMATION:
 NAME: SWEENEY, PAUL B.
 ADDRESS: 1000 WASHINGTON ST., SUITE 1100
 TELEPHONE: (617) 601-2595
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: 0508-008
 TELEPHONE: (610) 601-2595
 INFORMATION FOR SEQ ID NO. 65-3542.24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 115 amino acids
 TYPE: amino acid
 TOPOLOGY: 1
 MOLECULE TYPE: protein
 US-08-483-749A-24

Query Match 82.0%; Score 530; DB 1; Length 115;
 Best Local Similarity 82.4%; Pval 1.9e-12; Mismatches 7; Indels 4; Gaps 1;
 Matches 99; Conservative 10; Mismatches 7; Indels 4; Gaps 1;

QY 1 EVLVYSGEELKKKGGTYKISCSASGYIFLYGNNVYQAPKGLMMNMINTTGGPT 60
 DB 1 EVLVYSGEELKKKGGTYKISCSASGYIFLYGNNVYQAPKGLMMNMINTTGGPT 60

QY 61 ADFFGKPSLSLSASNYQINNLNEDATATYCALVGNPGKPAVMGGTLVYSA 119
 DB 61 ADFFGKPSLSLSASNYQINNLNEDATATYCALVGNPGKPAVMGGTLVYSA 115

RESULT 15
 US-08-113-804-6
 Sequence 6, Application US/08133804
 Patent No. 5531224
 GENERAL INFORMATION:
 APPLICANT: Biogen, Inc., James S.
 APPLICANT: Oppermann, Hermann
 APPLICANT: Ring, David B.
 TITLE OF INVENTION: Biocytetic Binding Proteins For
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Tecca, Hurwitz & Thibault/Patent Department
 ADDRESS: 1000 State Place, 55 State Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP CODE: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: GENESYS/PC/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/133,804
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Kelley, Robin D.
 REGISTRATION NUMBER: 34,637
 TELEPHONE: (617) 248-7477
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-248-7100
 INVENTOR: 617-248-7100
 SEQUENCE CHARACTERISTICS:
 LENGTH: 243 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein
 US-08-113-804-6
 Query Match 82.0%; Score 530; DB 1; Length 243;
 Best Local Similarity 82.4%; Pval No. 2.2e-41;
 Matches 99; Conservative 17; Indels 4; Gaps 1;

QY 1 EVLVYSGEELKKKGGTYKISCSASGYIFLYGNNVYQAPKGLMMNMINTTGGPT 60
 DB 1 EVLVYSGEELKKKGGTYKISCSASGYIFLYGNNVYQAPKGLMMNMINTTGGPT 60

QY 61 ADFFGKPSLSLSASNYQINNLNEDATATYCALVGNPGKPAVMGGTLVYSA 119
 DB 61 ADFFGKPSLSLSASNYQINNLNEDATATYCALVGNPGKPAVMGGTLVYSA 115

Search completed: November 7, 2003, 07:30:07
 CDD time : 18.4786 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on:

November 7, 2003, 07:21:18, Search time 13.9866 Seconds

742,504 Million cell updates/sec

Title:

US-09-661-992b-82_COPY_135_242

RefSeq score:

1 DQ4Y0SPRFLVMSQDWT.....QQDY0SPRFLVMSQDWT 108

Sequence:

BL0SIN62

Scoring table:

Gapop 10.0, Gapex 0.5

Searched:

283308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters:

283308

Minimum hit seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

1. PIR 76.4
2. PIR2.1
3. PIR3.1
4. PIR4.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	510.5	89.2	225	2	837484
2	487	85.1	127	2	837484
3	487	83.7	107	2	809964
4	473	82.7	115	2	837484
5	466	81.5	139	1	KW6511
6	456	79.7	107	2	D51285
7	450	78.5	107	2	D51285
8	445	79.5	119	2	P02455
9	443	77.8	107	2	832121
10	434	75.9	115	2	A25924
11	432.5	75.6	108	2	P03043
12	432.5	75.6	107	2	R10013
13	419	73.3	108	2	P10204
14	419	73.3	107	2	837484
15	412	72.0	107	2	A48155
16	412	72.0	107	2	837484
17	407	71.2	131	2	P10207
18	404	70.6	107	2	809967
19	404	70.6	108	2	A47159
20	402	70.3	220	2	A31790
21	399	69.8	136	1	KW6521
22	399	69.8	136	1	KW6521
23	398.5	69.7	135	2	K00023
24	398	69.6	108	2	B42047
25	396	69.2	107	2	B28195
26	396	69.2	108	2	B43371
27	394.5	69.0	108	2	P02454
28	394.5	69.0	115	2	838807
29	394	68.9	115	2	838807

30	383	68.7	98	2	BH1072	19 kappa chain - m
31	383	68.7	111	2	B37266	19 kappa chain - m
32	392	68.5	100	2	H36011	19 kappa chain - m
33	392	68.5	114	1	K41010	19 kappa chain - m
34	392	68.5	114	1	K41010	19 kappa chain - m
35	392	68.5	240	2	860684	19 kappa chain - m
36	391.5	68.4	113	2	841103	19 kappa chain - m
37	391.5	68.4	133	1	K3H017	19 kappa chain - m
38	391.5	68.4	113	2	D22770	19 kappa chain - m
39	391.5	68.4	133	1	K3H017	19 kappa chain - m
40	391	68.4	134	2	R12114	19 kappa chain - m
41	390	68.2	127	2	840367	19 kappa chain - m
42	389.5	68.1	107	2	836775	19 kappa chain - m
43	389.5	68.1	107	2	836775	19 kappa chain - m
44	389.5	68.1	118	2	P70356	19 kappa chain - m
45	389	68.0	112	2	E30538	19 kappa chain - m

ALIGNMENTS

RESULT 1

19 kappa chain - mouse (fragment)

C136266:US-09-661-992b-82_COPY_135_242

Cloned: US-09-661-992b-82_COPY_135_242

Reference number: 837484

Submitted to the EMBL Data Library, February 1993

Accession: F04584

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Matches 93; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

QY 2 IOMTOSPELVANADRYITTCASQSVSDVAMVQKQKQSGKLLMYASNRITVDP 61
 DB 22 IVMQTFKELVANSGRVITTCASQSVSDVAMVQKQKQSGKLLMYASNRITVDP 81
 QY 62 FTGSGVGTFPFTISTVOEDALVAYCOQDSPTFGGKLEIK 107
 DB 82 FTGSGVGTFPFTISTVOEDALVAYCOQDSPTFGGKLEIK 127

RESULT 3

Ig kappa chain V-1 region (105-26) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 12-Feb-1993 [sequence revision 12-Feb-1993 #extc_change 21-Jan-2000
 C/Accession: 5091964
 A/Title: Nucleotide sequence of the variable region of the heavy chain of the
 Eur. J. Immunol. 20: 771-777, 1990
 A/Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
 A/Reference number: 5091955; MIMD:9069328; PMID:2347362
 A/Molecule type: mRNA
 A/Residues: 1-107 <EXT>
 A/Cross-references: EMBL:X51852; MIMD:955393; PIRN:CA36145.1; PID:9302229
 C/Commentary: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: antibody; immunoglobulin homology
 P.15-30/Domain: Immunoglobulin homology <MIM>

Query Match 82.7%; Score 473; DB 2; Length 107;
 Best Local Similarity 82.4%; Pred. No. 7, 2e-36;
 Matches 90; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 DIOMTOSPELVANADRYITTCASQSVSDVAMVQKQKQSGKLLMYASNRITVDP 60
 DB 1 EIVMTQPELVANSGRVITTCASQSVSDVAMVQKQKQSGKLLMYASNRITVDP 60
 QY 61 FTGSGVGTFPFTISTVOEDALVAYCOQDSPTFGGKLEIK 107
 DB 61 FTGSGVGTFPFTISTVOEDALVAYCOQDSPTFGGKLEIK 107

RESULT 4

Ig kappa chain precursor V region (ser-b) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 05-Jun-1988 [sequence revision 05-Jun-1988 #extc_change 21-Jan-2000
 C/Accession: 5091964
 A/Title: Nucleotide sequence of the variable region of the heavy chain of the
 Proc. Natl. Acad. Sci. U.S.A. 85: 9134-9138, 1988
 A/Title: Structural differences in a single gene encoding the V-kappa-seg group of light
 A/Reference number: 5091955; MIMD:9069328; PMID:2347362
 A/Molecule type: DNA
 A/Residues: 1-115 <EXT>
 A/Cross-references: DB:W14360; MIMD:9197464; PIRN:AAA3903.1; PID:9197465
 A/Commentary: DB:W14360; MIMD:9197464; PIRN:AAA3903.1; PID:9197465
 A/Keywords: antibody; immunoglobulin homology
 P.15-30/Domain: Immunoglobulin homology <MIM>

Query Match 82.7%; Score 473; DB 2; Length 115;
 Best Local Similarity 82.4%; Pred. No. 7, 2e-36;
 Matches 89; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IOMTOSPELVANADRYITTCASQSVSDVAMVQKQKQSGKLLMYASNRITVDP 61
 DB 22 IVMQTFKELVANSGRVITTCASQSVSDVAMVQKQKQSGKLLMYASNRITVDP 81
 QY 62 FTGSGVGTFPFTISTVOEDALVAYCOQDSPTFGGKLEIK 107
 DB 82 FTGSGVGTFPFTISTVOEDALVAYCOQDSPTFGGKLEIK 127

RESULT 5

Ig kappa chain precursor V region (MPC11) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-May-1994 [sequence revision 18-Nov-1994 #extc_change 21-Jan-2000
 C/Accession: A30823; EMBL:50753; MIMD:9069328; PMID:2347362
 A/Title: Nucleotide sequence of the variable region of the heavy chain of the
 Cell 79: 681-689, 1992
 A/Title: Functional significance and evolutionary development of the 5'-terminal
 A/Reference number: A30823; EMBL:50753; MIMD:9069328; PMID:2347362
 A/Molecule type: DNA
 A/Residues: 1-71 <EXT>

A/Note: The nucleotide sequence of the variable region of the heavy chain of the
 R. Robbitt, P.H. Hanley, P.H. Mathysen, G.J. Ro, B.A.
 Can. J. Biochem. 58: 116-187, 1980
 A/Title: The variable region, arrangement, and rearrangement of immunoglobulin genes
 A/Reference number: A30823; EMBL:50753; MIMD:9069328; PMID:2347362
 A/Molecule type: mRNA
 A/Residues: 41-149 <MIM>
 A/Cross-references: EMBL:50753; MIMD:9069328; PMID:2347362
 A/Commentary: DB:W14360; MIMD:9197464; PIRN:AAA3903.1; PID:9197465
 A/Keywords: antibody; immunoglobulin homology
 P.15-30/Domain: Immunoglobulin homology <MIM>

Query Match 82.4%; Score 466; DB 1; Length 149;
 Best Local Similarity 82.4%; Pred. No. 4e-35;
 Matches 93; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTOSPELVANADRYITTCASQSVSDVAMVQKQKQSGKLLMYASNRITVDP 60
 DB 42 DIOMTOSPELVANADRYITTCASQSVSDVAMVQKQKQSGKLLMYASNRITVDP 101
 QY 61 FTGSGVGTFPFTISTVOEDALVAYCOQDSPTFGGKLEIK 108
 DB 61 FTGSGVGTFPFTISTVOEDALVAYCOQDSPTFGGKLEIK 149

Ig kappa chain V and J regions; monoclonal antibody 5C7.N8.1 - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-May-1994 [sequence revision 18-Nov-1994 #extc_change 20-Jun-2000
 C/Accession: D53285
 A/Title: Nucleotide sequence of the variable region of the heavy chain of the
 Mol. Immunol. 28: 1061-1072, 1991
 A/Title: Molecular characterization of monoclonal anti-steroid antibodies: primary
 A/Reference number: A53585; MIMD:92017897; PMID:1322102
 A/Commentary: DB:W14360; MIMD:9197464; PIRN:AAA3903.1; PID:9197465
 A/Keywords: antibody; immunoglobulin homology
 P.15-30/Domain: Immunoglobulin homology <MIM>

Query Match 82.4%; Score 466; DB 1; Length 149;
 Best Local Similarity 82.4%; Pred. No. 4e-35;
 Matches 93; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

QY 1 DIOMTOSPELVANADRYITTCASQSVSDVAMVQKQKQSGKLLMYASNRITVDP 60
 DB 42 DIOMTOSPELVANADRYITTCASQSVSDVAMVQKQKQSGKLLMYASNRITVDP 101
 QY 61 FTGSGVGTFPFTISTVOEDALVAYCOQDSPTFGGKLEIK 108
 DB 61 FTGSGVGTFPFTISTVOEDALVAYCOQDSPTFGGKLEIK 149

A:Residues: 1-107 <SN>

A:CDom - reference: DB:024773, NID:g20597, PIRN:BA02229.1, PID:g20598
C:Species: Mus musculus (house mouse)
C:Accession: P02655
C:Comment: This protein recognizes a restricted idiotype associated with antibodies spec
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterocysteine; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IM>

Query Match

Best Local Similarity 78.7%; Score 455; DB 2; Length 107;
Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

DB

1 IOWTOSKFLVSGRVTTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 61
2 IWTGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 61

DB

62 PFGSGGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 107
63 PFGSGGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 107

DB

RESULT 7

P02655

IG kappa chain V region (NCI) - mouse (freemart)
C:Species: Mus musculus (house mouse)
C:Accession: P02655
C:Comment: This protein recognizes a restricted idiotype associated with antibodies spec
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterocysteine; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IM>

Query Match

Best Local Similarity 79.5%; Score 455; DB 2; Length 113;
Matches 87; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

DB

1 IOWTOSKFLVSGRVTTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 60
2 IWTGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 61

DB

61 PFGSGGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 107
62 PFGSGGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 107

DB

73 PFGSGGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 113

DB

RESULT 8

S32192

IG kappa chain V region - mouse (freemart)
C:Species: Mus musculus (house mouse)
C:Accession: S32192
C:Comment: This protein recognizes a restricted idiotype associated with antibodies spec
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterocysteine; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IM>

Query Match

Best Local Similarity 78.7%; Score 455; DB 2; Length 107;
Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

DB

1 IOWTOSKFLVSGRVTTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 61
2 IWTGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 61

DB

61 PFGSGGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 107
62 PFGSGGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 107

DB

RESULT 9

S32191

IG kappa chain V region - mouse (freemart)
C:Species: Mus musculus (house mouse)
C:Accession: S32191
C:Comment: This protein recognizes a restricted idiotype associated with antibodies spec
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterocysteine; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IM>

Query Match

Best Local Similarity 78.7%; Score 455; DB 2; Length 107;
Matches 87; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

DB

1 IOWTOSKFLVSGRVTTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 61
2 IWTGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 61

DB

61 PFGSGGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 107
62 PFGSGGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 107

DB

RESULT 10

A25924

IG kappa chain precursor V region (Ser-) - mouse
C:Species: Mus musculus (house mouse)
C:Accession: A25924
C:Comment: This protein recognizes a restricted idiotype associated with antibodies spec
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterocysteine; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IM>

Query Match

Best Local Similarity 80.4%; Score 445; DB 2; Length 107;
Matches 86; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

DB

1 IOWTOSKFLVSGRVTTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 60
2 IWTGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 61

DB

61 PFGSGGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 107
62 PFGSGGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 107

DB

RESULT 11

A25924

IG kappa chain precursor V region (Ser-) - mouse
C:Species: Mus musculus (house mouse)
C:Accession: A25924
C:Comment: This protein recognizes a restricted idiotype associated with antibodies spec
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterocysteine; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IM>

Query Match

Best Local Similarity 80.4%; Score 445; DB 2; Length 107;
Matches 86; Conservative 6; Mismatches 15; Indels 0; Gaps 0;

DB

1 IOWTOSKFLVSGRVTTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 60
2 IWTGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 61

DB

61 PFGSGGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 107
62 PFGSGGTFEATSVGGRVITTCAGSDNSVAVVYQOORFPGFLLTASNTTQTPD 107

DB

A:Accession: K03105
 A:Molecule type: mRNA
 A:Residues: 1-107 <SHR>
 A:Cross-References: GB:U19766; NID:G197039; PID:RAA8893.1; PID:G197040
 C:Superfamily: Immunoglobulin Region; Immunoglobulin homology
 C:Superfamily: Immunoglobulin Region; Immunoglobulin homology
 F:16-90/Domains: immunoglobulin homology <Ime>

Query Match 72.08; Score 412; DB 2; Length 107;

Matches 79; Conservatve 10; Mismatches 18; Indels 0; Gaps 0;

QY 1 DLDVTSKFLVSAKRVTTTKASGVSNVWAFQQKQSGFLMWTNSNRTGSD 60
 1 DLDVTSKFLVSAKRVTTTKASGVSNVWAFQQKQSGFLMWTNSNRTGSD 60
 DQ 1 DLDVTSKFLVSAKRVTTTKASGVSNVWAFQQKQSGFLMWTNSNRTGSD 60
 1 DLDVTSKFLVSAKRVTTTKASGVSNVWAFQQKQSGFLMWTNSNRTGSD 60
 QY 61 RTSGVGDTPTTSTVQADNAVTFQGVDSPTFGGPTLEIK 107
 61 RTSGVGDTPTTSTVQADNAVTFQGVDSPTFGGPTLEIK 107
 DQ 61 RTSGVGDTPTTSTVQADNAVTFQGVDSPTFGGPTLEIK 107
 61 RTSGVGDTPTTSTVQADNAVTFQGVDSPTFGGPTLEIK 107

Search completed: November 7, 2003, 07:36:19
 Job time: 15.0866 secs

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OM protein - protein search, using sw method

Run on:

November 7, 2003, 07:21:18, Search time 7.76638 Seconds

652,278 Million cells updates/sec

Title: US-09-661-992b-82_COPY_135_242

Percent score: 572

Sequence: 1 DIGNOSPRELJNACDNT.....QDVSGPTFGCKMLKLR 108

Scoring table: BLOSUM62

Gapop 10.0, Deapet 0.5

Searched:

127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	366	81.5	149	1	P01633 mus musculus
2	399	69.8	136	1	P01633 mus musculus
3	391.5	68.4	133	1	P01633 mus musculus
4	391	68.4	133	1	P01633 mus musculus
5	391	68.4	133	1	P01633 mus musculus
6	386	67.5	108	1	P01652 mus musculus
7	378	66.1	108	1	P01652 mus musculus
8	376	65.7	108	1	P01652 mus musculus
9	375	65.0	108	1	P01652 mus musculus
10	372	64.8	108	1	P01652 mus musculus
11	370.5	64.8	108	1	P01652 mus musculus
12	370	64.4	108	1	P01652 mus musculus
13	367	64.2	108	1	P01652 mus musculus
14	367	64.2	108	1	P01652 mus musculus
15	366	64.0	108	1	P01652 mus musculus
16	365	63.8	108	1	P01652 mus musculus
17	365	63.8	108	1	P01652 mus musculus
18	363.5	63.5	109	1	P01652 mus musculus
19	363.5	63.5	109	1	P01652 mus musculus
20	363	63.4	109	1	P01652 mus musculus
21	362.5	63.4	109	1	P01652 mus musculus
22	361	63.1	108	1	P01652 mus musculus
23	361	63.1	108	1	P01652 mus musculus
24	360	62.9	108	1	P01652 mus musculus
25	359	62.8	108	1	P01652 mus musculus
26	358.5	62.7	108	1	P01652 mus musculus
27	357.5	62.5	113	1	P01652 mus musculus
28	356.5	62.5	113	1	P01652 mus musculus
29	356	62.2	108	1	P01652 mus musculus
30	356	62.2	108	1	P01652 mus musculus
31	354	61.9	108	1	P01652 mus musculus
32	354	61.9	108	1	P01652 mus musculus
33	354	61.9	108	1	P01652 mus musculus

34	353	61.7	108	1	P01645 mus musculus
35	351	61.4	108	1	P01645 mus musculus
36	350	61.2	108	1	P01645 mus musculus
37	350	61.2	108	1	P01645 mus musculus
38	350	61.2	108	1	P01645 mus musculus
39	348.5	60.9	109	1	P01654 mus musculus
40	348	60.8	108	1	P01654 mus musculus
41	348.5	60.5	108	1	P01654 mus musculus
42	348	60.5	108	1	P01654 mus musculus
43	345	60.3	109	1	P01654 mus musculus
44	345	60.3	109	1	P01654 mus musculus
45	345	60.1	121	1	P06312 homo sapiens

ALIGNMENTS

RESULT 1	STANDARD	RET	149 AA.
QVSA_MOUSE			
ID	P01633		
AC	1986		
NC	21-JUL-1986 (Rel. 01, Created)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	19 kDa chain V.V. region MRC1 precursor.		
OS	Escherichia Coli		
OC	Bacteriophages		
CC	Mammalia; Euteleostomi; Chordata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Chordata; Vertebrata; Mammalia; Mus.		
CK	NCBI TaxID:10090		
SK	SEQUENCE OF 1-71 FROM N.A.		
FX	MEDLINE:601944; PubMed:6288267		
FA	Kelly D.B., Colledge C., Perry R.P.		
FT	Functional significance and evolutionary development of the		
RT	19 kDa chain V.V. region MRC1 precursor.		
RI	Cal 29.681.669(1982).		
RN	[21		
RP	SEQUENCE OF 41-149 FROM N.A.		
RQ	MEDLINE:601944; PubMed:6288267		
RX	Kelly D.B., Colledge C., Perry R.P.		
RY	Functional significance and evolutionary development of the		
RZ	19 kDa chain V.V. region MRC1 precursor.		
RS	Cal 29.681.669(1982).		
RT	[21		
RU	SEQUENCE OF 41-149 FROM N.A.		
RV	MEDLINE:601944; PubMed:6288267		
VS	"The variability, arrangement, and rearrangement of immunoglobulin		
VT	genes".		
VX	Can. J. Biochem. 58:176-187(1980).		
VY	SEQUENCE OF 30-149.		
VZ	MEDLINE:7816617; PubMed:418775;		
WA	Smith G.P.		
WB	Sequence of the full-length immunoglobulin kappa-chain of mouse		
WC	111337-347(1978).		
WD	MISCELLANEOUS: THE NATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS		
WE	AMINO END, DUE TO A RANDOM DUPLICATION OF 16 NUCLEOTIDES AFTER		
WF	RESIDUE OF TYRICAL KAPPA CHAINS		
WG	RESIDUE OF TYRICAL KAPPA CHAINS		
WH	THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION		
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WN	*****		
WO	EMBL, J00541; AAA38776.1; ..		
WP	PIR, A08032; KEMM1.		
WQ	InterPro, IPR001110; IG-like.		
WR	InterPro, IPR005006; IG_MHC.		
WS	InterPro, IPR005196; IG_V.		
WT	SMART, SM00406; IG_V.		
WU	PROSITE, PS00335; IG_Like; 1.		
WV	Immunoglobulin V region; Signal; Repeat.		

FT DOMAIN 123 132 FRAMEWORK-4.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON_TER 133 134
 SEQUENCE 133 AA, 16632 MW, 5FB39306674AA4 CMC64,
 Query Match 68.4%; Score 391.5; DB 1; Length 133;
 Best Local Similarity 68.4%; Pred. No. 8.4e-35;
 Matches 76; Conservative 13; Mismatches 16; Indels 7; Gaps 2;
 QY 1 D1QNTGSPFFLVASGRVATVTCASGV-----SDVAVQKQSGSKPLMTYASNR 54
 DB 21 DIVVQSPFLVSLASGRATVTCASGV-----SDVAVQKQSGSKPLMTYASNR 80
 QY 55 YTVQNPPTSGSGVDPFTTISVQAEALVYFQDQYSGSPPTGSKTLEIR 108
 DB 81 ESDVNPPTSGSGVDPFTTISVQAEALVYFQDQYSGSPPTGSKTLEIR 133
 RESULT 4
 ID: K14A.HUMAN STANDARD; PRT; 114 AA.
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 47, Last annotation update)
 OS Homo sapiens (human)
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1] Traxid-9506;
 RP SEQUENCE.
 RX MEDLINE=76004342; PubMed=50995;
 RA Schneider M., Hirschman N., monoclonic immunoglobulin-F-chain of
 RT subgroup IV of the kappa type (Jance-Jones protein Len)."
 RL Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
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 CC EMBL=02090; CNA6793.1.
 CC HSP; P80562; 1RT.
 DR GO:GO:0005576; Cytoskeletal; NMS.
 DR GO:GO:0003823; Filament binding activity; NMS.
 DR InterPro: IPR001100; Ig-like.
 DR InterPro: IPR003006; Ig-MHC.
 DR InterPro: IPR003596; Ig_V.
 DR SMART; SM0046; IGV_1.
 DR PROSITE; PS00835; Ig Like, 1.
 KW Immunoglobulin V region, signal.
 FT SIGNAL 1 20
 FT DOMAIN 21 43
 FT DOMAIN 44 60
 FT DOMAIN 61 75
 FT DOMAIN 76 83
 FT DOMAIN 84 101
 FT DOMAIN 102 122
 FT DOMAIN 123 133
 FT DISULFID 43 114
 FT NON_TER 133 134
 SEQUENCE 133 AA, 16640 MW, 6643PFD17232645 CMC64,
 Query Match 67.4%; Score 391; DB 1; Length 134;
 Best Local Similarity 67.4%; Pred. No. 8e-35;
 Matches 76; Conservative 13; Mismatches 16; Indels 6; Gaps 1;

Matches 77; Conservative 13; Mismatches 18; Indels 6; Gaps 1;
 QY 1 D1QNTGSPFFLVASGRVATVTCASGV-----SDVAVQKQSGSKPLMTYASNR 54
 DB 1 DIVVQSPFLVSLASGRATVTCASGV-----SDVAVQKQSGSKPLMTYASNR 80
 QY 55 YTVQNPPTSGSGVDPFTTISVQAEALVYFQDQYSGSPPTGSKTLEIR 108
 DB 61 ESDVNPPTSGSGVDPFTTISVQAEALVYFQDQYSGSPPTGSKTLEIR 114
 RESULT 5
 ID: K14A.HUMAN STANDARD; PRT; 114 AA.
 AC P06314;
 DT 01-JUN-1988 (Rel. 06, Created)
 DT 15-SEP-1999 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 47, Last annotation update)
 OS Homo sapiens (human)
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1] Traxid-9506;
 RP SEQUENCE FROM N.A., PubMed=299713;
 RA March P., Miller P., Gould H.;
 RT "Detection of a unique human V kappa IV germline gene by a cloned
 RT cDNA probe."
 RL J. Mol. Biol. 121:5531-5544(1985).
 RP REVISION TO 76.
 RA March P.;
 RL Submitted (OCT-1986) to the EMBL/Genbank/DBJ databases.
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 CC or send an email to license@ebi.ac.uk).
 CC EMBL=02090; CNA6793.1.
 CC HSP; P80562; 1RT.
 DR GO:GO:0005576; Cytoskeletal; NMS.
 DR GO:GO:0003823; Filament binding activity; NMS.
 DR InterPro: IPR001100; Ig-like.
 DR InterPro: IPR003006; Ig-MHC.
 DR InterPro: IPR003596; Ig_V.
 DR SMART; SM0046; IGV_1.
 DR PROSITE; PS00835; Ig Like, 1.
 KW Immunoglobulin V region, signal.
 FT SIGNAL 1 20
 FT DOMAIN 21 43
 FT DOMAIN 44 60
 FT DOMAIN 61 75
 FT DOMAIN 76 83
 FT DOMAIN 84 101
 FT DOMAIN 102 122
 FT DOMAIN 123 133
 FT DISULFID 43 114
 FT NON_TER 133 134
 SEQUENCE 134 AA, 14966 MW, 64132PFD0738832 CMC64,
 Query Match 67.4%; Score 387; DB 1; Length 134;
 Best Local Similarity 67.4%; Pred. No. 8e-35;
 Matches 76; Conservative 13; Mismatches 19; Indels 6; Gaps 1;

Db 1 D10MTGSSKFLVSAAGDVYTTTCAASODTIVYMMKQKQKQKLYLTKASLTGVS 60
 61 RFTGSGVGTDFPTTISLOPEADAVYFCQGDQSPPTFGGKTLKIKR 108
 Db 61 RFTGSGSGVGTDFPTTISLOPEADAVYFCQGDLTGTLTGCGTKIKR 108

RESULT 8
 KY1H HUMAN STANDARD; PRT; 108 AA.
 ID KY1H HUMAN STANDARD; PRT; 108 AA.
 AC EY1500; 1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DB 19 kappa chain V-I region Hau.
 OS Homo sapiens (human)
 OC Mammalia; Chordata; Carnivora; Vertebrata; Euteleostomi;
 CC Mammalia; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo.
 NX NCBI_TaxID=9606;
 RX MEDLINE=7103280; PubMed=4097974;
 RA Mactenab S., Hiltchmann N.
 RT The primary structure of a monoclonal kappa-type immunoglobulin L-subchain " " (kappa-chain protein Hau); molecular weight 14 kDa.
 FT 1986-05-19. This is a BENCE-JONES PROTEIN.
 CC -1- MISCELLANEOUS: THE C-REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 HL Hopsa-Sevler E. Z. Physiol. Chem. 351:1291-1295 (1970).
 DB PIR; A01868; K18H01.
 DR HSP; P80362; INTL.
 DR GO; GO:0005576; C:cytoskeleton; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR Interpro; IPR007110; Ig-like.
 DR Interpro; IPR003566; Ig-MC.
 DR Interpro; IPR003566; Ig-V.
 DR SMART; SM00406; Iov; 1.
 DR PROSITE; PS00855; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 1 33 FRANKMOKR-1.
 FT DOMAIN 2 34 49 FRANKMOKR-2.
 FT DOMAIN 3 50 56 FRANKMOKR-3.
 FT DOMAIN 4 57 68 FRANKMOKR-4.
 FT DOMAIN 5 69 107 FRANKMOKR-5.
 FT DOMAIN 6 108 108 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3M616D80618 CRC64;
 Query Match 65.7%; Score 376; DB 1; Length 108;
 Beat Local Similarity 63.9%; Pred. No. 36-33;
 Matches 69; Conservative 21; Mismatches 18; Indels 0; Gaps 0;
 QY 1 D10MTGSSKFLVSAAGDVYTTTCAASODTIVYMMKQKQKQKLYLTKASLTGVS 60
 1 D10MTGSSKFLVSAAGDVYTTTCAASODTIVYMMKQKQKQKLYLTKASLTGVS 60
 DB 1 D10MTGSSKFLVSAAGDVYTTTCAASODTIVYMMKQKQKQKLYLTKASLTGVS 60
 61 RFTGSGVGTDFPTTISLOPEADAVYFCQGDQSPPTFGGKTLKIKR 108
 61 RFTGSGSGVGTDFPTTISLOPEADAVYFCQGDLTGTLTGCGTKIKR 108
 Db 61 RFTGSGSGVGTDFPTTISLOPEADAVYFCQGDLTGTLTGCGTKIKR 108

Db 19 kappa chain V-I region 00.
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Carnivora; Vertebrata; Euteleostomi;
 CC Mammalia; Chordata; Primates; Catarrhini; Hominoidea; Homo.
 NX NCBI_TaxID=9606;
 RX MEDLINE=70201507; PubMed=5447531;
 RA Mactenab S., Hiltchmann N.
 RT The primary structure of a monoclonal kappa-type immunoglobulin L-subchain " " (kappa-chain protein Hau); molecular weight 14 kDa.
 FT 1986-05-19. This is a BENCE-JONES PROTEIN.
 CC -1- MISCELLANEOUS: THE C-REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 HL Hopsa-Sevler E. Z. Physiol. Chem. 351:1291-1295 (1970).
 DB PIR; A01868; K18H01.
 DR HSP; P80362; INTL.
 DR GO; GO:0005576; C:cytoskeleton; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR Interpro; IPR007110; Ig-like.
 DR Interpro; IPR003566; Ig-MC.
 DR Interpro; IPR003566; Ig-V.
 DR SMART; SM00406; Iov; 1.
 DR PROSITE; PS00855; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 1 33 FRANKMOKR-1.
 FT DOMAIN 2 34 49 FRANKMOKR-2.
 FT DOMAIN 3 50 56 FRANKMOKR-3.
 FT DOMAIN 4 57 68 FRANKMOKR-4.
 FT DOMAIN 5 69 107 FRANKMOKR-5.
 FT DOMAIN 6 108 108 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11777 MW; 8283D4A241058278 CRC64;

Query Match 65.7%; Score 376; DB 1; Length 108;
 Beat Local Similarity 63.9%; Pred. No. 36-33;
 Matches 69; Conservative 21; Mismatches 18; Indels 0; Gaps 0;
 QY 1 D10MTGSSKFLVSAAGDVYTTTCAASODTIVYMMKQKQKQKLYLTKASLTGVS 60
 1 D10MTGSSKFLVSAAGDVYTTTCAASODTIVYMMKQKQKQKLYLTKASLTGVS 60
 DB 1 D10MTGSSKFLVSAAGDVYTTTCAASODTIVYMMKQKQKQKLYLTKASLTGVS 60
 61 RFTGSGVGTDFPTTISLOPEADAVYFCQGDQSPPTFGGKTLKIKR 108
 61 RFTGSGSGVGTDFPTTISLOPEADAVYFCQGDLTGTLTGCGTKIKR 108
 Db 61 RFTGSGSGVGTDFPTTISLOPEADAVYFCQGDLTGTLTGCGTKIKR 108

RESULT 10
 KY1H HUMAN STANDARD; PRT; 114 AA.
 ID KY1H HUMAN STANDARD; PRT; 114 AA.
 AC EY1500; 1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DB 19 kappa chain V-I region SI7A.
 OS Homo sapiens (human)
 OC Mammalia; Chordata; Carnivora; Vertebrata; Euteleostomi;
 CC Mammalia; Chordata; Primates; Catarrhini; Hominoidea; Homo.
 NX NCBI_TaxID=9606;
 RX MEDLINE=70201507; PubMed=5447531;
 RA Mactenab S., Hiltchmann N.
 RT The primary structure of a monoclonal kappa-type immunoglobulin L-subchain " " (kappa-chain protein Hau); molecular weight 14 kDa.
 FT 1986-05-19. This is a BENCE-JONES PROTEIN.
 CC -1- MISCELLANEOUS: THE C-REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 HL Hopsa-Sevler E. Z. Physiol. Chem. 351:1291-1295 (1970).
 DB PIR; A01868; K18H01.
 DR HSP; P80362; INTL.
 DR GO; GO:0005576; C:cytoskeleton; NAS.
 DR GO; GO:0003823; F:antigen binding activity; NAS.
 DR Interpro; IPR007110; Ig-like.
 DR Interpro; IPR003566; Ig-MC.
 DR Interpro; IPR003566; Ig-V.
 DR SMART; SM00406; Iov; 1.
 DR PROSITE; PS00855; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 1 33 FRANKMOKR-1.
 FT DOMAIN 2 34 49 FRANKMOKR-2.
 FT DOMAIN 3 50 56 FRANKMOKR-3.
 FT DOMAIN 4 57 68 FRANKMOKR-4.
 FT DOMAIN 5 69 107 FRANKMOKR-5.
 FT DOMAIN 6 108 108 BY SIMILARITY.
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11777 MW; 8283D4A241058278 CRC64;

Query Match 65.7%; Score 376; DB 1; Length 108;
 Beat Local Similarity 63.9%; Pred. No. 36-33;
 Matches 69; Conservative 21; Mismatches 18; Indels 0; Gaps 0;
 QY 1 D10MTGSSKFLVSAAGDVYTTTCAASODTIVYMMKQKQKQKLYLTKASLTGVS 60
 1 D10MTGSSKFLVSAAGDVYTTTCAASODTIVYMMKQKQKQKLYLTKASLTGVS 60
 DB 1 D10MTGSSKFLVSAAGDVYTTTCAASODTIVYMMKQKQKQKLYLTKASLTGVS 60
 61 RFTGSGVGTDFPTTISLOPEADAVYFCQGDQSPPTFGGKTLKIKR 108
 61 RFTGSGSGVGTDFPTTISLOPEADAVYFCQGDLTGTLTGCGTKIKR 108
 Db 61 RFTGSGSGVGTDFPTTISLOPEADAVYFCQGDLTGTLTGCGTKIKR 108

CC Bakercia; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
 OX NCBI_TaxID:9606;
 RN 11
 RN SOURCE
 RX MEDLINE:6832076; PubMed:5595110;
 RA Hilschmann N.;
 RT "Chemical structure of 2 Kappa-type Bence Jones proteins (Koy and
 Cam.)";
 RN 12
 RN Type:SevJar's Z. Physiol. Chem. 348:1077-1080(1967).
 RP REVISIONS TO 38 AND 41.
 RP Hilschmann N., Bernholc H.U., Bass N., Langer B., Fomeling H.,
 R (in) Franek P., Singer D. (eds.);
 RL Gamma globulins: structure and function, pp.57-74, Academic Press,
 New York (1969).
 RL -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
 CC -1- MARKER
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR: A91638; KIMRY.
 DR HSP: P03627; LML.
 DR D: D000837; COXTRACTALLAF; NAS.
 DR GO: GO:0003823; P:immune binding activity; NAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR Interpro: IPR07110; 16_1like.
 DR Interpro: IPR03036; 16_1like.
 DR Interpro: IPR03596; 16_1V.
 DR Pfam: PF00047; 19; 1.
 DR SMART: SM00406; 107; 1.
 DR TrEMBL: P03627; 16_1like; 1
 RX Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DOMAIN 108 108
 FT NON TER
 FT 108 108
 SO SEQUENCE 108 AA; 11782 MW; F5ACDE5A13D53A CRO64;
 Query Match 64.2%; Score 367; DB 1; Length 108;
 Best Local Similarity 64.8%; Pred. No. 2,7e-32;
 Matches 70; Conservative 14; Mismatches 24; Indels 0; Gaps 0;
 OY 1 D I O N G O K E T L I S A G P V T T C A S G S W D N I O K G O S P E L A M Y A N K R T G H D 60
 DB 1 D I O N G O S P E L A S A V D R V I T I O S D S I P I M Y Q O R G A P L L I D A S I L A G V S 60
 OY 61 R F T S G I G T P P T I S T V N Q A E L A V I P C O O D S P F T G S T K L E I R 108
 DB 61 R F S I G S G I G T P P T I S I O P E I A T I Y C O Q D N L P L T G S G T K V D F K 108

Search completed: November 7, 2003, 07:28:07
 Job time : 7.78638 secs

Db 1 KELLUSKGVNTTTCASGVSDVAVYQKQFSPLLTYTNNKTVPPFTSGSG 60
 69 TDTFTTSTQVADAVYFCQDVGSPPTFGGKLEIK 107
 Oy 1 DLTQGTGKPELVADGVYTTTCASGVSDVAVYQKQFSPKLMVYASRYTVPD 60
 1 DLTQGTGKPELVADGVYTTTCASGVSDVAVYQKQFSPKLMVYASRYTVPD 60
 Db 61 TDTFTTSTQVADAVYFCQDVGSPPTFGGKLEIK 99

RESULT 2

10 Q9VJ10 PRELIMINARY; PRT; 108 AA.
 AC Q9VJ10
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 23, Last annotation update)
 DE Anti-DNA light chain (Fragment).
 OS Homo sapiens (human).
 OC Vertebrata; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 NX NCBI_TaxID=10090;
 RX MEDLINE=96409289; PubMed=8614271;
 RM MLOC N.R., Alexander A.L., Phipps A.V., Fiebach P.S., Gilkeson C.S.,
 RT Anti-DNA from C3H/10F mice and lupus mice with nephritis."
 RL Eyr. J. Immunol. 26:225-233 (1996).
 DR EMBL, U99155; AAB02817.1; 11k.
 DR Interpro: IPR003006; 15 kMC.
 DR Interpro: IPR003596; 15 kV.
 DR Pfam: PF00047; 19; 1.
 DR SMART: SM00835; 15; 1.
 DR PROSITE: PS00835; 15; 1.
 FT NON TER 1
 FT LENGTH 108
 FT SEQUENCE 108 AA; 11893 MW; 685060756130PBE CRC64;

Query Match 69.8%; Score 399; DB 11; Length 108;
 Best Local Similarity 72.2%; Pred. No. 3; 8e-36;
 Matches 78; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

Oy 1 DLTQGTGKPELVADGVYTTTCASGVSDVAVYQKQFSPKLMVYASRYTVPD 60
 1 DLTQGTGKPELVADGVYTTTCASGVSDVAVYQKQFSPKLMVYASRYTVPD 60
 Db 1 DLTQGTGKPELVADGVYTTTCASGVSDVAVYQKQFSPKLMVYASRYTVPD 60
 1 DLTQGTGKPELVADGVYTTTCASGVSDVAVYQKQFSPKLMVYASRYTVPD 60
 Oy 61 RFTGSGSTGPTFTLTCASGVSDVAVYQKQFSPPTFGGKLEIK 108
 61 RFTGSGSTGPTFTLTCASGVSDVAVYQKQFSPPTFGGKLEIK 108

RESULT 3

10 Q968A9 PRELIMINARY; PRT; 107 AA.

AC Q968A9
 DT 03-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Anti-1-epsilon-chloroacetyl-anti-myosin immunoglobulin kappa light chain
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
 NX NCBI_TaxID=9606;
 RX MEDLINE=96315693; PubMed=9712075;
 RM MLOC N.R., Kallal M., Cunningham M.W.,
 RT "Molecular analysis of polyclonal monoclonal antibodies from
 antitumor V region genes."

Db 61 RFTGSGSTGPTFTLTCASGVSDVAVYQKQFSPPTFGGKLEIK 108
 61 RFTGSGSTGPTFTLTCASGVSDVAVYQKQFSPPTFGGKLEIK 108

PL J. Immunol. 161:2020-2031 (1998).
 DR EMBL, U96396; AAB6785.1; 11k.
 DR Interpro: IPR007110; 15; 11k.
 DR Interpro: IPR003006; 15 kMC.
 DR Pfam: PF00047; 19; 1.
 DR Pfam: PF00047; 19; 1.
 DR SMART: SM00406; 10; 1.
 DR PROSITE: PS00835; 15; 1.
 FT NON TER 1
 FT LENGTH 107
 FT SEQUENCE 107 AA; 11520 MW; 484385877716 CRC64;

Query Match 66.8%; Score 382.5; DB 4; Length 107;
 Best Local Similarity 74.2%; Pred. No. 4; 4e-34;
 Matches 74; Conservative 4; Mismatches 19; Indels 1; Gaps 1;

Oy 1 DLTQGTGKPELVADGVYTTTCASGVSDVAVYQKQFSPKLMVYASRYTVPD 60
 1 DLTQGTGKPELVADGVYTTTCASGVSDVAVYQKQFSPKLMVYASRYTVPD 60
 Db 61 RFTGSGSTGPTFTLTCASGVSDVAVYQKQFSPPTFGGKLEIK 108
 61 RFTGSGSTGPTFTLTCASGVSDVAVYQKQFSPPTFGGKLEIK 108

RESULT 4

10 Q9U79 PRELIMINARY; PRT; 108 AA.
 AC Q9U79
 DT 01-MAR-2000 (TrEMBLrel. 13, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 OS Homo sapiens (human).
 OC Vertebrata; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
 NX NCBI_TaxID=9606;
 RX MEDLINE=96277193; PubMed=9644934;
 RM MLOC N.R., Van der Nette J., Kalle N.N., Berny S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 clinical immunopathology." 87:184-192 (1998).
 DR EMBL, AF015035; AAB5271.1; 11k.
 DR HMM, AF015035; AAB5271.1; 11k.
 DR Interpro: IPR003006; 15 kMC.
 DR Interpro: IPR003596; 15 kV.
 DR Pfam: PF00047; 19; 1.
 DR SMART: SM00835; 15; 1.
 DR PROSITE: PS00835; 15; 1.
 FT NON TER 1
 FT LENGTH 108
 FT SEQUENCE 108 AA; 11787 MW; DBS45E1972AF4E CRC64;

Query Match 69.8%; Score 377; DB 4; Length 108;
 Best Local Similarity 70.7%; Pred. No. 9; 8e-34;
 Matches 70; Conservative 15; Mismatches 23; Indels 0; Gaps 0;

Oy 1 DLTQGTGKPELVADGVYTTTCASGVSDVAVYQKQFSPKLMVYASRYTVPD 60
 1 DLTQGTGKPELVADGVYTTTCASGVSDVAVYQKQFSPKLMVYASRYTVPD 60
 Db 61 RFTGSGSTGPTFTLTCASGVSDVAVYQKQFSPPTFGGKLEIK 108
 61 RFTGSGSTGPTFTLTCASGVSDVAVYQKQFSPPTFGGKLEIK 108

RESULT 5

10 Q9U70 PRELIMINARY; PRT; 108 AA.
 AC Q9U70
 DT 01-MAR-2000 (TrEMBLrel. 13, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region
 OS Homo sapiens (human).
 OC Vertebrata; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
 NX NCBI_TaxID=9606;
 RX MEDLINE=96277193; PubMed=9644934;
 RM MLOC N.R., Van der Nette J., Kalle N.N., Berny S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 clinical immunopathology." 87:184-192 (1998).
 DR EMBL, AF015035; AAB5271.1; 11k.
 DR HMM, AF015035; AAB5271.1; 11k.
 DR Interpro: IPR003006; 15 kMC.
 DR Interpro: IPR003596; 15 kV.
 DR Pfam: PF00047; 19; 1.
 DR SMART: SM00835; 15; 1.
 DR PROSITE: PS00835; 15; 1.
 FT NON TER 1
 FT LENGTH 108
 FT SEQUENCE 108 AA; 11787 MW; DBS45E1972AF4E CRC64;

Query Match 69.8%; Score 377; DB 4; Length 108;
 Best Local Similarity 70.7%; Pred. No. 9; 8e-34;
 Matches 70; Conservative 15; Mismatches 23; Indels 0; Gaps 0;

Oy 1 DLTQGTGKPELVADGVYTTTCASGVSDVAVYQKQFSPKLMVYASRYTVPD 60
 1 DLTQGTGKPELVADGVYTTTCASGVSDVAVYQKQFSPKLMVYASRYTVPD 60
 Db 61 RFTGSGSTGPTFTLTCASGVSDVAVYQKQFSPPTFGGKLEIK 108
 61 RFTGSGSTGPTFTLTCASGVSDVAVYQKQFSPPTFGGKLEIK 108

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ID 09U70 PRELIMINARY; PRT; 108 AA.
AC 01-MAY-2000 (TREMUR-rel. 13, Created)
DT 01-MAY-2000 (TREMUR-rel. 13, Last sequence update)
DT 01-MAR-2003 (TREMUR-rel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (human)
OC Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID:9606;
RN 1
RS SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=964934;
RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berny S.M.,
RA Myosin-reactive autoantibodies in rheumatic carditis and normal
RA young D.C.;
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR BMBJ; A035054; A05280.1; -.
DR HSBP; P01607; IREI.
DR Interpro; IPR00306; IG.MC.
DR Interpro; IPR003596; IG.V.
DR Pfam; PF00047; 19; 1.
DR SMART; SM0046; 16v.1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER
FT SEQUENCE 108 AA; 11633 MW; B7BECB41FC037 CRC64;
SQ
Query Match 65.7%; Score 376; DB 4; Length 108;
Beat Local Similarity 65.7%; Pred.No.1.3e-33;
Matches 72; Conservative 13; Mismatches 23; Indels 0; Gaps 0;
Cy 1 D1QWTSKSLASAGRRVITTCAGSGSNVAVWAKQKSGSPFLKLVASNRITVPD 60
Db 1 D1QWTSKSLASAGRRVITTCAGSGSNVAVWAKQKSGSPFLKLVASNRITVPD 60
Cy 61 RFTSGSGVDITFTISLPDADVAVFVQCGSPPTGGSTKLKLR 108
Db 61 RFTSGSGVDITFTISLPDADVAVFVQCGSPPTGGSTKLKLR 108
Db 61 RFTSGSGVDITFTISLPDADVAVFVQCGSPPTGGSTKLKLR 108
RESULT 6
ID 09U77 PRELIMINARY; PRT; 108 AA.
AC 01-MAY-2000 (TREMUR-rel. 13, Created)
DT 01-MAY-2000 (TREMUR-rel. 13, Last sequence update)
DT 01-MAR-2003 (TREMUR-rel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (human)
OC Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID:9606;
RN 1
RS SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=964934;
RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berny S.M.,
RA Myosin-reactive autoantibodies in rheumatic carditis and normal
RA fetus";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR BMBJ; A035053; A05273.1; -.
DR HSBP; P01607; IREI.
DR Interpro; IPR007110; IG_LIKE.
DR Interpro; IPR00306; IG.MC.
DR Interpro; IPR003596; IG.V.
DR Pfam; PF00047; 19; 1.
DR SMART; SM0046; 16v.1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER
FT SEQUENCE 107 AA; 11501 MW; 07065P080754748 CRC64;
SQ
Query Match 64.8%; Score 370.5; DB 4; Length 107;
Beat Local Similarity 65.7%; Pred.No.5e-33; 21; Indels 1; Gaps 1;
Matches 72; Conservative 14; Mismatches 22;
Cy 1 D1QWTSKSLASAGRRVITTCAGSGSNVAVWAKQKSGSPFLKLVASNRITVPD 60
Db 1 D1QWTSKSLASAGRRVITTCAGSGSNVAVWAKQKSGSPFLKLVASNRITVPD 60
Cy 61 RFTSGSGVDITFTISLPDADVAVFVQCGSPPTGGSTKLKLR 108
Db 61 RFTSGSGVDITFTISLPDADVAVFVQCGSPPTGGSTKLKLR 108
Db 61 RFTSGSGVDITFTISLPDADVAVFVQCGSPPTGGSTKLKLR 108

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FT NON TER 1 1
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11738 MW; C0668176C4D1E93 CRC64;
Query Match 65.7%; Score 376; DB 4; Length 108;
Beat Local Similarity 65.7%; Pred.No.1.3e-33;
Matches 71; Conservative 15; Mismatches 22; Indels 0; Gaps 0;
Cy 1 D1QWTSKSLASAGRRVITTCAGSGSNVAVWAKQKSGSPFLKLVASNRITVPD 60
Db 1 D1QWTSKSLASAGRRVITTCAGSGSNVAVWAKQKSGSPFLKLVASNRITVPD 60
Cy 61 RFTSGSGVDITFTISLPDADVAVFVQCGSPPTGGSTKLKLR 108
Db 61 RFTSGSGVDITFTISLPDADVAVFVQCGSPPTGGSTKLKLR 108
Db 61 RFTSGSGVDITFTISLPDADVAVFVQCGSPPTGGSTKLKLR 108
RESULT 7
ID 09U81 PRELIMINARY; PRT; 107 AA.
AC 01-MAY-2000 (TREMUR-rel. 13, Created)
DT 01-MAY-2000 (TREMUR-rel. 13, Last sequence update)
DT 01-MAR-2003 (TREMUR-rel. 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (fragment).
OS Homo sapiens (human)
OC Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID:9606;
RN 1
RS SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=964934;
RA Wu X., Liu B., Van der Werf P.L., Kalis N.N., Berny S.M.,
RA Myosin-reactive autoantibodies in rheumatic carditis and normal
RA fetus";
RT Clin. Immunol. Immunopathol. 87:184-192(1998).
DR BMBJ; A035053; A05269.1; -.
DR HSBP; P01607; IREI.
DR Interpro; IPR007110; IG_LIKE.
DR Interpro; IPR00306; IG.MC.
DR Interpro; IPR003596; IG.V.
DR Pfam; PF00047; 19; 1.
DR SMART; SM0046; 16v.1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER
FT SEQUENCE 107 AA; 11501 MW; 07065P080754748 CRC64;
SQ
Query Match 64.8%; Score 370.5; DB 4; Length 107;
Beat Local Similarity 65.7%; Pred.No.5e-33; 21; Indels 1; Gaps 1;
Matches 72; Conservative 14; Mismatches 22;
Cy 1 D1QWTSKSLASAGRRVITTCAGSGSNVAVWAKQKSGSPFLKLVASNRITVPD 60
Db 1 D1QWTSKSLASAGRRVITTCAGSGSNVAVWAKQKSGSPFLKLVASNRITVPD 60
Cy 61 RFTSGSGVDITFTISLPDADVAVFVQCGSPPTGGSTKLKLR 108
Db 61 RFTSGSGVDITFTISLPDADVAVFVQCGSPPTGGSTKLKLR 108
Db 61 RFTSGSGVDITFTISLPDADVAVFVQCGSPPTGGSTKLKLR 108

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RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.
RA Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DB HSP1: P80362.1 (178BEMBL:22, Created)
DB HSP2: P80362.1 (178BEMBL:22, Last annotation update)
DR Interpro: IPR007110; 1g-1ike
DR Interpro: IPR003066; 1g-MHC
DR Interpro: IPR003597; 1g-MHC
DR SMART: SM00406; 10v.1
DR PROSITE: PS00353; 10-Like; 1
FT NON_TER
SC SEQUENCE 107 AA; 11794 MW; 2815ED6604A26C3 CRC64;

Query Match
Score 62.9%; Score 360; DB 11; Length 107;
Best Local Similarity 65.4%; Pred. No. 7.1e-32;
Matches 69; Conservative 19; Mismatches 16; Indels 6; Gaps 1;

OY 4 MTGSGKELVLSAGRPRTYTVKASGVNSD-----VAMTQKQFGSPFLVAMVANSNYTPD 57
DB 1 MTGSGKELVLSAGRPRTYTVKASGVNSD-----VAMTQKQFGSPFLVAMVANSNYTPD 57
58 VPPRFGSGSGLDPTFTTSTVOAEDAVYFCQDQSGSPFFTCGGTTL 104
OY 61 VPPRFGSGSGLDPTFTTSTVOAEDAVYFCQDQSGSPFFTCGGTTL 104
DB 61 VPPRFGSGSGLDPTFTTSTVOAEDAVYFCQDQSGSPFFTCGGTTL 107

RESULT 12
OPU33
AD G91W48
DT 01-MAY-2000 (178BEMBL:23, Created)
DT 01-MAY-2000 (178BEMBL:23, Last sequence update)
DT 01-MAY-2000 (178BEMBL:23, Last annotation update)
DR Interpro: IPR007110; 1g-1ike
DR Interpro: IPR003066; 1g-MHC
DR Interpro: IPR003597; 1g-MHC
DR SMART: SM00406; 10v.1
DR PROSITE: PS00353; 10-Like; 1
FT NON_TER
SC SEQUENCE 108 AA; 11934 MW; 9F9C3A23E9A6E2BA CRC64;

Query Match
Score 62.8%; Score 359; DB 4; Length 108;
Best Local Similarity 65.0%; Pred. No. 9.3e-32;
Matches 68; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

OY 1 DLTGSGKELVLSAGRPRTYTVKASGVNSDVAWVQKQFGSPFLVAMVANSNYTPD 60
DB 1 DLTGSGKELVLSAGRPRTYTVKASGVNSDVAWVQKQFGSPFLVAMVANSNYTPD 60
1 ELYMGSPATLSVPEGRATLSCRASGVSYSNLAIVQKQFGSPFLVAMVANSNYTPD 60
61 RFSGSGSGLDPTFTTSTVOAEDAVYFCQDQSGSPFFTCGGTTL 108

RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.
RA Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DB HSP1: P80362.1 (178BEMBL:22, Created)
DB HSP2: P80362.1 (178BEMBL:22, Last annotation update)
DR Interpro: IPR007110; 1g-1ike
DR Interpro: IPR003066; 1g-MHC
DR Interpro: IPR003597; 1g-MHC
DR SMART: SM00406; 10v.1
DR PROSITE: PS00353; 10-Like; 1
FT NON_TER
SC SEQUENCE 108 AA; 11934 MW; 9F9C3A23E9A6E2BA CRC64;

Query Match
Score 62.8%; Score 359; DB 4; Length 108;
Best Local Similarity 65.0%; Pred. No. 9.3e-32;
Matches 68; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

OY 1 DLTGSGKELVLSAGRPRTYTVKASGVNSDVAWVQKQFGSPFLVAMVANSNYTPD 60
DB 1 DLTGSGKELVLSAGRPRTYTVKASGVNSDVAWVQKQFGSPFLVAMVANSNYTPD 60
1 ELYMGSPATLSVPEGRATLSCRASGVSYSNLAIVQKQFGSPFLVAMVANSNYTPD 60
61 RFSGSGSGLDPTFTTSTVOAEDAVYFCQDQSGSPFFTCGGTTL 108

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RESULT 13
OGENEX1
ID G91W48
DT 01-OCT-2002 (178BEMBL:22, Created)
DT 01-OCT-2002 (178BEMBL:22, Last annotation update)
DR Interpro: IPR007110; 1g-1ike
DR Interpro: IPR003066; 1g-MHC
DR Interpro: IPR003597; 1g-MHC
DR SMART: SM00406; 10v.1
DR PROSITE: PS00353; 10-Like; 1
FT NON_TER
SC SEQUENCE 234 AA; 25530 MW; 63165DE8FD32FE CRC64;

Query Match
Score 62.8%; Score 359; DB 4; Length 234;
Best Local Similarity 63.0%; Pred. No. 3.1e-11;
Matches 68; Conservative 21; Mismatches 19; Indels 0; Gaps 0;

OY 1 DLTGSGKELVLSAGRPRTYTVKASGVNSDVAWVQKQFGSPFLVAMVANSNYTPD 60
DB 1 DLTGSGKELVLSAGRPRTYTVKASGVNSDVAWVQKQFGSPFLVAMVANSNYTPD 60
21 ELYMGSPATLSVPEGRATLSCRASGVSYSNLAIVQKQFGSPFLVAMVANSNYTPD 80
61 RFSGSGSGLDPTFTTSTVOAEDAVYFCQDQSGSPFFTCGGTTL 108
DB 81 RFSGSGSGLDPTFTTSTVOAEDAVYFCQDQSGSPFFTCGGTTL 128

RESULT 14
G91W48
ID G91W48
AC G91W48; 2001 (178BEMBL:23, Created)
DT 01-DEC-2001 (178BEMBL:23, Last sequence update)
DT 01-MAY-2003 (178BEMBL:23, Last annotation update)
DR Interpro: IPR007110; 1g-1ike
DR Interpro: IPR003066; 1g-MHC
DR Interpro: IPR003597; 1g-MHC
DR SMART: SM00406; 10v.1
DR PROSITE: PS00353; 10-Like; 1
FT NON_TER
SC SEQUENCE 234 AA; 25529 MW; B0D0D6E8E87312D2 CRC64;

Query Match
Score 61.0%; Score 349; DB 11; Length 234;
Best Local Similarity 61.1%; Pred. No. 3e-10;

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Matches 66; Conservative 14; Mismatches 28; Indels 0; Gaps 0;
QY      1 DIOMTQSPPEFLVAGSDVYITTCASQVSNDVAATQCGQSPKLTLYMASRRYGVDP 60
DB      21 DIOMTQTSLSNLSMDGVYISCSADQSLNMTQKSGDQVALLHTSRSLTAVPS 80
QY      61 RFTGSGYGTDFETFTSTQVRELDVAFQCGQYSPTPGGTGLKLR 108
DB      81 RFTSSGSGTDSITLISNLSGEDVITRFQCGQNTPTFTSGSTLKVRA 128

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RESULT 15

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OS9W37.09037       PRELIMINARY; FRT; 238 AA.
ID 099K37.
DT 01-JUN-2001 (TRIMBLrel. 17, Created)
DT 01-JUN-2001 (TRIMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TRIMBLrel. 23, Last annotation update)
OS 099K37.09037 (238 AA)
OG Mus musculus (Mouse)
OC Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RM 111_TaxID=10090;
RP SEQUENCE FROM N.A.
RA Straubberg N.A., 2001 to the EMBL/GenBank/DBJ databases.
RL Mus musculus (NC02035)
DR EMBL; NC02035; AB02035-1;
DR HSSP; P01579; 2FDJ.
DR InterPro; IPR001110; 19-like.
DR InterPro; IPR003596; 19-MEC.
DR InterPro; IPR00447; 197_2_197.
DR Pfam; PF00447; 197_2_197.
DR SMART; SM00406; 197; 1.
DR PROSITE; PS00328; 197; 2.
DR PROSITE; PS00328; 197; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 2634 MW; FE2BD6A0B80130A CRC64;
Query Match
Best local Similarity 61.9%; Score 346.5; DB 11; Length 238;
Matches 70; Conservative 15; Mismatches 23; Indels 5; Gaps 2;
QY      1 DIOMTQSPPEFLVAGSDVYITTCASQVSNDVAATQCGQSPKLTLYMASRRYGVDP 55
DB      21 DIOMTQTSLSNLSMDGVYISCSADQSLNMTQKSGDQVALLHTSRSLTAVPS 79
QY      56 TQPPRTGSGYGTDFETFTSTQVRELDVAFQCGQYSPTPGGTGLKLR 108
DB      80 SDVPRSSGSGTDSITLISNLSGEDVITRFQCGQNTPTFTSGSTLKVRA 132

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Search completed: November 7, 2003, 07:34:33
 Job time : 36.7155 secs

XX 13-SEP-2000; 2000MC-BP08936.
 XX 14-SEP-1999; 99AT-0001576.
 XX (BAXT) BAXTER AG.
 XX Schellinger F, Kerschbaum R, Falkner F, Dörner F;
 XX HPI. 2001-290358/30.
 XX N-PSDB; AAF30723.
 XX
 XX New factor IX/factor IXa antibodies and their derivatives useful for
 XX increasing the survival of haemophilic patients with haemorrhagic
 XX PT congenital disorders such as haemophilia A and haemorrhagic diathesis -
 XX claim 8; Fig 14; 138pp; English.
 XX
 XX The present sequence is that of a single chain Fv (scFv) derivative
 XX of antibody 193/AD3, comprising the heavy (VH) and light (VL) chain
 XX variable regions of 193/AD3 joined by a flexible linker
 XX peptide. The scFv was obtained by PCR amplification of cDNA for
 XX the variable regions of the heavy and light chain of antibody 193/AD3
 XX (an example of anti-human Factor IX (FIX)/activated Factor IX (aFIX)
 XX antibodies of the invention. Anti-FIX/FIXa and their derivatives,
 XX including scFv and CDR fragments, have Factor VIIIa (FVIIIa) cofactor
 XX activity and are useful for the treatment of haemophilic patients
 XX in the absence of FVIII or FVIIIa and in the case of FVIII
 XX inhibitor patients. The antibodies and derivatives are used in a
 XX method for the treatment of haemophilic patients with haemorrhagic
 XX congenital disorders, especially haemophilia A and haemorrhagic
 XX diathesis.
 XX
 XX Sequence 242 Ab.
 XX
 XX Query Match 100.0%; Score 572; DB 22; Length 242;
 XX Best Local Similarity 100.0%; Pred. No. 3; 1e-39;
 XX Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 D I Q M T G P E P L I A S A D R V Y T T C A S G S S N D V A Y Q O F Q S G P L L M Y T A S N R Y T G V D P 60
 XX DB 135 D I Q M T G P E P L I A S A D R V Y T T C A S G S S N D V A Y Q O F Q S G P L L M Y T A S N R Y T G V D P 194
 XX QY 61 P F T S G I G D F P F I S T V Q A E D L A V F Q O D Y S S P F P G G T A L E I K R 108
 XX DB 195 P F T S G I G D F P F I S T V Q A E D L A V F Q O D Y S S P F P G G T A L E I K R 242

RESULT 2

AAE70828
 XX AAE70828 standard; Protein; 154 AA.
 XX
 XX AAE70828;
 XX 25-MAR-2003 (Unclustcd)
 XX 31-MAR-1995 (first entry)
 XX
 XX Mab 4197X light chain variable region.
 XX Immunoconin, heavy chain, light chain, variable region; antibody;
 XX IgG1A; cytototoxic; cancer; lens opacification; epithelial cell;
 XX pH9.5; 4197X; monoclonal antibody; Mab.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Region 51..64 CDR1
 XX /note= "complementarity determining region 1"
 XX Region 80..86
 XX /label= CDR2

FT /note= "complementarity determining region 2"
 FT Region 119..127
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 XX MO9503828-A1.
 XX
 XX 09-FEB-1995.
 XX 15-JUL-1994; 94WO-US07919.
 XX 02-AUG-1993; 93US-0101329.
 XX (HOUS-) HOUSTON BIOTECHNOLOGY INC.
 XX Goud RW, Kallender PJ, Wallace TL, Wood MS;
 XX HPI. 1995-02036/11.
 XX N-PSDB; AAF08367.
 XX
 XX New single chain immunotoxin - binds specifically to epithelial
 XX cells, for inhibiting development of sec. carcinoma after
 XX extra-capsular cathect excision.
 XX
 XX Disclosure; Fig. 3; 68pp; English.
 XX
 XX An immunotoxin (given in AAE70827) comprising the heavy (VH) and light
 XX chain (VL) variable regions of anti-lens epithelium 1953 Mab 4197X
 XX linked to ricin-A. CDRs encoding the VL and VH regions of 4197X
 XX (AA08387-89, respectively) were obtained from hybridoma mAb,
 XX amplified by PCR and engineered for inclusion in the immunotoxin
 XX (updated on 05-MAR-2003 to correct FN field.)
 XX
 XX Sequence 134 AA;
 XX
 XX Query Match 99.5%; Score 529; DB 16; Length 154;
 XX Best Local Similarity 93.5%; Pred. No. 6; 4e-36;
 XX Matches 100; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX QY 2 I Q M T G P E P L I A S A D R V Y T T C A S G S S N D V A Y Q O F Q S G P L L M Y T A S N R Y T G V D P 61
 XX DB 31 I Y M T G P E P L I A S A D R V Y T T C A S G S S N D V A Y Q O F Q S G P L L M Y T A S N R Y T G V D P 90
 XX QY 62 P F T S G I G D F P F I S T V Q A E D L A V F Q O D Y S S P F P G G T A L E I K R 108
 XX DB 91 P F T S G I G D F P F I S T V Q A E D L A V F Q O D Y S S P F P G G T A L E I K R 137

RESULT 3

AAE29157
 XX AAE29157 standard; Protein; 128 AA.
 XX
 XX AAE29157;
 XX 27-JUN-2003 (first entry)
 XX
 XX Chimeric 31.1 antibody light chain variable region.
 XX 31.1 antibody; pancreatic cancer; pancreatic carcinoma; antibody therapy;
 XX light chain variable region.
 XX
 XX Unidentified.
 XX
 XX Key Location/Qualifiers
 XX Region 21..128 Signal-peptide
 XX Protein
 XX MO200274251-A2.
 XX 26-SEP-2002.

XX 15-MAR-2003; 2002MO-US09193.
 PF 15-MAR-2001; 2001US-276284P.
 DR 15-MAR-2001; 2001US-276284P.
 PA (ITB1-) INT BIOENGINEERING SYSTEMS INC.
 XX Acton M, Trang KY;
 DR WPI, 2002-759857/82.
 CC N-PEDS; A0404577.
 DR
 PF New nucleic acid encoding light and heavy chain variable regions of the
 PT antibody 31.1, useful for expressing chimerized 31.1 antibodies for
 creating pancreatic cancer or for diagnosing pancreatic carcinoma -
 CC Claim 4; Fig 2, 40pp; English.
 XX
 CC The present invention relates to novel nucleic acid sequences encoding
 CC light and heavy chain variable regions of the antibody 31.1. Sequences
 CC of the nucleic acid are useful in expressing chimerized 31.1 antibodies,
 CC which are used for diagnosing pancreatic carcinoma or for treating
 CC pancreatic carcinoma. They are also used in antibody therapy. The present
 CC sequence is chimeric 31.1 antibody light chain variable region.
 XX Sequence 128 AA;
 SS
 Query Match 92.3%; Score 528; DB 23; Length 128;
 Best Local Similarity 99.5%; Pred. No. 6,5e-36;
 Matches 100; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Oy 2 IYMTGSPFRLVMSADNVTTCAGSGSYNDVAVYQCGQSPFRLVYASNTVGPDR 61
 DB 22 IYMTGSPFRLVMSADNVTTCAGSGSYNDVAVYQCGQSPFRLVYASNTVGPDR 81
 Oy 62 FTGSGYGFDFPFTSTVQAEHLAVYPCQDYSPPFGSGTLETKR 108
 DB 82 FTGSGYGFDFPFTSTVQAEHLAVYPCQDYSPPFGSGTLETKR 128
 RESULT 4
 AAR39818
 XX AAR39818 standard; Protein; 106 AA.
 AC AAR39818;
 XX 25-MAR-2003 (updated)
 DT 11-JUN-1994 (first entry)
 XX HP1/2 VV.
 DS Monoclonal antibody; allergen; light chain; asthma; VLA-4;
 XX very late antigen; hypersensitivity.
 XX Homo sapiens.
 YS
 PN MO313796-A1.
 XX
 PD 22-JUL-1993.
 PF 12-JUN-1993; 93MO-US00030.
 XX
 PR 13-JUN-1993; 92US-0821768.
 XX (B10J) BIOGEN INC.
 XX
 P1 Lobb R;
 XX
 XX WPI, 1993-242914/30.
 DR N-PEDS; A040459.
 XX
 PT Use of anti-VLA-4 antibodies e.g. HP1/2, HP2/1, HP2/4, 125 or
 PT P4C2 antibodies - for inhibiting late phase response to allergen

PT In treating chronic allergen-induced asthma
 PF
 SS Claim 4; Page 29; 40pp; English.
 XX
 CC Asthma is treated by admin. of an anti-VLA (very late antigen)-4
 CC antibody, esp. monoclonal antibody HP1/2. The antibody is able to
 CC bind to the alpha 4 subunit of VLA-4 so as to (a) inhibit late phase
 CC response to an allergen to which the subject is hypersensitive or (b)
 CC elicit a late phase response to an allergen to which the subject is
 CC (updated on 25-MAR-2003 to correct PM field)
 XX
 SS Sequence 106 AA;
 SS
 Query Match 91.4%; Score 523; DB 14; Length 106;
 Best Local Similarity 94.3%; Pred. No. 1,4e-35;
 Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 IYMTGSPFRLVMSADNVTTCAGSGSYNDVAVYQCGQSPFRLVYASNTVGPDR 61
 DB 2 IYMTGSPFRLVMSADNVTTCAGSGSYNDVAVYQCGQSPFRLVYASNTVGPDR 61
 Oy 62 FTGSGYGFDFPFTSTVQAEHLAVYPCQDYSPPFGSGTLETKR 106
 DB 62 FTGSGYGFDFPFTSTVQAEHLAVYPCQDYSPPFGSGTLETKR 106
 RESULT 5
 AAR39567
 ID AAR39567 standard; Protein; 106 AA.
 XX
 AC AAR39567;
 XX 25-MAR-2003 (updated)
 DT 08-FEB-1994 (first entry)
 DS Sequence of the variable region of the light chain of the anti-VLA-4
 XX monoclonal antibody HP1/2 (HP1/2 V kappa).
 XX
 XX Monoclonal antibody; anti-very late antigen-4; VLA-4; HP1/2;
 XX variable light chain.
 XX
 OS Synthetic.
 XX
 XX MO315764-A1.
 XX
 PD 19-AUG-1993.
 XX
 XX 02-FEB-1993; 93MO-US00924.
 XX
 PR 12-FEB-1992; 92US-083139.
 XX (B10J) BIOGEN INC.
 XX
 P1 Lobb R;
 XX
 XX WPI, 1993-272566/34.
 DR N-PEDS; A0406080.
 XX
 PT Treatment of inflammatory bowel disease - using anti-very late
 PT antigen-4 antibody, polypeptide or other molecule recognizing
 PT anti-very late antigen-4, reducing acute inflammation in
 PT ulcerative colitis, Crohn's disease, etc.
 XX
 PS Disclosure; Page 26; 35pp; English.
 XX
 CC Anti-VLA-4 antibody - anti-very late antigen-4 antibody. One anti-
 CC VLA-4 monoclonal antibody is designated HP1/2 (Gibco, Grand Island,
 CC Inc. Cambridge, MA). The variable regions of the heavy and light
 CC chains of the anti-VLA-4 antibody HP1/2 were cloned, sequenced and
 CC immunoglobulin combination with constant regions of human
 CC antibody is similar in specificity and potency to the murine HP1/2
 CC antibody, and may be useful in methods for treating ulcerative

RESULT 8
 XX 1-SEP-1999
 XX ID AAV23985 standard; Protein: 106 Aa.
 XX AC AAV23985;
 XX DT 20-MAR-2003 (updated)
 XX DT 22-SEP-1999 (first entry)
 XX
 XX Antibody HPI/2 light chain variable region.
 XX
 XX Light chain variable region; very late antigen-4; VLA-4; antibody HPI/2;
 XX inflammatory bowel disease; B1 epitope; E2 epitope; alpha 4 subunit;
 XX ulcerative colitis; Crohn's disease.
 XX Mus sp.
 XX US5932214-A.
 XX
 XX 03-AUG-1999.
 XX
 XX 15-OCT-1997; 97US-0950660.
 XX
 XX 31-MAY-1995; 95US-046124.
 XX PR 12-FEB-1992; 92US-0851339.
 XX PR 02-FEB-1993; 93MO-US00924.
 XX PR 11-AUG-1994; 94US-0284603.
 XX PR 18-JUN-1995; 95US-0319857.
 XX
 XX (BIOV) BIOGEN INC.
 XX
 XX Burkly LC; Lobb RE;
 XX WPI: 1999-443570/37.
 XX N-PSDB; AAX6185.
 XX
 XX Treating inflammatory bowel disease with VLA-4 blockers
 XX
 XX Disclosure; Columns 25-26; 26pp; English.
 XX
 XX The present sequence represents the light chain variable region of the
 XX murine anti-human VLA-4 antibody HPI/2.
 XX The protein can be used in the method of the invention. The specification
 XX describes methods for treating inflammatory bowel disease with a
 XX composition comprising an antibody, or its fragments, able to bind to
 XX VLA-4.
 XX The antibody is useful for treating ulcerative colitis and Crohn's disease.
 XX (Updated on 20-MAR-2003 to correct PR field.)
 XX
 XX Sequence 106 Aa.
 XX
 XX Query Match 91.4%; Score 523; DB 20; Length 106;
 XX Best Local Similarity 94.3%; Pred. No. 1,4e-35;
 XX Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0.
 XX
 XX 2 IOWTSEKELVLSGGRVITTCASQGVNDVAVYQCFQSPGILLAVYASNYTGVPR 61
 XX 2 IWRVGTGKFLVLSGGRVITTCASQGVNDVAVYQCFQSPGILLAVYASNYTGVPR 61
 XX 62 FTGSGYGTDFFTTSTVOAEADLAVYFQQDYGSPFTFGGATLKI 106
 XX 62 FTGSGYGTDFFTTSTVOAEADLAVYFQQDYGSPFTFGGATLKI 106
 XX
 XX RESULT 9
 XX AAV10104 standard; Protein: 106 Aa.
 XX DT 20-MAR-2003 (updated)
 XX AC AAV10104;
 XX DT 04-JUN-1999 (first entry)

XX
 XX Anti VLA-4 antibody HPI/2 VK protein sequence.
 XX
 XX VLA-4; antibody; anti VLA-4 antibody HPI/2; VR chain; alpha 4 subunit;
 XX inflammatory bowel disease; B1 epitope; E2 epitope; alpha 4 subunit;
 XX vascular cell adhesion molecule-1; insulin-dependent diabetes; therapy.
 XX
 XX Homo sapiens.
 XX US5988507-A.
 XX
 XX 30-MAR-1999.
 XX
 XX 22-MAY-1995; 95US-0447118.
 XX PR 09-FEB-1993; 93US-0039330.
 XX PR 03-FEB-1994; 94US-0001456.
 XX
 XX (BIOV) BIOGEN INC.
 XX
 XX Burkly LC;
 XX WPI: 1999-243165/20.
 XX N-PSDB; AAX7914.
 XX
 XX Treating insulin-dependent diabetes by blocking VLA-4 antigen
 XX
 XX Disclosure; Column 27-28; 28pp; English.
 XX
 XX This sequence is the anti VLA-4 antibody HPI/2 VK chain.
 XX The antibody is useful for treating insulin-dependent
 XX type 1 diabetes, comprising administering to a prediabetic animal (or one
 XX showing partial beta-cell destruction) one or more compositions of an
 XX antibody that binds to the alpha 4 subunit of VLA-4 (very late
 XX antigen-4).
 XX The antibody is useful for treating ulcerative colitis and Crohn's disease.
 XX The treatment is used to prevent development of
 XX insulin-dependent diabetes.
 XX
 XX Sequence 106 Aa.
 XX
 XX Query Match 91.4%; Score 523; DB 20; Length 106;
 XX Best Local Similarity 94.3%; Pred. No. 1,4e-35;
 XX Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0.
 XX
 XX 2 IOWTSEKELVLSGGRVITTCASQGVNDVAVYQCFQSPGILLAVYASNYTGVPR 61
 XX 2 IWRVGTGKFLVLSGGRVITTCASQGVNDVAVYQCFQSPGILLAVYASNYTGVPR 61
 XX 62 FTGSGYGTDFFTTSTVOAEADLAVYFQQDYGSPFTFGGATLKI 106
 XX 62 FTGSGYGTDFFTTSTVOAEADLAVYFQQDYGSPFTFGGATLKI 106
 XX
 XX RESULT 10
 XX AAV6742 standard; Protein: 106 Aa.
 XX AC AAV6742;
 XX DT 20-MAR-2003 (updated)
 XX DT 16-APR-1999 (first entry)
 XX
 XX Light chain variable region of antibody HPI/2.
 XX
 XX Light chain variable region of antibody HPI/2;
 XX alpha 4 beta 1 integrin very late antigen-4; VLA-4;
 XX chronic antigen-induced asthma; VLA-4-leukocyte migration;
 XX leukocyte infiltration; signal transduction inhibition.
 XX
 XX Mus sp.

PN US5871734-A.
 XX 16-FEB-1999.
 PD
 XX 21-MAR-1997; 97US-08222830.
 XX
 XX 31-MAY-1995; 95US-0456493.
 PR 13-JUN-1993; 92US-0821768.
 PR 12-JUN-1993; 91US-0800030.
 PR 18-JUN-1995; 95US-0374311.
 XX
 PA (BIO) BIOGEN INC.
 XX
 XX Burkly LC, Lobb RB.
 PR WPI; 1999-16573/14.
 DR N-ESDB; AAM15094.
 XX
 PT Treating allergic asthma with very late antigen-4 binding agent -
 XX to inhibit late phase response and decrease airway hypersensitivity
 XX
 XX Disclosure; Columns 23-24; 31pp; English.
 XX
 CC The present sequence represents the light chain variable region of
 CC antibody HP/2. This antibody binds alpha-4 beta-1 integrin very
 CC specifically and inhibits the binding of alpha-4 beta-1 integrin to
 CC extracellular matrix components. Inhibition of alpha-4 beta-1 integrin
 CC migration prevents secondary effects of leukocyte infiltration
 CC (release of toxins, inducers of soluble inflammatory cell mediators
 CC or chemotactic agents) and inhibition of signal transduction causing
 CC cell proliferation and tumor growth.
 CC (Updated on 20-MAR-2003 to correct PR field.)
 CC
 SQ Sequence 106 AA;
 XX
 Query Match 91.4%; Score 523; DB 20; Length 106;
 Best Local Similarity 94.3%; Pred. No. 1,4e-35;
 Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IOMTOSKPEFLVNSAGRWYITTCASQSVSNVAVVQOKQSPFLVLYSNRYGVOPR 61
 DB 2 IWTGTFEFLVNSAGRWYITTCASQSVSNVAVVQOKQSPFLVLYSNRYGVOPR 61
 QY 62 FTSGSGTGTDFFTISTVQADLAVYFCQDYSPTFGSGTFLKI 106
 DB 62 FTSGSGTGTDFFTISTVQADLAVYFCQDYSPTFGSGTFLKI 106
 RESULT 11
 ID AAB73463 standard; Protein; 106 AA.
 AC AAB73463;
 XX
 DT 02-JUL-2001 (first entry)
 DX
 MX Murine anti-VLA-4 monoclonal antibody HP/2 VL.
 XX
 XX Integrin antagonist; VLA-4 antagonist; alpha-4-beta-1 integrin;
 XX very late antigen; monoclonal antibody HP/2; mouse; murine;
 XX chronic diabetic nephropathy; hypertensive nephrosclerosis;
 XX diabetic renal hypertrophy; hypertensive glomerulonephritis;
 XX hypertensive glomerulonephritis; chronic glomerulonephritis;
 XX light chain variable region; VL.
 XX
 OS Mus sp.
 XX
 XX MO200113936-AL.
 XX
 PD 22-MAR-2001.

XX 14-SEP-2000; 2000WO-0525140.
 XX
 XX 14-SEP-1999; 99US-0153826.
 XX
 XX (BIO) BIOGEN INC.
 XX (UNLO) IMPERIAL COLLEER SCI TECHNOLOGY & MED.
 XX
 XX Allen A, Pusey C, Lobb R.
 PR WPI; 2001-273408/28.
 DR N-ESDB; AAF6602.
 XX
 XX Treating a mammal in, or at a risk of developing, chronic renal
 XX failure, involving administering at least one integrin antagonist to the
 XX mammal.
 XX
 XX Claim 12; Page 1; 62pp; English.
 XX
 CC The invention relates to a method for treating a mammal with,
 CC or at risk of developing, chronic renal failure, involving the
 CC administration of at least one integrin antagonist. The integrin
 CC antagonist is a polypeptide chain consisting of alpha-1-subunit-
 CC alpha-2-subunit and alpha-3-subunit. The antagonists are antibodies
 CC containing integrins. In particular, the antagonists are antibodies
 CC specific for VLA-1 (very late antigen-1, alpha-1-beta-1 integrin) or
 CC alpha-4 beta-1 integrin (VLA-4). In particular, the antagonists are
 CC integrin and its cognate ligand and VLA-4 in the case of VLA-4).
 CC The method of the invention may be used to treat chronic renal failure,
 CC end-stage renal disease, chronic diabetic nephropathy, diabetic
 CC hypertensive glomerulonephritis, chronic glomerulonephritis, peridialy
 CC nephritis or renal dysplasia. The present sequence represents the light
 CC chain variable region (VL) of the murine anti-VLA-4 monoclonal antibody
 CC 18 given in US5932214, columns 25-26.
 CC
 SQ Sequence 106 AA;
 XX
 Query Match 91.4%; Score 523; DB 22; Length 106;
 Best Local Similarity 94.3%; Pred. No. 1,4e-35;
 Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IOMTOSKPEFLVNSAGRWYITTCASQSVSNVAVVQOKQSPFLVLYSNRYGVOPR 61
 DB 2 IWTGTFEFLVNSAGRWYITTCASQSVSNVAVVQOKQSPFLVLYSNRYGVOPR 61
 QY 62 FTSGSGTGTDFFTISTVQADLAVYFCQDYSPTFGSGTFLKI 106
 DB 62 FTSGSGTGTDFFTISTVQADLAVYFCQDYSPTFGSGTFLKI 106
 RESULT 12
 ID ABO08539 standard; Protein; 106 AA.
 AC ABO08539;
 XX
 DT 02-JUN-2003 (first entry)
 DX
 MX Mouse anti-VLA-4 antibody HP/2 kappa chain variable region.
 XX
 XX Mouse; antibody; VLA-4; alpha-beta-1 integrin; VCM-1; ID;
 XX immunological detection molecule; inflammatory bowel disease;
 XX ulcerative colitis; Crohn's disease; Crohn's disease;
 XX antitumor; antiinflammatory; VCM-2 IgG; kappa chain variable region.
 XX
 OS Mus musculus.
 XX
 XX US6482409-B1.
 XX
 PD

FT Peptide 549.554
 FT /label= TAG
 FT /notes="hexa-histidine tail"
 PK M095010828-A1.
 PK 09-FEB-1995.
 PK 15-JUL-1994; 94MO-US07919.
 PK 02-AUG-1993; 93US-0201329.
 PK (HMOUS-) HOUSTON BIOTECNOLOGY INC.
 PI Gould RM, Kallisher PJ, Wallace TL, Wood WS;
 PI WPI, 1995-082036/11.
 CC N-PS09; A0085386.
 CC New single chain immuno-toxin - binds specifically to epithelial
 PT cells, for inhibiting development of sec. carcinoma after
 PT excisional/capsular carcinoma excision.
 PS Discloure; Fig.4; 6pp; English.
 CC The immunotoxin given in A870827 comprises the heavy and light chain
 CC variable regions of anti-lane epithelium 19c3 Mab 4127, linked to
 CC ricin-A and a hexa-histidine tag. The DNA construct encoding the
 CC immunotoxin was expressed from pHB3 in E. coli.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SO Sequence 554 Aa;
 SO
 Query Match 90.6%; Score 518; DB 16; Length 554;
 SO
 Matches 98; Conservative 4; Mismatches 26-34; Indels 0; Gaps 0;
 OY 2 10MTGSRKFLVSAAGRVYTTCKASGSVSNVAMVQKQKQSPKLMVYSNRITGVDP 61
 DB 169 IWTGTFKFLVSAAGRVYTTCKASGSVSNVAMVQKQKQSPKLMVYSNRITGVDP 228
 OY 62 FTGSGVGTDFPFTISVQADLAVYFCQDQVSPPTFGGQTRLEVK 107
 DB 229 FTGSGVGTDFPFTISVQADLAVYFCQDQVSPPTFGGQTRLEVK 274
 RESULT 15
 ID AAR23413
 AC AAR23413;
 AC 25-MAR-2003 (updated)
 DT 11-JAN-1993 (first entry)
 XX
 XX Light chain variable domain of Mab HM93 to TNFalpha epitope.
 KM monoclonal antibody; humanized; chimeric; CDR; neoplastic therapy;
 KM shock; antilymphocyte therapy; endotoxin shock; septic shock;
 KM sepsis; cardiovascular shock; tumour necrosis factor alpha;
 KM multi-organ failure.
 XX
 OS Chimeric.
 OS
 OS M09211383-A1.
 PD 09-JUL-1992.
 PD 20-DEC-1991; 91MO-G802300.
 PD 21-DEC-1990; 90MO-G802017.
 PD 03-MAY-1991; 91GB-0009645.
 PK
 PK
 PK

PA (CLUT) CELLTECH LTD.
 PA Adult TB, Althwal DS, Bodmer WM, Entage JS;
 PK WPI, 1992-250102/30.
 PK Recombinant antibody specific for human TNF-alpha - for treatment
 PT of shock and immuno-regulatory and inflammatory disorders, also
 PT used in diagnosis
 PS Claim 2; Fig 4; 57pp; English.
 CC This sequence is that of the light chain variable domain of a chimeric
 CC antibody to an epitope of human tumour necrosis factor. The
 CC sequence shows 21 differences compared with C86 (R23411.2) - in
 CC the light chain at positions 50, 96, and in the framework at 1, 19,
 CC 32, 46, 46', 103, and 106, and in the heavy chain in Cys C86 at
 CC 52, 48, and 95, and in the framework at 1, 40, 56, 90, 97, 121, 97,
 CC and 105.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 SO Sequence 107 Aa;
 SO
 Query Match 89.5%; Score 512; DB 13; Length 107;
 SO
 Matches 94; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
 OY 1 10MTGSRKFLVSAAGRVYTTCKASGSVSNVAMVQKQKQSPKLMVYSNRITGVDP 60
 DB 1 IWTGTFKFLVSAAGRVYTTCKASGSVSNVAMVQKQKQSPKLMVYSNRITGVDP 60
 OY 61 FTGSGVGTDFPFTISVQADLAVYFCQDQVSPPTFGGQTRLEVK 107
 DB 61 FTGSGVGTDFPFTISVQADLAVYFCQDQVSPPTFGGQTRLEVK 107
 SO
 Search completed: November 7, 2003, 07:27:00
 Job time : 47.574 secs

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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:10:13 / Search time 94.7143 seconds
(without alignment)

195,799 Million cell updates/sec

File: US-09-661-992b-82_copy_135_242

Perfect score: 5271 DIGNOTSKRLVUSAGDRT.....QDVGSPPFGGKTLRIR 108

Sequence: 1 DIGNOTSKRLVUSAGDRT.....QDVGSPPFGGKTLRIR 108

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 644079 seqs, 17174292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Databases:

Published Applications AA.*
1: /csm2_6/pdata/2/pubpa/US07_PUBCOMB.pep.*
2: /csm2_6/pdata/2/pubpa/PC7_NEW_PUB.pep.*
3: /csm2_6/pdata/2/pubpa/US06_NEW_PUB.pep.*
4: /csm2_6/pdata/2/pubpa/US05_NEW_PUB.pep.*
5: /csm2_6/pdata/2/pubpa/US04_NEW_PUB.pep.*
6: /csm2_6/pdata/2/pubpa/PC7US_PUBCOMB.pep.*
7: /csm2_6/pdata/2/pubpa/US08_NEW_PUB.pep.*
8: /csm2_6/pdata/2/pubpa/US08_PUBCOMB.pep.*
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10: /csm2_6/pdata/2/pubpa/US09_PUBCOMB.pep.*
11: /csm2_6/pdata/2/pubpa/US09_PUBCOMB.pep.*
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15: /csm2_6/pdata/2/pubpa/US10_NEW_PUB.pep.*
16: /csm2_6/pdata/2/pubpa/US00_PUBCOMB.pep.*
17: /csm2_6/pdata/2/pubpa/US00_PUBCOMB.pep.*
18: /csm2_6/pdata/2/pubpa/US00_PUBCOMB.pep.*

Pred. No. is the number of results predicted by the change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Pred. No.	Score	Query Match	Length	ID	Description
1	523	91.4	106	US-10-428-662-10	Sequence 10, App1
2	523	91.4	106	US-10-428-662-10	Sequence 2, App1
3	523	91.4	106	US-10-428-662-10	Sequence 11, App1
4	512	89.5	107	US-10-428-049-17	Sequence 17, App1
5	507	88.6	107	US-10-428-049-13	Sequence 13, App1
6	498	87.1	107	US-10-283-88-6	Sequence 6, App1
7	498	87.1	107	US-10-283-88-6	Sequence 7, App1
8	479	83.7	128	US-10-428-662-67	Sequence 67, App1
9	479	83.7	128	US-10-428-662-67	Sequence 68, App1
10	466	81.5	128	US-10-428-662-63	Sequence 63, App1
11	466	81.5	128	US-10-428-662-63	Sequence 64, App1
12	448	78.3	128	US-10-428-049-16	Sequence 16, App1
13	448	78.3	128	US-10-428-049-16	Sequence 72, App1
14	442	77.3	128	US-10-422-049-14	Sequence 36, App1
15	442	77.3	128	US-08-773-784-36	Sequence 36, App1

16	442	77.3	333	US-10-059-281-61	Sequence 61, App1
17	439	76.7	107	US-09-509-088-130	Sequence 10, App
18	439	76.7	107	US-09-509-088-130	Sequence 11, App
19	439	76.7	131	US-09-269-921-104	Sequence 104, App
20	439	76.7	131	US-10-218-283-104	Sequence 104, App
21	437	76.4	331	US-10-059-281-169	Sequence 169, App
22	435	76.0	250	US-09-887-883-2	Sequence 2, App1
23	431	75.3	107	US-09-509-088-134	Sequence 134, App
24	429	74.7	107	US-09-566-2064-79	Sequence 79, App1
25	427	74.7	107	US-09-566-2064-49	Sequence 49, App1
26	425	74.3	127	US-10-268-1051-1	Sequence 1, App1
27	425	74.3	127	US-10-268-1051-1	Sequence 15, App1
28	425	74.3	127	US-10-268-1051-1	Sequence 16, App1
29	424	74.1	133	US-09-874-141-51	Sequence 51, App1
30	423	74.0	106	US-09-824-286-4	Sequence 4, App1
31	423	74.0	107	US-09-956-2064-61	Sequence 61, App1
32	422	74.0	127	US-09-956-2064-95	Sequence 95, App1
33	422	73.9	213	US-10-215-1808-76	Sequence 76, App1
34	422.5	73.9	213	US-10-266-1328-76	Sequence 76, App1
35	422.5	73.9	213	US-10-266-1328-76	Sequence 76, App1
36	422.5	73.9	234	US-10-268-1494-24	Sequence 24, App1
37	422.5	73.9	234	US-10-268-1494-24	Sequence 24, App1
38	422.5	73.9	234	US-10-268-1494-24	Sequence 24, App1
39	421	73.6	126	US-09-760-725-6	Sequence 6, App1
40	421	73.6	126	US-09-355-925-6	Sequence 6, App1
41	421	73.6	126	US-09-355-925-6	Sequence 6, App1
42	421	73.6	126	US-09-509-088-136	Sequence 136, App
43	421	73.6	126	US-10-428-088-136	Sequence 6, App1
44	421	73.6	126	US-10-428-088-136	Sequence 6, App1
45	421	73.6	126	US-10-315-125-6	Sequence 6, App1
				US-10-218-253-106	Sequence 106, App

ALIGNMENTS

RESULT 1
US-10-428-662-10
Sequence 10, Application US/10428662
ORIGIN: US09-509-088-130
APPLICANT: Lobb, Roy R.
APPLICANT: Tempert, Philip R.
APPLICANT: US/10428662
FILE REFERENCE: 10274-007001
CURRENT FILING DATE: 2003-05-02
PRIOR FILING DATE: 1993-01-12
PRIOR APPLICATION NUMBER: US 06/004,798
PRIOR APPLICATION NUMBER: PCT/US94/00266
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Padded for Windows Version 4.0
SEQ ID NO 10
US-10-428-662-10
TYR1: P
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: light chain variable region
US-10-428-662-10
Query Match 91.4%; Score 523; DB 12; Length 106;
Best Local Similarity 94.3%; Pred. No. 46; 44;
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
2 IYVQGGPFLVADADPTVYIKSGASGVDAVQKQCGSKLVAASNTYVDPD 61
DB IYVQGGPFLVADADPTVYIKSGASGVDAVQKQCGSKLVAASNTYVDPD 61
QY PFGSGGPGFFSTFQVADHVLAVYACQDQVSPFPFGGKTLRIR 106

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DB
66 FTOSGVDFTFTITVOAEMALVAFPCODVSPFFGPGCTKLEI 106

RESULT 2
US-10-095-496-2
1 Sequence 2, Application US/10095496
2 Publication No. US2003007969A1
3 APPLICANT: Cobb, Roy
4 APPLICANT: Allen, Andrew
5 APPLICANT: Passy, Charles
6 APPLICANT: Hagedorn, College of Science, Technology and Medicine
7 TITLE OF INVENTION: Therapies for Chronic Renal Failure
8 TITLE OF INVENTION: Using One or More Intergrin Antagonists
9 FILE REFERENCE: 6082 NUMBER: US/01/095,496
10 CURRENT FILING DATE: 2002-03-12
11 PRIOR FILING DATE: 2000-09-14
12 PRIOR FILING DATE: 2000-09-14, 153,326
13 PRIOR FILING DATE: 1999-09-14
14 NUMBER OF SEQ ID NOS: 21
15 SEQ ID NOS: 1-21
16 LENGTH: 106
17 SOFTWARE: FastSeq for Windows Version 4.0
18 TYPE: PRT
19 ORGANISM: Artificial Sequence
20 OTHER INFORMATION: Hb1/2 Light chain variable region
21 US-10-095-496-2

Query: Hbch
          91.4% Score 523; DB 15; Length 106;
          Blast Local Similarity 94.3%; Pct Ident 90.94e-44;
          Matches 99/ Conservative 3/ Mismatches 93/ Indels 0/ Gaps 0
QY
2 LCQSGFTFTFTITVOAEMALVAFPCODVSPFFGPGCTKLEI 106
2 IWPOTFTFLLSGSGRRFTITGSCGVTVAVWAVQCFQSGPFLIYASNNITVQVPR 61
DB
62 FTOSGVDFTFTITVOAEMALVAFPCODVSPFFGPGCTKLEI 106

RESULT 3
US-10-282-978-4
1 Sequence 4, Application US/10252978
2 Publication No. US2003009599A1
3 APPLICANT: Cobb, Roy R.
4 APPLICANT: Bartly, Linda C.
5 TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE
6 CURRENT APPLICATION NUMBER: US/09/157,452
7 CURRENT FILING DATE: 2002-08-23
8 PRIOR APPLICATION NUMBER: US/09/157,452
9 PRIOR FILING DATE: 1998-09-22
10 PRIOR FILING DATE: 1997-10-15
11 PRIOR FILING DATE: 1994-08-11
12 PRIOR FILING DATE: 1993-02-08
13 PRIOR FILING DATE: 1993-02-08, 07/895,139
14 NUMBER OF SEQ ID NOS: 16
15 SEQ ID NOS: 1-16
16 SOFTWARE: FastSeq for Windows Version 3.0
17 LENGTH: 106
18 TYPE: PRT

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[illegible]

PRIOR APPLICATION NUMBER: 08/456,418
 PRIOR FILING DATE: 1995-06-01
 PRIOR APPLICATION NUMBER: 08/373,882
 PRIOR FILING DATE: 1995-06-01
 PRIOR APPLICATION NUMBER: 07/920,376
 PRIOR FILING DATE: 1992-09-28
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 107
 TYPE: PRT
 ORGANISM: Murine
 US-10-422-045-13

Query Match 88.6%; Score 507; DB 12; Length 107;
 Best Local Similarity 90.6%; Pred. No. 3,4e-42;

Matches 96; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 Oy 2 IYMTGSPFLVSLAGGVITTCAGAGSNDVAMVYKQPGSPKLLMTVANSRYGVPR 61
 Db 2 IYMTGSPFLVSLAGGVITTCAGAGSNDVAMVYKQPGSPKLLMTVANSRYGVPR 61
 Oy 62 FTSGSGVDTFTLTISVQAEADLVAFVCOQDYSPPFTGGSTLTKIK 107
 Db 62 FTSGSGVDTFTLTISVQAEADLVAFVCOQDYSPPFTGGSTLTKIK 107

RESULT 6

US-10-283-838-6

Sequence 6; Application US/0283838

Sequence 6; Patent In Release #1.0, Version #1.25

GENERAL INFORMATION

APPLICANT: Per Antnason, Per Bjork, Mikael Dohlehan,

John Hansen, Reje Kalland, Lars

Correspondence Address: Howitt, Kimball & Krieger

Street: 117 West Loop South, 10th Floor

City: Houston

State: TX

ZIP: 77027-8095

Computer Readable Form:

Medium Type: floppy disk

Operating System: PC-DOS/MS-DOS

Software: PatentIn Release #1.0, Version #1.25

Current Application Data: US/10/283,838

Application Number: 283,838

Classification: <unknown>

Prior Application Data: US/08/456,418

Application Number: 456,418

Filing Date: March 29, 1996

Registration Number: 25,886

Reference/Doclet Number: 14966/1

Telecommunication Information:

Telephone: 1350-0099

Telex: 1350-0099

Information for SEQ ID NO: 6:

Sequence Characteristics:

Length: 107 amino acids

Molecule Type: peptide

Topology: linear

Sequence Description: SEQ ID NO: 6:

US-10-283-838-6

Query Match 87.1%; Score 438; DB 15; Length 107;
 Best Local Similarity 87.9%; Pred. No. 2.6e-41;

Matches 94; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Oy 1 DIYMTGSPFLVSLAGGVITTCAGAGSNDVAMVYKQPGSPKLLMTVANSRYGVPR 60
 Db 1 DIYMTGSPFLVSLAGGVITTCAGAGSNDVAMVYKQPGSPKLLMTVANSRYGVPR 60
 Oy 61 FTSGSGVDTFTLTISVQAEADLVAFVCOQDYSPPFTGGSTLTKIK 107
 Db 61 FTSGSGVDTFTLTISVQAEADLVAFVCOQDYSPPFTGGSTLTKIK 107

RESULT 7

US-09-900-766-1

Sequence 7; Application US/0990766

Sequence 7; Patent In Release #1.0, Version #1.25

GENERAL INFORMATION

Publication No. US2003009655A1

APPLICANT: FORBES, GORDAN

APPLICANT: ANTONSSON, PER

APPLICANT: MALSB, EVON

APPLICANT: ANTONSSON, PER

Title of Invention: A NOVEL, ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY

Current Application Number: US/09/900,766

Current Filing Date: 2001-07-06

Number of SEQ ID NOS: 7

Software: PatentIn version 3.0

Length: 672

Type: PRT

Organism: Artificial Sequence

Sequence: PEPTIDE

Location: (1)-(672)

Other Information: Conjugate protein

US-09-900-766-1

Query Match 85.7%; Score 490; DB 11; Length 672;
 Best Local Similarity 86.5%; Pred. No. 1.1e-39;

Matches 93; Conservative 5; Mismatches 9; Indels 0; Gaps 0;
 Oy 2 IYMTGSPFLVSLAGGVITTCAGAGSNDVAMVYKQPGSPKLLMTVANSRYGVPR 61
 Db 460 IYMTGSPFLVSLAGGVITTCAGAGSNDVAMVYKQPGSPKLLMTVANSRYGVPR 619
 Oy 62 FTSGSGVDTFTLTISVQAEADLVAFVCOQDYSPPFTGGSTLTKIK 108
 Db 520 FTSGSGVDTFTLTISVQAEADLVAFVCOQDYSPPFTGGSTLTKIK 566

RESULT 8

US-10-428-662-71

Sequence 71; Application US/10428662

Sequence 71; Patent In Release #1.0, Version #1.25

GENERAL INFORMATION

APPLICANT: Lobb, Roy R.

APPLICANT: Gavr, Frank J.

Title of Invention: ANTIBODY ANTIV-14M ANTIBODY MOLECULES

Current Application Number: US/10/428,662

Current Filing Date: 2003-05-02

Prior Filing Date: 1995-05-31

Prior Application Number: US 08/004,798

Prior Filing Date: 1993-01-12

Prior Filing Date: 1994-01-07

Number of SEQ ID NOS: 109

Software: PatentIn version 4.0

/ SEQ ID NO 71
 / LENGTH 124
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / OTHER INFORMATION: Light chain variable region
 US-10-428-662-71

Query Match Similarity 83.7%; Score 429; DB 12; Length 124;
 Best Local Similarity 83.7%; Pred. No. 2, 1e-39;
 Matches 90; Conservative 7; Mismatches 0; Gaps 0;

Oy 2 IOMTGSPEFLVSGADRTTTCAGSISVNDVAVYQKQSGSPFLMTYSASRRITGVPD 61
 Db 20 IIMQSPSLASVSDVDVITTCAGSISVNDVAVYQKQSGSPFLMTYSASRRITGVPD 79

Oy 62 FTGSGVGTDFITFTISVQADLVAVYPCQGVSPPTFGGKTLKLR 106
 Db 80 FSGSGVGTDFITFTISVQADLVAVYPCQGVSPPTFGGKTLKLR 124

RESULT 9
 US-10-428-662-67
 / Sequence 67; Application US/10428662
 / Publication No. US20030185819A1
 / GENERAL INFORMATION:
 / ORGANISM: Artificial Sequence
 / APPLICANT: Carr, Frank J.
 / TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES

/ CURRENT FILING DATE: 2003-05-02
 / PRIOR APPLICATION NUMBER: US/10/428,662
 / PRIOR FILING DATE: 2003-05-02
 / PRIOR APPLICATION NUMBER: US/08/454,899G
 / PRIOR FILING DATE: 2003-05-02
 / PRIOR APPLICATION NUMBER: US/08/004,798
 / PRIOR FILING DATE: 1993-01-12
 / PRIOR APPLICATION NUMBER: ECT/US94/00266
 / PRIOR FILING DATE: 1994-01-07
 / SOFTWARE: FASTSEQ for Windows Version 4.0
 / SEQ ID NO 67
 / LENGTH 128
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / OTHER INFORMATION: Light chain variable region
 US-10-428-662-67

Query Match Similarity 83.7%; Score 479; DB 12; Length 128;
 Best Local Similarity 81.5%; Pred. No. 2, 2e-39;
 Matches 88; Conservative 10; Indels 0; Gaps 0;

Oy 1 DIOMTGSPEFLVSGADRTTTCAGSISVNDVAVYQKQSGSPFLMTYSASRRITGVPD 60
 Db 20 DIOMTGSPEFLVSGADRTTTCAGSISVNDVAVYQKQSGSPFLMTYSASRRITGVPD 79

Oy 61 FTGSGVGTDFITFTISVQADLVAVYPCQGVSPPTFGGKTLKLR 108
 Db 80 FSGSGVGTDFITFTISVQADLVAVYPCQGVSPPTFGGKTLKLR 127

RESULT 10
 US-10-428-662-63
 / Sequence 63; Application US/10428662
 / Publication No. US20030185819A1
 / GENERAL INFORMATION:
 / ORGANISM: Artificial Sequence
 / APPLICANT: Carr, Frank J.
 / TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
 / FILE REFERENCE: 10274-007001
 / CURRENT APPLICATION NUMBER: US/10/428,662

/ CURRENT FILING DATE: 2003-05-02
 / PRIOR APPLICATION NUMBER: US/08/454,899G
 / PRIOR FILING DATE: 1993-05-31
 / PRIOR APPLICATION NUMBER: US/08/004,798
 / PRIOR FILING DATE: 1993-05-31
 / PRIOR APPLICATION NUMBER: ECT/US94/00266
 / PRIOR FILING DATE: 1994-01-07
 / SOFTWARE: FASTSEQ for Windows Version 4.0
 / SEQ ID NO 63
 / LENGTH 128
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / OTHER INFORMATION: Light chain variable region
 US-10-428-662-63

Query Match Similarity 81.5%; Score 466; DB 12; Length 128;
 Best Local Similarity 80.4%; Pred. No. 4, 1e-36;
 Matches 86; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Oy 2 IOMTGSPEFLVSGADRTTTCAGSISVNDVAVYQKQSGSPFLMTYSASRRITGVPD 61
 Db 21 IIMQSPSLASVSDVDVITTCAGSISVNDVAVYQKQSGSPFLMTYSASRRITGVPD 80

Oy 62 FTGSGVGTDFITFTISVQADLVAVYPCQGVSPPTFGGKTLKLR 108
 Db 81 FSGSGVGTDFITFTISVQADLVAVYPCQGVSPPTFGGKTLKLR 127

RESULT 11
 US-10-428-662-31
 / Sequence 31; Application US/10428662
 / Publication No. US20030185819A1
 / GENERAL INFORMATION:
 / ORGANISM: Artificial Sequence
 / APPLICANT: Carr, Frank J.
 / TITLE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES

/ CURRENT FILING DATE: 2003-05-02
 / PRIOR APPLICATION NUMBER: US/10/428,662
 / PRIOR FILING DATE: 2003-05-02
 / PRIOR APPLICATION NUMBER: US/08/454,899G
 / PRIOR FILING DATE: 2003-05-02
 / PRIOR APPLICATION NUMBER: US/08/004,798
 / PRIOR FILING DATE: 1993-01-12
 / PRIOR APPLICATION NUMBER: ECT/US94/00266
 / PRIOR FILING DATE: 1994-01-07
 / SOFTWARE: FASTSEQ for Windows Version 4.0
 / SEQ ID NO 31
 / LENGTH 128
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / OTHER INFORMATION: Light chain variable region
 US-10-428-662-31

Query Match Similarity 80.6%; Score 461; DB 12; Length 128;
 Best Local Similarity 78.7%; Pred. No. 1, 3e-37;
 Matches 85; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Oy 1 DIOMTGSPEFLVSGADRTTTCAGSISVNDVAVYQKQSGSPFLMTYSASRRITGVPD 60
 Db 20 DIOMTGSPEFLVSGADRTTTCAGSISVNDVAVYQKQSGSPFLMTYSASRRITGVPD 79

Oy 61 FTGSGVGTDFITFTISVQADLVAVYPCQGVSPPTFGGKTLKLR 108
 Db 80 FSGSGVGTDFITFTISVQADLVAVYPCQGVSPPTFGGKTLKLR 127

RESULT 12
 US-10-422-049-18


```

CORRESPONDENCE ADDRESS:
ADDRESSES: DAVID A. JACKSON, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM: d1sk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
APPLICATION NUMBER: US 08/779,784
FILING DATE: 07-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA: US 08/236,520
APPLICATION NUMBER: US 08/236,520
FILING DATE: 07-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
EXPIRATION DATE: 26-SEP-2001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
ORGANISM: Homo sapiens
ORGANISM: Mus musculus
US-08-779-784-36

Query Match: 77.3%, Score 442, DB 8, Length 128;
Seq. ID: 26742, Score 442, DB 8, Length 128;
Matches: 85; Conservative 8; Mismatches 15; Gaps 0;

QY 1 DTCMTGSEPLVNADEPVTTTCAGSGSVMDNANQCGQSGKLVYANKTCTCPD 60
DB 21 DVTGSHHSTGVDPDVTTCAGSDVSTAVAYQCGQSPRLTYSKFRVTCVPD 80
QY 61 RFTGSGGTGTFITSTVQENLAVYTCQDPQSPFTFGGTXLXLR 108
DB 81 RFTGSGGTGTFITSTVQENLAVYTCQDPQSPFTFGGTXLXLR 128

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Search Completed: November 7, 2003, 08:16:51
 Job time : 95.7343 secs

GenCore version 5.1.6
Copyright (c) 1995 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18

Search time 11.6611 seconds
(without alignments)
288.098 Million cell updates/sec

Perfect score: 572
Sequence: 1 D1MGCSRELYAAGDRTV.....QQVSPYTCCKTEIKK 108

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 32877 seqs 4231058 residues

Total number of hits satisfying chosen parameters: 32877

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: 1: Tissue Patents Ab.*
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3: /cgm2/6/prodata/1/isa/BA.COMB.pep.*
4: /cgm2/6/prodata/1/isa/BA.COMB.pep.*
5: /cgm2/6/prodata/1/isa/BA.COMB.pep.*
6: /cgm2/6/prodata/1/isa/BA.COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
sequence identical to the query sequence. The probability of finding
and is derived by analysis of the local score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	523	91.4	106	US-08-622-8109-4	Sequence 4, Appl1
2	523	91.4	106	US-08-157-4528-4	Sequence 4, Appl1
3	523	91.4	106	US-08-157-4528-4	Sequence 4, Appl1
4	523	91.4	106	US-08-157-4528-4	Sequence 4, Appl1
5	523	91.4	106	US-08-157-4528-4	Sequence 4, Appl1
6	523	91.4	106	US-08-157-4528-4	Sequence 4, Appl1
7	498	87.1	107	US-08-625-6325-6	Sequence 7, Appl1
8	474	82.9	105	US-08-065-089-17	Sequence 10, Appl1
9	466	81.5	128	US-08-463-128-10	Sequence 10, Appl1
10	466	81.5	128	US-08-463-128-10	Sequence 10, Appl1
11	461	80.6	128	US-08-463-128-10	Sequence 6, Appl1
12	461	80.6	128	US-08-463-128-10	Sequence 6, Appl1
13	461	80.6	128	US-08-463-128-10	Sequence 6, Appl1
14	461	80.6	128	US-08-463-128-10	Sequence 6, Appl1
15	443	77.4	109	US-08-437-6425-5	Sequence 5, Appl1
16	443	77.4	109	US-08-437-6425-5	Sequence 5, Appl1
17	443	77.4	109	US-08-437-6425-5	Sequence 5, Appl1
18	443	77.4	109	US-08-437-6425-5	Sequence 5, Appl1
19	443	77.4	109	US-08-437-6425-5	Sequence 5, Appl1
20	443	77.4	109	US-08-437-6425-5	Sequence 5, Appl1
21	437	76.4	617	US-08-840-713-37	Sequence 3, Appl1
22	437	76.4	617	US-08-840-713-37	Sequence 3, Appl1
23	437	76.4	617	US-08-840-713-37	Sequence 3, Appl1
24	437	76.4	617	US-08-840-713-37	Sequence 3, Appl1
25	437	76.4	617	US-08-840-713-37	Sequence 3, Appl1
26	437	76.4	617	US-08-840-713-37	Sequence 3, Appl1
27	435	76.0	250	US-08-461-184-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-08-622-8109-4
Query No. 58721
GENERAL INFORMATION:
APPLICANT: Lobby Roy R.; Burky, Linda C.
TITLE OF INVENTION: Treatment for Asthma with VLA-4 Blocking
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: LAIVRE & COCKFIELD, LLP
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SEQUENCE RELEASE: 11/0
CURRENT APPLICATION DATA: Release #2.0
APPLICATION NUMBER: US/06/122,810/8
FILING DATE: 03-MAR-1997
PRIORITY APPLICATION DATA: US 06/165,193
FILING DATE: 31-MAY-1995
PRIORITY APPLICATION DATA: US 06/174,331
APPLICATION NUMBER: 1995
PRIORITY APPLICATION DATA: US 06/256,631
FILING DATE: 12-JUL-1994
PRIORITY APPLICATION DATA: RCT/US93/00030
FILING DATE: 12-JAN-1993
APPLICATION DATA: 07/821,768
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Louis (PLM)
REGISTRATION NUMBER: 35,965
TELEPHONE: (617)722-7100
TELEFAX: (617)722-4214
INSTRUMENT: CDS
SEQUENCE CDS ID NO.: 4
LENGTH: 106 amino acids
TYPE: amino acid

TOPOLGCV: linear
MOLECULE TYPE: protein

US-08-822-830b-4

Query Match

Best Local Similarity 91.4% Score 523; DB 2; Length 106;
Pct Local Similarity 94.3% Pct No. 3e-46;
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IOWTSGPFFVLASGGRVITTCAGSGVSNVAVYVCOGSGPFLMYASNRITGVPR 61
DB 2 IVMGTFEFLVSGRVTTCAGSGVSNVAVYVCOGSGPFLMYASNRITGVPR 61
QY 62 FTSGSGVDTFTTSTVQMDLAVYVCOGSGPFTFGQVLEI 106
DB 62 FTSGSGVDTFTTSTVQMDLAVYVCOGSGPFTFGQVLEI 106

RESULT 2

US-09-157-452b-4
Sequence 4, Application US/08950660

Patent No. 5932214

GENERAL INFORMATION: Roy R. Buckley, Linda C.

TITLE OF INVENTION: Treatment For Inflammatory Bowel Disease

NUMBER OF INVENTORS: 11

CORRESPONDENCE ADDRESS: COPTREID

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

ZIP: 02109-1975

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/950,660

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/456,124

FILING DATE: 08/373,857

APPLICATION NUMBER: US 08/373,857

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 12-JAN-1995

APPLICATION NUMBER: US 08/284,603

FILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/00924

FILING DATE: 02-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/835,119

FILING DATE: 12-FEB-1992

ATTORNEY/AGENT INFORMATION:

NAME: WYER, LOUIS (PLM)

REFERENCE/DOCKET NUMBER: 965

TELECOMMUNICATION INFORMATION: BGP-031USCP2

TELEPHONE: (617)221-7400

INFORMATION FOR SEQ ID NO: 1

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 91.4% Score 523; DB 2; Length 106;
Best Local Similarity 94.3% Pct No. 1.3e-46;
Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IOWTSGPFFVLASGGRVITTCAGSGVSNVAVYVCOGSGPFLMYASNRITGVPR 61
DB 2 IVMGTFEFLVSGRVTTCAGSGVSNVAVYVCOGSGPFLMYASNRITGVPR 61
QY 62 FTSGSGVDTFTTSTVQMDLAVYVCOGSGPFTFGQVLEI 106
DB 62 FTSGSGVDTFTTSTVQMDLAVYVCOGSGPFTFGQVLEI 106

RESULT 3

US-09-157-452b-4
Sequence 4, Application US/0915452b

Patent No. 6482409

GENERAL INFORMATION: Roy R. Buckley, Linda C.

TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE

NUMBER OF INVENTORS: 11

CORRESPONDENCE ADDRESS: COPTREID

STREET: 60 State Street, Suite 510

CITY: Boston

STATE: Massachusetts

ZIP: 02109-1975

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/950,660

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/456,124

FILING DATE: 08/373,857

APPLICATION NUMBER: US 08/373,857

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 12-JAN-1995

APPLICATION NUMBER: US 08/284,603

FILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/00924

FILING DATE: 02-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/835,119

FILING DATE: 12-FEB-1992

ATTORNEY/AGENT INFORMATION:

NAME: WYER, LOUIS (PLM)

REFERENCE/DOCKET NUMBER: 965

TELECOMMUNICATION INFORMATION: BGP-031USCP2

TELEPHONE: (617)221-7400

INFORMATION FOR SEQ ID NO: 1

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

Query Match 91.4% Score 523; DB 4; Length 106;
Best Local Similarity 94.3% Pct No. 1.3e-46;
Matches 99; Conservative 3; Mismatches 4; Indels 0; Gaps 0

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: MONTGOMERY, Janet M.
 REFERENCE/DOCKET NUMBER: 92, 307-A, D002 CIT PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-715-1000
 TELEFAX: 312-715-1234
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 106 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US93-00924-4

Query Match 9.44% Score 523, DB 5, Length 106;
 Best Local Similarity 94.34% Pctd No. 1,3e-46;
 Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IOWTGSPEFLVNSADRYTTTCKASQSVTNVAMVQKPGKPKLLIYVNSRRTGYVR 61
 DB 2 IWMQTFPEFLVNSADRYTTTCKASQSVTNVAMVQKPGKPKLLIYVNSRRTGYVR 61
 QY 62 PFGSGYDPTFTTISVQADLAVYVCOQDYSPTFGSGTLEIK 106
 DB 62 PFGSGYDPTFTTISVQADLAVYVCOQDYSPTFGSGTLEIK 106

RESULT 5
 PCT-US93-00924-4
 Sequence 4, Application PC/TUS930924
 GENERAL INFORMATION:
 APPLICANT: LOBB, Roy R.
 REFERENCE/DOCKET NUMBER: 4
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Allegretti & Witcoff, Ltd.
 CITY: Chicago
 STATE: IL
 COUNTRY: US
 COMPILED BY: JAMES ROY,
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 106 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US93-00924-4

Query Match 91.44% Score 523, DB 5, Length 106;
 Best Local Similarity 94.34% Pctd No. 1,3e-46;
 Matches 99; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IOWTGSPEFLVNSADRYTTTCKASQSVTNVAMVQKPGKPKLLIYVNSRRTGYVR 61
 DB 2 IWMQTFPEFLVNSADRYTTTCKASQSVTNVAMVQKPGKPKLLIYVNSRRTGYVR 61

DB 2 IWMQTFPEFLVNSADRYTTTCKASQSVTNVAMVQKPGKPKLLIYVNSRRTGYVR 61
 QY 62 PFGSGYDPTFTTISVQADLAVYVCOQDYSPTFGSGTLEIK 106
 DB 62 PFGSGYDPTFTTISVQADLAVYVCOQDYSPTFGSGTLEIK 106

RESULT 6
 US-08-197-834-7
 Sequence 6, Application US/08197834
 Patent No. 5639455
 GENERAL INFORMATION:
 APPLICANT: HANSON, TEIJE
 APPLICANT: HANSON, TEIJE
 APPLICANT: HANSON, TEIJE
 TITLE OF INVENTION: IMMUNOSUPPRESSANT
 NUMBER OF SEQUENCES: 7
 ADDRESS: P.C.,
 ADDRESSEE: OHLSON, STEVAL, MCCELLAND, WALTER & NEUGSTADT,
 STREET: 1755 S. Jefferson Davis Highway, Suite 400
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPILED BY: JAMES ROY,
 MEDIUM TYPE: IBM PC floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patench Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 106 amino acids
 TYPE: AMINO ACID
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-197-834-7

Query Match 90.78% Score 519, DB 1, Length 246;
 Best Local Similarity 92.58% Pctd No. 9e-46;
 Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DIOWTGSPEFLVNSADRYTTTCKASQSVTNVAMVQKPGKPKLLIYVNSRRTGYVR 60
 DB 2 DILWQTFPEFLVNSADRYTTTCKASQSVTNVAMVQKPGKPKLLIYVNSRRTGYVR 61
 QY 61 PFGSGYDPTFTTISVQADLAVYVCOQDYSPTFGSGTLEIK 107
 DB 62 PFGSGYDPTFTTISVQADLAVYVCOQDYSPTFGSGTLEIK 108

RESULT 7
 US-08-693-692B-6
 Sequence 6, Application US/08695692B
 GENERAL INFORMATION:
 APPLICANT: Per Antonsson, Per Bjork, Mikael Dohleren,
 APPLICANT: Johan Hansson, Teije Kalland, Lars

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/ APPLICANT: Altheausen and Gorman Forebears
/ TITLE OF INVENTION: MODIFIED/CHIMERIC SUPPLEMENTARYGENES
/ TITLE OF INVENTION: AND THEIR USE
/ NUMBER OF SEQUENCES: 24
/ CORRESPONDENCE ADDRESS:
/ ATTORNEY/AGENT INFORMATION:
/ STREET: 1177 West Loop South, 10th floor
/ CITY: Houston
/ STATE: TX
/ COUNTRY: USA
/ ZIP: 77027-9095
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/695,692B
/ PRIORITY NUMBER: 12, 1996
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 661245-5
/ PRIORITY NUMBER: 29,5396
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Krieger, Paul E.
/ REGISTRATION NUMBER: 29,886
/ TELECOMMUNICATION INFORMATION: 986/1
/ TELEPHONE: 713-850-0909
/ TELEFAX: 713-850-0165
/ INSPECTION CHARGE: $25.00
/ SPECIFIC CHARGES: 6:
/ LENGTH: 107 amino acids
/ TYPE: amino acid
/ MOLECULE TYPE: linear
/ US-08-695,692B-6: peptide

Query Match: 87.1%; Score 428; DB 4; Length 107;
Base local similarity: 94; Pct Matches 94; Indels 0; Gaps 0;
Matches 94; Conservative 4; Mismatches 9;

Qy 1 DVTMTSPFPLVSGADPTTTCASGVNNAWYQCFQSPRLTAVTSRTVGP 60
Db 1 DVTMTSPFPLVSGADPTTTCASGVNNAWYQCFQSPRLTAVTSRTVGP 60
Qy 61 RFTGSGVDTFTFTISTVDAEDLAVFCQDYSPPFGQATLH 107
Db 61 RFTGSGVDTFTFTISTVDAEDLAVFCQDYSPPFGQATLH 107

RESULT 8
US-08-695,692B-17
/ Sequence 17: Application US/09065059
/ Patent No. 6068841
/ GENERAL INFORMATION:
/ OPERATING SYSTEM: PC-486
/ APPLICANT: KANAKA, Masamichi
/ APPLICANT: YAMATA, Hideo
/ APPLICANT: OKAWA, Masamichi
/ APPLICANT: OKAWA, Masamichi
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ATTORNEY/AGENT INFORMATION:
/ STREET: 11111 11th Street, Wall & Emory
/ CITY: Alexandria
/ STATE: Virginia
/ COUNTRY: USA
/ ZIP: 22304-4111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible

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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/065,059
/ PRIORITY NUMBER: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bucca Ph.D., Daniel
/ REGISTRATION NUMBER: P-42,368
/ TELECOMMUNICATION INFORMATION: 156-151
/ TELEPHONE: 703-518-5100
/ TELEFAX: 703-584-1124
/ INSPECTION CHARGE: $25.00
/ SPECIFIC CHARGES: 17:
/ LENGTH: 105 amino acids
/ TYPE: amino acid
/ STANDARD: single
/ MOLECULE TYPE: linear
/ US-09-065-059-17: peptide

Query Match: 82.0%; Score 474; DB 3; Length 105;
Base local similarity: 84.8%; Pct Matches 89; Indels 0; Gaps 0;
Matches 89; Conservative 6; Mismatches 10;

Qy 1 DVTMTSPFPLVSGADPTTTCASGVNNAWYQCFQSPRLTAVTSRTVGP 60
Db 1 DVTMTSPFPLVSGADPTTTCASGVNNAWYQCFQSPRLTAVTSRTVGP 60
Qy 61 RFTGSGVDTFTFTISTVDAEDLAVFCQDYSPPFGQATLH 105
Db 61 RFTGSGVDTFTFTISTVDAEDLAVFCQDYSPPFGQATLH 105

RESULT 9
US-08-463,128-10
/ Sequence 10: Application US/09463128
/ Patent No. 6565755
/ GENERAL INFORMATION:
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ APPLICANT: Board of Regents, U.
/ APPLICANT: Washington (except USA)
/ TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ATTORNEY/AGENT INFORMATION:
/ STREET: 1315 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10019-3000
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/463,128
/ PRIORITY NUMBER: 05-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/11060
/ FILING DATE: 11-11-1993
/ PCT DATE: 05/97/702
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Haley Jr., James F.
/ REGISTRATION NUMBER: 27,794
/ TELECOMMUNICATION INFORMATION: 30321P
/ TELEPHONE: (212) 596-9000

```

TELEFAX: (212) 596-9090
 INFORMATION FOR SEQ ID NO: 10:
 SOURCE: CHARACTERISTICS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-463-128-10

Query Match 81.5%; Score 466; DB 1; Length 128;
 Best Local Similarity 80.4%; Pred. No. 1,2e-40;
 Matches 86; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Cy 2 IOMTSGPEFLVSNADQVYITTCAGSOSVNDVAMCOCKPQSGKLLVYASNNYTYGPR 61
 Db 21 IYMTSGPEFLVSNADQVYITTCAGSOSVNDVAMCOCKPQSGKLLVYASNNYTYGPR 80
 Cy 61 FPGSGYGFPTFTISLOPEDIATVYCOOYSSPTFGQTKVEIKR 108
 Db 61 FPGSGYGFPTFTISLOPEDIATVYCOOYSSPTFGQTKVEIKR 127

RESULT 10

US-08-463-296-10
 Sequence 10; Application US/08/463298
 Patent No. 584339A
 GENERAL INFORMATION:

APPLICANT: Repayamopolou, Thalia (USA only)
 APPLICANT: Board of Regents, U.S.A.
 TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS: 6 NEVAY
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10020

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: COMPATIBLE
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/463,298
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PGT/0893/11060
 FILING DATE: 13-NOV-1992
 APPLICATION NUMBER: US 07/977,702
 FILING DATE: 13-NOV-1992

ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: B173CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 FAX: (212) 596-9000
 INFORMATION FOR SEQ ID NO: 10:
 LENGTH: 128 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-463-298-10

Query Match 81.5%; Score 466; DB 2; Length 128;
 Best Local Similarity 80.4%; Pred. No. 1,2e-40;
 Matches 86; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Cy 2 IOMTSGPEFLVSNADQVYITTCAGSOSVNDVAMCOCKPQSGKLLVYASNNYTYGPR 61
 Db 21 IYMTSGPEFLVSNADQVYITTCAGSOSVNDVAMCOCKPQSGKLLVYASNNYTYGPR 80
 Cy 61 FPGSGYGFPTFTISLOPEDIATVYCOOYSSPTFGQTKVEIKR 108
 Db 61 FPGSGYGFPTFTISLOPEDIATVYCOOYSSPTFGQTKVEIKR 127

RESULT 11

US-08-436-339A-10
 Sequence 10; Application US/08/3339A
 Patent No. 584339A
 GENERAL INFORMATION:

APPLICANT: Repayamopolou, Thalia (USA only)
 APPLICANT: Board of Regents, U.S.A.
 TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS: 6 NEVAY
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10020

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: IBM PC COMPATIBLE
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/436,339A
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/463,128
 FILING DATE: 05-JUN-1995
 APPLICATION NUMBER: 1344-1993/0893/11060
 FILING DATE: 13-NOV-1992
 APPLICATION NUMBER: US 07/977,702
 FILING DATE: 13-NOV-1992

ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: B173CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 596-9000
 FAX: (212) 596-9000
 INFORMATION FOR SEQ ID NO: 10:
 LENGTH: 128 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-436-339A-10

Query Match 81.5%; Score 466; DB 2; Length 128;
 Best Local Similarity 80.4%; Pred. No. 1,2e-40;
 Matches 86; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Cy 2 IOMTSGPEFLVSNADQVYITTCAGSOSVNDVAMCOCKPQSGKLLVYASNNYTYGPR 61
 Db 21 IYMTSGPEFLVSNADQVYITTCAGSOSVNDVAMCOCKPQSGKLLVYASNNYTYGPR 80
 Cy 61 FPGSGYGFPTFTISLOPEDIATVYCOOYSSPTFGQTKVEIKR 108
 Db 61 FPGSGYGFPTFTISLOPEDIATVYCOOYSSPTFGQTKVEIKR 127

RESULT 12

US-08-463-128-6

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Sequence 6, Application US/09463128
Patent No. 5695755
GENERAL INFORMATION:
APPLICANT: Papeyannopolou, Thalia (USA only)
INVENTOR: Papeyannopolou, Thalia (USA only)
APPLICANT: Washington (except USA)
TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
CELLS
TITLE OF INVENTION: CELLS
CURRENT APPLICATION DATA: 08/463,128
CORRESPONDENCE ADDRESS: 10
ADDRESS: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10020
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 08/463,128
APPLICATION NUMBER: US/08/463,128
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIORITY INFORMATION:
PCT/US93/11060
APPLICATION NUMBER: US 07/977,702
FILING DATE: 11-11-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B173CIP
TELEPHONE: (212) 596-9090
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463,128-6
Query Match
Match Local Similarity 80.6%; Score 461; DB 1; Length 128;
Best Local Similarity 78.7%; Pred. No. 3.7e-40;
Matches 85; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
DB
Oy 1 D1QNTGSEKFLVAGADRVTTTCKASGVSNDAVMAVQKRGKQAPLMTVYASNRRTGPD 60
20 D1LDTGSSLSASVGRVTTTCKASGVSNDAVMAVQKRGKQAPLMTVYASNRRTGPD 79
Oy 61 RPTGSGVDTFFTTISVQADLAVYCOODYSSPTFGGQTKVKIKR 108
80 RFSGSGSDTFFTTISLQPEDLAVTTCODYSSPTFGGQTKVKIKR 127
DB
RESULT 13
Sequence 6, Application US/08463298
Patent No. 5824304
GENERAL INFORMATION:
APPLICANT: Papeyannopolou, Thalia (USA only)
INVENTOR: Papeyannopolou, Thalia (USA only)
APPLICANT: Washington (except USA)
TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
CELLS
TITLE OF INVENTION: CELLS
CURRENT APPLICATION DATA: 08/463,128
CORRESPONDENCE ADDRESS: 10
ADDRESS: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York

```

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STATE: New York
COUNTRY: U.S.A.
ZIP: 10020
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 08/463,298
APPLICATION NUMBER: US/08/463,298
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIORITY INFORMATION:
PCT/US93/11060
APPLICATION NUMBER: US 07/977,702
FILING DATE: 11-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B173CIP
TELEPHONE: (212) 596-9090
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463,298-6
Query Match
Match Local Similarity 80.6%; Score 461; DB 2; Length 128;
Best Local Similarity 78.7%; Pred. No. 3.7e-40;
Matches 85; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
DB
Oy 1 D1QNTGSEKFLVAGADRVTTTCKASGVSNDAVMAVQKRGKQAPLMTVYASNRRTGPD 60
20 D1LDTGSSLSASVGRVTTTCKASGVSNDAVMAVQKRGKQAPLMTVYASNRRTGPD 79
Oy 61 RPTGSGVDTFFTTISVQADLAVYCOODYSSPTFGGQTKVKIKR 108
80 RFSGSGSDTFFTTISLQPEDLAVTTCODYSSPTFGGQTKVKIKR 127
DB
RESULT 14
Sequence 6, Application US/0846339A
Patent No. 5824304
GENERAL INFORMATION:
APPLICANT: Papeyannopolou, Thalia (USA only)
INVENTOR: Papeyannopolou, Thalia (USA only)
APPLICANT: Washington (except USA)
TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
CELLS
TITLE OF INVENTION: CELLS
CURRENT APPLICATION DATA: 08/463,128
CORRESPONDENCE ADDRESS: 10
ADDRESS: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10020
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 08/463,39A
APPLICATION NUMBER: US/08/463,39A
FILING DATE: 05-JUN-1995
CLASSIFICATION:
PRIORITY INFORMATION:

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1 APPLICATION NUMBER: US 08/463,128
2 FILING DATE: 05-JUN-1995
3 APPLICATION NUMBER: US 07/0593/11060
4 FILING DATE: 11-11-1993
5 APPLICATION NUMBER: US 07/977,702
6 FILING DATE: 13-NOV-1992
7 ATTORNEY/AGENT INFORMATION:
8 REGISTRATION NUMBER: 27,794
9 REFERENCE/DOCKET NUMBER: B173CIP
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (212) 566-0000
12 TELEFAX: (212) 566-0000
13 INFORMATION FOR SEQ ID NO: 6:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 128 amino acids
16 TYPE: amino acid
17 TOPOLOGY: linear
18 MOLECULE TYPE: protein
19 US-08-436-339A-6
20
21 Query Match
22 Best Local Similarity 80.6%; Score 443; DB 2; Length 128;
23 Matches 85; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
24
25 QY 1 DIQWTSPEFLVLSAGSRVITTCASQSVNDVAVYQCGQSPPELLMTYASNYGYVD 60
26 DB 20 DILVTSFSLNSVGRVITTCASQSVNDVAVYQCGQSPPELLMTYASNYGYVD 79
27
28 QY 61 RFTSGSGDTDFITTSVQAEALAVYQCGQSPPELLMTYASNYGYVD 108
29 DB 80 RFTSGSGDTDFITTSVQAEALAVYQCGQSPPELLMTYASNYGYVD 127
30
31 RESULT 15
32 US-07-934-373C-5
33 Sequence 5, Application US/07934373C
34 Patent No. 5681370
35 INVENTOR: Leonard G. Presta
36 APPLICANT: Paul J. Carter
37 TITLE OF INVENTION: Immunoglobulin Variants
38 NUMBER OF SEQUENCES: 48
39 CORRESPONDENCE ADDRESS:
40 ADDRESSER: Genentech, Inc.
41 STREET: 1 DNA Way
42 CITY: South San Francisco
43 STATE: California
44 COUNTRY: USA
45 ZIP: 94080
46
47 COMPUTER READABLE FORM:
48 SEQ. NO. 1, 128, 1,44 kb floppy disk
49 COMPUTER: IBM PC compatible
50 OPERATING SYSTEM: PC-DOS/MS-DOS
51 SOFTWARE: WinPatIn (Genentech)
52 CURATOR: NATHAN DAVIS/07/934,373C
53 APPLICATION NUMBER: 07/934,373C
54 FILING DATE: 21-Aug-1992
55 CLASSIFICATION: 530
56 PRIOR APPLICATION DATA: PCT/US92/05126
57 PCT NO. 92/05126
58 FILING DATE: 15-JUN-1992
59 PRIOR APPLICATION DATA:
60 PCT NO. 92/05126
61 ATTORNEY/AGENT INFORMATION:
62 NAME: Lee, Wendy M.
63 REGISTRATION NUMBER: 40,378
64 TELECOMMUNICATION INFORMATION:
65 TELEPHONE: 650/225-1994
66 TELEFAX: 650/952-9881
67 INFORMATION FOR SEQ ID NO: 5:

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1 SEQUENCE CHARACTERISTICS:
2 LENGTH: 109 amino acids
3 TYPE: amino acid
4 TOPOLOGY: linear
5 US-07-934-373C-5

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1 Query Match
2 Best Local Similarity 77.4%; Score 443; DB 2; Length 109;
3 Matches 85; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
4
5 QY 1 DIQWTSPEFLVLSAGSRVITTCASQSVNDVAVYQCGQSPPELLMTYASNYGYVD 60
6 DB 1 DILVTSFSLNSVGRVITTCASQSVNDVAVYQCGQSPPELLMTYASNYGYVD 79
7
8 QY 61 RFTSGSGDTDFITTSVQAEALAVYQCGQSPPELLMTYASNYGYVD 108
9 DB 61 RFTSGSGDTDFITTSVQAEALAVYQCGQSPPELLMTYASNYGYVD 108

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Search completed: November 7, 2003, 07:30:08
Job time: 16.8611 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18; Search time 15.6702 seconds

742,581 Million call updates/sec

US-09-661-992b-84_COPY_1_121

Sequence: 1 EVQVSGGVGGLVPGSGSLK.....HNGSGPDVNGQGLTWISS 121

Scoring table:

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: 1: PIR 76.4*

2: Trn1*

3: P12*

4: P13*

5: P14*

6: P15*

7: P16*

8: P17*

9: P18*

10: P19*

11: P20*

12: P21*

13: P22*

14: P23*

15: P24*

16: P25*

17: P26*

18: P27*

19: P28*

20: P29*

21: P30*

22: P31*

23: P32*

24: P33*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	557	86.6	122	E27888	1g heavy chain V x
2	546.5	85.0	119	E27888	1g heavy chain V x
3	542	84.3	120	B671	1g heavy chain pre
4	531.1	82.6	120	E27888	1g heavy chain V x
5	531.1	82.6	120	E27888	1g heavy chain V x
6	530.5	82.5	121	E27888	1g heavy chain V x
7	529.5	82.3	118	H27888	1g heavy chain V x
8	528.4	81.5	120	E27888	1g heavy chain V x
9	518	80.6	120	E27888	1g heavy chain V x
10	515.5	80.2	119	E27888	1g heavy chain V x
11	515.5	80.2	119	E27888	1g heavy chain V x
12	515.5	80.2	119	E27888	1g heavy chain V x
13	507.5	79.7	122	E27888	1g heavy chain V x
14	508	79.0	119	E27888	1g heavy chain V x
15	508	79.0	119	E27888	1g heavy chain V x
16	507.5	79.0	122	E27888	1g heavy chain V x
17	507.5	79.0	122	E27888	1g heavy chain V x
18	507	78.8	120	E27888	1g heavy chain V x
19	506	78.7	138	E27888	1g heavy chain V x
20	504.5	78.5	119	E27888	1g heavy chain V x
21	504.5	78.5	119	E27888	1g heavy chain V x
22	504.5	78.5	119	E27888	1g heavy chain V x
23	504.5	78.5	119	E27888	1g heavy chain V x
24	501.5	78.0	121	E27888	1g heavy chain V x
25	499.5	77.5	121	E27888	1g heavy chain V x
26	498	77.4	124	E27888	1g heavy chain V x
27	497.5	77.4	124	E27888	1g heavy chain V x
28	497.5	77.4	124	E27888	1g heavy chain V x
29	493.5	77.1	121	E27888	1g heavy chain V x

30	492	76.5	117	2	P10249	1g heavy chain V x
31	490	76.2	119	2	C36005	1g heavy chain V x
32	489	76.2	119	2	A41413	1g heavy chain V x
33	488	75.9	118	2	E27888	1g heavy chain V x
34	487.5	75.9	118	2	E27888	1g heavy chain V x
35	487.5	75.9	118	2	P10249	1g heavy chain V x
36	485.5	75.5	108	2	P10249	1g heavy chain V x
37	485	75.4	111	2	P10107	1g heavy chain V x
38	485	75.4	111	2	P10107	1g heavy chain V x
39	484	75.3	142	2	C34903	1g heavy chain pre
40	483.5	75.2	119	2	S23277	1g heavy chain V x
41	482	75.0	119	2	E27888	1g heavy chain V x
42	482	75.0	119	2	E27888	1g heavy chain V x
43	477	74.4	98	1	H10586	1g heavy chain V x
44	474.5	73.8	113	2	E27888	1g heavy chain V x
45	473.5	73.6	119	2	P10131	1g heavy chain V regio

ALIGNMENTS

RESULT 1

E27888

1g heavy chain V region (H35-C6) - mouse

C:Species: Mus musculus (house mouse)

C:Accession: E27888

R:Clon: A.J.; Brownlee, G.G.; Staudt, L.N.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response

A:Accession: E27888

A:Molecule type: DNA

A:Residues: 1-122 <CDT>

A:Note: This sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

F/15-29/Domain: Immunoglobulin homology <CDT>

Query Match: 86.6%; Score: 557; DB 2; Length: 122;

Best local similarity: 87.7%; Pred. No. 1.5e-41;

Matches: 107; Conservative: 6; Mismatch: 5; Indels: 2;

Gap: 2;

1 EVQVSGGVGGLVPGSGSLK.....HNGSGPDVNGQGLTWISSGSSYTY 60

1 DVKVSQGVGGLVPGSGSLK.....HNGSGPDVNGQGLTWISSGSSYTY 60

61 PSYRGEFTRIRNKKLVYQMSKSEEDPVMYCTPRD-GHGYS-SPTVNGQGLTW 118

61 PSYRGEFTRIRNKKLVYQMSKSEEDPVMYCTPRD-GHGYS-SPTVNGQGLTW 120

QY 119 VS 120

DB 121 VS 122

RESULT 2

E27888

1g heavy chain V region (H35-C6) - mouse

C:Species: Mus musculus (house mouse)

C:Accession: E27888

R:Clon: A.J.; Brownlee, G.G.; Staudt, L.N.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response

A:Accession: E27888

A:Molecule type: DNA

A:Residues: 1-119 <CDT>

A:Note: This sequence was determined from the germline gene

C/Comment: This chain was isolated from a biphidoma protein that binds influenza virus C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterocenter; immunoglobulin
P:15-96/Domain: immunoglobulin homology <IMb>

Query Match

Best Local Similarity 85.0%; Score 546.5; DB 2; Length 119;
Matched 105; Conservative 7; Mismatches 1; Indels 1; Gaps 1;

1 EVQVSGGGLVKGSGIKSCASGFTSTYSWVWQTPKRLKLVWATISGGSTYY 60
1 DKVSGGGLVKGSGIKSCASGFTSTYSWVWQTPKRLKLVWATISGGSTYY 60
61 PSYVKRFTISDNANNTLYQMSLSLSDTANVCYF-GETYDYMDYQGGTIVTS 119

RESULT 3

B26471
IG heavy chain precursor V region (IMK33) - mouse

C/Species: Mus musculus (house mouse)
C/Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C/Accession: B26471, S70410
R:Hubbick, P. J., Hubner-Parajz, C., Mattee, R.; Lanz, H.; Haug, H.; Beaucamp, K.
Gene 53, Clontech, 1988 nucleotide sequence of heavy- and light-chain cDNAs from a cDNA library
A/reference number: A91572; MIMD:87248059; PMID:311009

A/Accession: B26471
A/nucleotide type: mRNA
A/Accession: B26471

A/cross-reference: GB:IM163; NID:9195405; PIM:AAA3292.1; PID:g195406
R:Leclercq, S.G.; Garthwaite, P.J.

J. Exp. Med. 172, 1171-1172, 1990

A/Title: Boundary of protein-coding region in immunoglobulin genes: 5' boundary
A/Accession: S70410; MIMD:8107975; PMID:2259702

A/Status: translation not shown

A/nucleotide type: mRNA

A/cross-reference: EMBL:X53776; NID:952475; PIM:CAA3792.1; PID:g52476

C/Accession: B26471

A/Title: Immunoglobulin V region; immunoglobulin homology

C/Species: Mus musculus (house mouse)

P:1-19/Domain: signal sequence #status predicted <SIG>

P:30-152/Product: Ig heavy chain V region IMK33 #status predicted <IMV>

P:14-97/Domain: immunoglobulin homology <IMb>

Query Match

Best Local Similarity 84.3%; Score 542; DB 2; Length 155;
Matched 104; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

1 EVQVSGGGLVKGSGIKSCASGFTSTYSWVWQTPKRLKLVWATISGGSTYY 60
20 EVQVSGGGLVKGSGIKSCASGFTSTYSWVWQTPKRLKLVWATISGGSTYY 79
61 PSYVKRFTISDNANNTLYQMSLSLSDTANVCYFCDGSGSGSPFWQGGTIVTS 118
80 PSYVKRFTISDNANNTLYQMSLSLSDTANVCYFCDGSGSGSPFWQGGTIVTS 139
119 VSS 121
140 VSS 142

RESULT 4

PH0097
IG heavy chain V region (anti-cyclosporin B) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 16-Aug-1996
C/Accession: PH0097
R:Schmitter, D.; Poch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Queniaux, V.F.J.; V

Mol. Immunol. 27, 1029-1036, 1990

A/Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporin B

A/reference number: PH0097; MIMD:9104649; PMID:2122240

A/Accession: PH0097

A/nucleotide type: mRNA

A/Status: 118 <CH>

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterocenter; immunoglobulin

P:15-96/Domain: immunoglobulin homology <IMb>

P:50-66/Region: complementarity-determining 3

P:9-105/Region: complementarity-determining 3

Query Match

Best Local Similarity 86.0%; Score 535.5; DB 2; Length 118;
Matched 104; Conservative 5; Mismatches 7; Indels 5; Gaps 1;

1 EVQVSGGGLVKGSGIKSCASGFTSTYSWVWQTPKRLKLVWATISGGSTYY 60
1 DKVSGGGLVKGSGIKSCASGFTSTYSWVWQTPKRLKLVWATISGGSTYY 60
61 PSYVKRFTISDNANNTLYQMSLSLSDTANVCYFCDGSGSGSPFWQGGTIVTS 115

121 S 121
116 S 116

RESULT 5

SS5516
IG heavy chain V region (p20 - mouse (fragment))

C/Species: Mus musculus (house mouse)
C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C/Accession: SS5516

R:Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-prenkephalin antibody

A/reference number: SS5516; MIMD:9523793; PMID:7516650

A/Accession: SS5516

A/nucleotide type: mRNA

A/Status: preliminary

A/cross-reference: EMBL:X62889; NID:9854304; PIM:CAA57925.1; PID:g854305

A/Title: Immunoglobulin V region; immunoglobulin homology

C/Superfamily: heterocenter; immunoglobulin

P:14-97/Domain: immunoglobulin homology <IMb>

Query Match

Best Local Similarity 82.6%; Score 531; DB 2; Length 120;
Matched 104; Conservative 3; Mismatches 13; Indels 0; Gaps 0;

1 EVQVSGGGLVKGSGIKSCASGFTSTYSWVWQTPKRLKLVWATISGGSTYY 60
1 VQVSGGGLVKGSGIKSCASGFTSTYSWVWQTPKRLKLVWATISGGSTYY 61
62 PSYVKRFTISDNANNTLYQMSLSLSDTANVCYFCDGSGSGSPFWQGGTIVTS 121
61 PSYVKRFTISDNANNTLYQMSLSLSDTANVCYFCDGSGSGSPFWQGGTIVTS 120

RESULT 6

H2788
IG heavy chain V region (H27-40) - mouse

C/Species: Mus musculus (house mouse)
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C/Accession: H2788
R:Schmitter, D.; Poch, O.; Zeder, G.O.; Staudt, L.M.; Gerhardt, W.
EMBO J. 5, 1577-1587, 1986
A/Title: Structural and functional implications of a restricted antibody response
A/reference number: A31043; MIMD:8610658; PMID:3427335

A:Status: preliminary
 A:Molecule type: mRNA
 A:Accession: U02593; NID:954312; PIRN:CA047329.1; PID:954313
 A:Cross-references: EMBL:982593; NID:954312; PIRN:CA047329.1; PID:954313
 C:Keywords: heterotrimer; immunoglobulin
 C:Keywords: heterotrimer; immunoglobulin
 F:14-97/Domain: immunoglobulin homology <IM>

Query Match
 Best Local Similarity 84.24; Pred. No. 1,56-38;
 Matches 101; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

OY 2 VOLVESGGSLVFGGSLKSCASGFTSTTMMVROTPERLEMAVATISGSGSTYY 61
 1 VOLVESGGSLVFGGSLKSCASGFTSTTMMVROTPERLEMAVATISGSGSTYY 60
 OY 62 DSVNGRFTSRNNAKNTLLQMSLSKEETPMVCTCRGAGGSGSPYWGQGTTLTVAS 121
 61 DSVNGRFTSRNNAKNTLLQMSLSKEETPMVCTCRGAGGSGSPYWGQGTTLTVAS 120

RESULT 11

B32789
 Ig heavy chain V region (H46-2483) - mouse
 C:Species: Mus musculus (house mouse)
 C:Update: 15-Dec-1988 Sequence_revision 15-Dec-1988 #exec_change 16-Aug-1996
 R:Clifton, A.J.; Bromberg, G.G.; Strand, L.M.; Gerhard, W.
 BMD0 J. 5, 1577-1871, 1986
 A>Title: Structural and functional implications of a restricted antibody response to a C
 A:Accession: B31790; MIMD:86300659; PMID:247335
 A:Molecule type: DNA
 A:Residues: 1,119 <CAT>
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Accession: B31790; MIMD:86300659; PMID:247335
 C:Comment: This chain was determined from the germline gene
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:15-99/Domain: immunoglobulin homology <IM>

Query Match
 Best Local Similarity 80.24; Score 515.5; DB 2; Length 119;
 Matches 102; Conservative 3; Mismatches 12; Indels 5; Gaps 2;

OY 1 EVOLVESGGSLVFGGSLKSCASGFTSTTMMVROTPERLEMAVATISGSGSTYY 60
 1 EVOLVESGGSLVFGGSLKSCASGFTSTTMMVROTPERLEMAVATISGSGSTYY 60
 OY 61 PSYNGRFTSRNNAKNTLLQMSLSKEETPMVCTCRGAGGSGSPYWGQGTTLTVAS 118
 61 PSYNGRFTSRNNAKNTLLQMSLSKEETPMVCTCRGAGGSGSPYWGQGTTLTVAS 117

OY 119 VS 120
 DB 118 VS 119

RESULT 12

B32788
 Ig heavy chain V region (H46-2483) - mouse
 C:Species: Mus musculus (house mouse)
 C:Update: 15-Dec-1988 Sequence_revision 15-Dec-1988 #exec_change 16-Aug-1996
 R:Clifton, A.J.; Bromberg, G.G.; Strand, L.M.; Gerhard, W.
 BMD0 J. 5, 1577-1871, 1986
 A>Title: Structural and functional implications of a restricted antibody response to a C
 A:Accession: B31790; MIMD:86300659; PMID:247335
 A:Molecule type: DNA
 A:Residues: 1,123 <CAT>
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Accession: B31790; MIMD:86300659; PMID:247335
 C:Comment: This sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:15-99/Domain: immunoglobulin homology <IM>

Query Match
 Best Local Similarity 79.74; Score 512.5; DB 2; Length 123;
 Matches 98; Conservative 10; Mismatches 12; Indels 3; Gaps 1;

OY 1 EVOLVESGGSLVFGGSLKSCASGFTSTTMMVROTPERLEMAVATISGSGSTYY 60
 1 EVOLVESGGSLVFGGSLKSCASGFTSTTMMVROTPERLEMAVATISGSGSTYY 60
 OY 61 PSYNGRFTSRNNAKNTLLQMSLSKEETPMVCTCRGAGGSGSPYWGQGTTLTVAS 117
 61 PSYNGRFTSRNNAKNTLLQMSLSKEETPMVCTCRGAGGSGSPYWGQGTTLTVAS 120

OY 118 TMS 120
 DB 121 TMS 123

RESULT 13

B31790
 Ig heavy chain V region (17/9) - mouse
 C:Species: Mus musculus (house mouse)
 C:Update: 31-Mar-1990 #exec_change 23-May-1997
 R:Schulze-Gahmen, U.; Bittl, J.M.; Azeva, J.; Stutz, B.A.; Kenten, J.H.; Wilson
 J. Biol. Chem. 263, 17100-17105, 1988 #abs: primary sequence, and binding data f
 A:Accession: B31790; MIMD:89034213; PMID:3112833
 A:Molecule type: mRNA
 A:Residues: 1,254 <CAT>
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Accession: B31790; MIMD:89034213; PMID:3112833
 C:Comment: This chain was determined from the germline gene
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:15-99/Domain: immunoglobulin homology <IM>

Query Match
 Best Local Similarity 81.04; Pred. No. 4,12e-37;
 Matches 99; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

OY 1 EVOLVESGGSLVFGGSLKSCASGFTSTTMMVROTPERLEMAVATISGSGSTYY 60
 1 EVOLVESGGSLVFGGSLKSCASGFTSTTMMVROTPERLEMAVATISGSGSTYY 60
 OY 61 PSYNGRFTSRNNAKNTLLQMSLSKEETPMVCTCRGAGGSGSPYWGQGTTLTVAS 120
 61 PSYNGRFTSRNNAKNTLLQMSLSKEETPMVCTCRGAGGSGSPYWGQGTTLTVAS 119

OY 121 S 121
 DB 120 A 120

RESULT 14

B34353
 anti-peptide Fab' B3172 heavy chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Update: 22-Jun-1990 Sequence_revision 22-Jun-1990 #exec_change 23-Jul-1999
 R:Stutz, B.A.; Steinfield, R.L.; Fleeger, T.M.; Balderas, R.S.; Smith, L.R.; Lerner
 J. Biol. Chem. 264, 15721-15725, 1989
 A>Title: Preliminary crystallographic data and primary sequence for anti-peptide
 A:Accession: B34353; MIMD:89354461; PMID:2504725
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Accession: B34353; MIMD:89354461; PMID:2504725
 C:Comment: This sequence was determined from the germline gene
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:15-99/Domain: immunoglobulin homology <IM>

A:Accession: B34353; MIMD:89354461; PMID:2504725
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Accession: B34353; MIMD:89354461; PMID:2504725
 C:Comment: This sequence was determined from the germline gene

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Query Match          79.04; Score 508; DB 2; Length 119;
Best Local Similarity 81.84; Pred. No. 2.5e-37;
Matches 101; Conservative 67; Mismatches 34; Indels 8; Gaps 2;

QY      1 EVQLVDSGGGLVPRGSAALSCASGPTFTSTMSVWQTPERKLELVNATISGGSGSYTY 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1 EVQLVDSGGGLVPRGSAALSCASGPTFTSTMSVWQTPERKLELVNATISGGSGSYTY 60
QY      61 PSVYNGRFTISDNKATLYLQMSLSKSDPTAYCTPGDHGYS--FDWGGQTTL 117
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      61 PSVYNGRFTISDNKATLYLQMSLSKSDPTAYCTPGDHGYS--FDWGGQTTL 115
QY      118 TVSS 121
        ||| |||
DB      116 TVSS 119

RESULT 15
PH0098
G:heavy chain V region (anti-cyclosporin G) - mouse (fragment)
C:IMMUNOGLOBULIN V REGION (mouse)
C.Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #ext_change 16-Aug-1996
C.Accession: PH0098
M:Accession: D.1, Foch, O.; Zeder, G.; Heinrich, G.F.; Kocher, H.P.; Quehenlau, V.P.J.; V
M:Accession: 15-Jan-1993 #sequence_revision 15-Jan-1993 #ext_change 16-Aug-1996
A:Title: Analysis of the structural diversity of monoclonal antibodies to cyclosporine.
A:Reference number: PH0097; MUID:91042649; PMID:212240
A:Accession: PH0098
M:Accession: 15-Jan-1993 #sequence_revision 15-Jan-1993 #ext_change 16-Aug-1996
A:Residues: 1-119 <CH>
A:Note: the authors translated the codon GTG for residue 104 as GLY
C:superfamily: immunoglobulin V region; immunoglobulin homology
S:keywords: heterocyclase; immunoglobulin
S:keywords: heterocyclase; immunoglobulin
F:31-39/Region: complementarity-determining 1
F:50-66/Region: complementarity-determining 2
F:99-106/Region: complementarity-determining 3

Query Match          79.04; Score 508; DB 2; Length 119;
Best Local Similarity 81.84; Pred. No. 2.5e-37;
Matches 99; Conservative 71; Mismatches 11; Indels 4; Gaps 1;

QY      1 EVQLVDSGGGLVPRGSAALSCASGPTFTSTMSVWQTPERKLELVNATISGGSGSYTY 60
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1 DYKVESGGGLVPRGSAALSCASGPTFTSTMSVWQTPERKLELVNATISGGSGSYTY 60
QY      61 PSVYNGRFTISDNKATLYLQMSLSKSDPTAYCTPGDHGYS--FDWGGQTTL 120
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      61 PSVYNGRFTISDNKATLYLQMSLSKSDPTAYCTPGDHGYS--FDWGGQTTL 116
QY      121 $ 121
        ||| |||
DB      117 $ 117

```

Search completed: November 7, 2003, 07:36:19
 Job time : 15.7702 secs

GenCode version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 | Search time 8.7363 seconds
(without alignment)

US-09-661-992b-84_COPY_1_121
652,278 Million cell updates/sec

Sequence: 1 EVUWSSGGALVKEGSSLKL.....HVGSSPFWGCGITLTVSS 121

Scoring table: ELOCSDW2
Gapop 10.0, Gapext 0.5

Numbered: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	ID	Description
1	476	74.0	98	1 HV57 MOUSE	P18528 mus musculus
2	466	72.5	117	1 HV55 MOUSE	P18526 mus musculus
3	461	71.7	117	1 HV54 MOUSE	P18525 mus musculus
4	461	71.7	117	1 HV54 MOUSE	P18529 mus musculus
5	457.5	71.2	97	1 HV56 MOUSE	P18527 mus musculus
6	441.5	68.0	1125	1 HV58 MOUSE	P01772 homo sapien
7	431.5	67.0	1122	1 HV57 HUMAN	P01768 homo sapien
8	430.5	67.0	1122	1 HV57 HUMAN	P18524 mus musculus
9	430.5	67.0	1122	1 HV57 HUMAN	P01771 homo sapien
10	430	66.9	117	1 HV53 MOUSE	P01809 mus musculus
11	412.4	65.9	1121	1 HV52 HUMAN	P01781 homo sapien
12	412.4	65.9	1121	1 HV52 HUMAN	P01804 mus musculus
13	414	64.4	116	1 HV57 HUMAN	P01780 mus musculus
14	410.5	63.8	116	1 HV57 HUMAN	P01804 mus musculus
15	407.5	63.4	111	1 HV55 MOUSE	P01762 homo sapien
16	405.5	63.1	1122	1 HV54 HUMAN	P01767 homo sapien
17	405.5	62.6	1122	1 HV54 HUMAN	P01767 homo sapien
18	402.5	62.6	1122	1 HV54 HUMAN	P01767 homo sapien
19	402	62.5	115	1 HV55 MOUSE	P01807 mus musculus
20	402	62.5	115	1 HV55 MOUSE	P01762 homo sapien
21	400.5	62.4	119	1 HV53 HUMAN	P01795 mus musculus
22	400	62.2	144	1 HV26 MOUSE	P01801 mus musculus
23	398	61.9	117	1 HV52 HUMAN	P01785 canis fam1
24	398	61.9	117	1 HV52 HUMAN	P01811 mus musculus
25	395	61.4	116	1 HV55 HUMAN	P01811 mus musculus
26	393.5	61.2	117	1 HV55 HUMAN	P01811 mus musculus
27	393.5	61.2	117	1 HV55 HUMAN	P01811 mus musculus
28	393	61.1	119	1 HV53 HUMAN	P01770 homo sapien
29	393	61.1	119	1 HV53 HUMAN	P01770 homo sapien
30	391.5	60.9	119	1 HV50 MOUSE	P01796 mus musculus
31	391	60.8	113	1 HV27 MOUSE	P01799 mus musculus
32	391	60.8	113	1 HV27 MOUSE	P01799 mus musculus
33	391	60.8	123	1 HV24 MOUSE	P01793 mus musculus

34	390	60.7	115	1 HV33 MOUSE	P01802 mus musculus
35	380	60.7	120	1 HV32 HUMAN	P01766 homo sapien
36	380	60.5	123	1 HV31 MOUSE	P01760 mus musculus
37	380	60.5	123	1 HV31 MOUSE	P01760 mus musculus
38	387.5	60.3	119	1 HV34 HUMAN	P01774 homo sapien
39	387.5	60.3	122	1 HV20 MOUSE	P01789 mus musculus
40	385	59.9	113	1 HV28 MOUSE	P01795 mus musculus
41	385	59.9	113	1 HV28 MOUSE	P01795 mus musculus
42	385	59.9	123	1 HV23 MOUSE	P01795 mus musculus
43	384.5	59.8	122	1 HV21 MOUSE	P01795 mus musculus
44	384	59.5	119	1 HV30 HUMAN	P01770 homo sapien
45	382.5	59.5	120	1 HV30 HUMAN	P01780 homo sapien

ALIGNMENTS

Result	ID	Query	Standard	Pct	98 AA
1	1 HV57 MOUSE	STANDARD	PCT	98 AA	
2	1 HV57 MOUSE	STANDARD	PCT	98 AA	
3	1 HV57 MOUSE	STANDARD	PCT	98 AA	
4	1 HV57 MOUSE	STANDARD	PCT	98 AA	
5	1 HV57 MOUSE	STANDARD	PCT	98 AA	
6	1 HV57 MOUSE	STANDARD	PCT	98 AA	
7	1 HV57 MOUSE	STANDARD	PCT	98 AA	
8	1 HV57 MOUSE	STANDARD	PCT	98 AA	
9	1 HV57 MOUSE	STANDARD	PCT	98 AA	
10	1 HV57 MOUSE	STANDARD	PCT	98 AA	
11	1 HV57 MOUSE	STANDARD	PCT	98 AA	
12	1 HV57 MOUSE	STANDARD	PCT	98 AA	
13	1 HV57 MOUSE	STANDARD	PCT	98 AA	
14	1 HV57 MOUSE	STANDARD	PCT	98 AA	
15	1 HV57 MOUSE	STANDARD	PCT	98 AA	
16	1 HV57 MOUSE	STANDARD	PCT	98 AA	
17	1 HV57 MOUSE	STANDARD	PCT	98 AA	
18	1 HV57 MOUSE	STANDARD	PCT	98 AA	
19	1 HV57 MOUSE	STANDARD	PCT	98 AA	
20	1 HV57 MOUSE	STANDARD	PCT	98 AA	
21	1 HV57 MOUSE	STANDARD	PCT	98 AA	
22	1 HV57 MOUSE	STANDARD	PCT	98 AA	
23	1 HV57 MOUSE	STANDARD	PCT	98 AA	
24	1 HV57 MOUSE	STANDARD	PCT	98 AA	
25	1 HV57 MOUSE	STANDARD	PCT	98 AA	
26	1 HV57 MOUSE	STANDARD	PCT	98 AA	
27	1 HV57 MOUSE	STANDARD	PCT	98 AA	
28	1 HV57 MOUSE	STANDARD	PCT	98 AA	
29	1 HV57 MOUSE	STANDARD	PCT	98 AA	
30	1 HV57 MOUSE	STANDARD	PCT	98 AA	
31	1 HV57 MOUSE	STANDARD	PCT	98 AA	
32	1 HV57 MOUSE	STANDARD	PCT	98 AA	
33	1 HV57 MOUSE	STANDARD	PCT	98 AA	
34	1 HV57 MOUSE	STANDARD	PCT	98 AA	
35	1 HV57 MOUSE	STANDARD	PCT	98 AA	
36	1 HV57 MOUSE	STANDARD	PCT	98 AA	
37	1 HV57 MOUSE	STANDARD	PCT	98 AA	
38	1 HV57 MOUSE	STANDARD	PCT	98 AA	
39	1 HV57 MOUSE	STANDARD	PCT	98 AA	
40	1 HV57 MOUSE	STANDARD	PCT	98 AA	
41	1 HV57 MOUSE	STANDARD	PCT	98 AA	
42	1 HV57 MOUSE	STANDARD	PCT	98 AA	
43	1 HV57 MOUSE	STANDARD	PCT	98 AA	
44	1 HV57 MOUSE	STANDARD	PCT	98 AA	
45	1 HV57 MOUSE	STANDARD	PCT	98 AA	


```

DR InterPro; IPR003596; Ig_V.
DR Pfam; PF0047; Ig_1.
DR PROSITE; PS0083; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL.
FT CHAIN.
FT DOMAIN.
FT DOMAIN.
FT DOMAIN.
FT DOMAIN.
FT DISULFID.
FT NON_TER.
SQ SEQUENCE 117 AA; 12872 MW; 234055C6A469861 CRC64;

Query Match
Best Local Similarity 88.8%; Pred. No. 4,3e-39; Gaps 0;
Matches 87; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

1 EVQLVESGGGLVQPGGSLRLQISGQSRFTTYSNWVRQPERKRLRWATISGGQSYTY 60
20 EYLVLSGGGLVQPGGSLRLQISGQSRFTTYSNWVRQPERKRLRWATISGGQSYTY 79
61 PSYVGRFTISDNNKNTLYQSSLSKSDTMNYTCR 98
80 PSYVGRFTISDNNKNTLYQSSLSKSDTMNYTCR 117

RESULT 5
HVS8 MOUSE STANDARD; PRT; 117 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-NOV-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-76 precursor.
DE Ig heavy chain V region 5-76 precursor.
DE Bkaryocra; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
DE NCBI_TaxId=10090;
DE SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RA MEDLINE=89273149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of mosaic mutation in immunoglobulin Vn genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH183 SUBFAMILY.
CC -1- SIMILARITY:
DE HSP; P01810; 2983; 16-11kD.
DE InterPro; IPR007105; Ig_Like.
DE InterPro; IPR003065; Ig_MHC.
DE Pfam; PF0047; Ig_1.
DE SMART; SM00406; IgV_1.
DE PROSITE; PS0083; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN.
FT DOMAIN.
FT DOMAIN.
FT DOMAIN.
FT DOMAIN.
FT DISULFID.
FT NON_TER.
SQ SEQUENCE 117 AA; 12093 MW; 93A04762D789890 CRC64;

Query Match
Best Local Similarity 88.8%; Pred. No. 4,3e-39; Gaps 0;
Matches 87; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

```

```

QY 1 EVQLVESGGGLVQPGGSLRLQISGQSRFTTYSNWVRQPERKRLRWATISGGQSYTY 60
DB 20 EYLVLSGGGLVQPGGSLRLQISGQSRFTTYSNWVRQPERKRLRWATISGGQSYTY 79
61 PSYVGRFTISDNNKNTLYQSSLSKSDTMNYTCR 98
80 PSYVGRFTISDNNKNTLYQSSLSKSDTMNYTCR 117

RESULT 6
HVS6 MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-NOV-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-76 precursor.
DE Ig heavy chain V region 5-76 precursor.
DE Bkaryocra; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
DE NCBI_TaxId=10090;
DE SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of mosaic mutation in immunoglobulin Vn genes during
RT the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH183 SUBFAMILY.
CC -1- SIMILARITY:
DE HSP; P01810; 2983; 16-11kD.
DE InterPro; IPR007105; Ig_Like.
DE InterPro; IPR003065; Ig_MHC.
DE Pfam; PF0047; Ig_1.
DE SMART; SM00406; IgV_1.
DE PROSITE; PS0083; IG_LIKE; 1.
KW Immunoglobulin V region.
FT CHAIN.
FT DOMAIN.
FT DOMAIN.
FT DOMAIN.
FT DOMAIN.
FT DISULFID.
SQ SEQUENCE, AND DISULFIDE BONDS.
MEDLINE=8929111; PubMed=688494;

```


CC -1- MISCELLANEOUS: THIS MD CHAIN WAS ISOLATED FROM THE PLASMA OF A
 CC -1- PATIENT WITH MACROGLOBULINEMIA.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02054; GIBBUL.
 DR HSSP; P01772; 2PB4.
 DR GO; GO:0005576; G-protein-coupled receptor activity, NMS.
 DR GO; GO:0003823; F-actin binding activity, NMS.
 DR InterPro; IPR001110; Immunoglobulin-like domain; NMS.
 DR InterPro; IPR000066; Ig-MHC.
 DR InterPro; IPR003596; Ig-V.
 DR Pfam; PF00047; IgV_1.
 DR Pfam; PF00048; IgV_2.
 DR PROSITE; PS50835; Ig LITE; 1.
 KY Immunoglobulin V region; Pyridoxine carboxylic acid.
 FT DOMAIN 1 112
 FT NON TER 122
 FT SEQUENCE 122 AA; 13668 MW; A42D0E17D25F7C2 CRC64;
 SQ
 Query Match
 Best Local Similarity 66.4%; Score 430.5; DB 1; Length 122;
 Matches 81; Conservative 19; Mismatches 21; Indels 1; Gaps 1;
 QY
 1 EVOLVING:VGGGVGSGVKKLSGASGFTSTYSNHWNRQPTPEKRLAWATISGCSSTYY 60
 1 QVLEVGGGVGVGSGVKKLSGASGFTSTYSNHWNRQPTPEKRLAWATISGCSSTYY 60
 DB
 61 PSYKRGFTISRDNAKNTLYLQNSLKSEEDNMTYCTGNGG-HEGSGSFDVGGGGLTY 119
 61 ASVYKRGFTISRDNAKNTLYLQNSLKSEEDNMTYCTGNGG-HEGSGSFDVGGGGLTY 120
 QY
 120 SS 121
 DB
 121 SS 122
 RESULT 10
 ID HVJ3 HUMAN STANDARD: PRT; 117 AA.
 AC P18534;
 DT 01-NOV-1990 (Rel. 16; Created)
 DT 15-JUL-1996 (Rel. 01; Last sequence update)
 DT 15-JUL-1999 (Rel. 38; Last annotation update)
 OS Ig heavy chain V region RP precursor.
 OS Mus musculus (Mouse).
 OC Bursaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclerothamnii; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN
 (1)
 RS SEQUENCE FROM N.A.
 RX MEDLINE=89279149; PubMed=2496654;
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT Early onset of somatic mutation in immunoglobulin VH genes during
 RT B cell primary 14S-200 (J Exp Med 1993; 178:1989).
 RT J Exp Med 178:1989 (1993).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH17.8 SUBFAMILY.
 CC PIR; J07053; HWSRP.
 DR HSSP; P01810; 2PB4.
 DR InterPro; IPR003596; Ig-V.
 DR Pfam; PF00047; IgV_1.
 DR Pfam; PF00048; IgV_2.
 DR PROSITE; PS50835; Ig LITE; 1.
 KY Immunoglobulin V region; Hydriloma; Signal.
 FT SIGNAL 1 19
 FT DOMAIN 20 142
 FT NON TER 50 54
 FT DOMAIN 55 68
 FT DOMAIN 69 85
 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 86 117
 FT DISULFD 115
 FT NON TER 117
 SQ SEQUENCE 12666 MW; 2033293F90F72B CRC64;
 QY
 Best Local Similarity 66.3%; Score 430; DB 1; Length 117;
 Matches 83; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
 QY
 1 EVOLVING:VGGGVGSGVKKLSGASGFTSTYSNHWNRQPTPEKRLAWATISGCSSTYY 60
 20 VLVVGGGVGSGVKKLSGASGFTSTYSNHWNRQPTPEKRLAWATISGCSSTYY 79
 DB
 61 PSYKRGFTISRDNAKNTLYLQNSLKSEEDNMTYCTGNGG-HEGSGSFDVGGGGLTY 98
 80 DTVKRGFTISRDNAKNTLYLQNSLKSEEDNMTYCTGNGG-HEGSGSFDVGGGGLTY 117
 RESULT 11
 ID HVJ3 HUMAN STANDARD: PRT; 121 AA.
 AC P18534;
 DT 21-JUL-1996 (Rel. 01; Created)
 DT 21-JUL-1996 (Rel. 01; Last sequence update)
 DT 15-SEP-2003 (Rel. 42; Last annotation update)
 OS Ig heavy chain V region HIL.
 OS Homo sapiens (Human).
 OC Bursaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN
 (1)
 RS SEQUENCE.
 RX MEDLINE=79124695; PubMed=420800;
 RA Ghu Y.-Y., Lopez de Castro J.A., Poljak R.J.;
 RT Early onset of somatic mutation in the VH region of human myeloma
 RT cryoimmunoglobulin Ig HIL.
 RT Biochemistry 18:553-560 (1979).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGJ1 MYELOMA
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02054; GIBBUL.
 DR HSSP; P01772; 2PB4.
 DR GO; GO:0005576; G-protein-coupled receptor activity, NMS.
 DR GO; GO:0003823; F-actin binding activity, NMS.
 DR InterPro; IPR001110; Immunoglobulin-like domain; NMS.
 DR InterPro; IPR003596; Ig-MHC.
 DR InterPro; IPR003596; Ig-V.
 DR Pfam; PF00047; IgV_1.
 DR Pfam; PF00048; IgV_2.
 DR SMART; SM0006; IgV_1.
 DR PROSITE; PS50835; Ig LITE; 1.
 KY Immunoglobulin V region; Pyridoxine carboxylic acid.
 FT SIGNAL 1 1
 FT MOD RES 1 1
 FT NON TER 121 121
 FT SEQUENCE 121 AA; 13366 MW; 480FC3610E92DAB CRC64;
 SQ
 Query Match
 Best Local Similarity 65.3%; Score 424; DB 1; Length 121;
 Matches 80; Conservative 16; Mismatches 25; Indels 0; Gaps 0;
 QY
 1 EVOLVING:VGGGVGSGVKKLSGASGFTSTYSNHWNRQPTPEKRLAWATISGCSSTYY 60
 1 QVLEVGGGVGSGVKKLSGASGFTSTYSNHWNRQPTPEKRLAWATISGCSSTYY 60
 DB
 61 PSYKRGFTISRDNAKNTLYLQNSLKSEEDNMTYCTGNGG-HEGSGSFDVGGGGLTY 120
 61 GSVKRGFTISRDNAKNTLYLQNSLKSEEDNMTYCTGNGG-HEGSGSFDVGGGGLTY 120
 QY
 121 S 121
 DB
 121 S 121

NR PROSITE; PS50835; IG-LIKE; 1.
 NM Immunoglobulin V region.
 FT NON TER 116 116
 SQ SEQUENCE 116 AA; 12730 MW; 2C67CA9AAAA1282 CRC64;

Query March 63.8%; Score 410.5; DB 1; Length 116;
 Best Local Similarity 67.8%; Pred. No. 5e-34;
 Matches 82; Conservative 10; Mismatches 24; Indels 5; Gaps 1;

Gy 1 EVGVHSSGGLVKEGSLKLCGLSGFTSTYSNYSKOTPEKLEKLVNMTISGGSTTY 60
 |||||
 Db 1 EVGLVSSGGLVQFGRSLRSCLSGFBPEKGVTVQFQKLELVNMTISGGSTZY 60
 |||||

Gy 6: PSYVRSFTISNDIAKNTLYLQMSLSKSEDTANYCTHDGCHGSGSPFYWGQYTLTVS 120
 |||||
 Db 6: VDSVNRFTISNDIAKNTLYLQMSLSKSEDTANYCTHDGCHGSGSPFYWGQYTLTVS 115
 |||||

Gy 121 S 121
 Db 116 F 116

RESULT 15

ID 3: HV35 MOUSE STANDARD; PRT; 111 AA.
 AC P01804;
 DT 21-JUL-1986 (Rel. 01, Created)
 DE 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 15-SEP-2003 (Rel. 42, Last annotation update)
 DT 1g heavy chain V-II region HPC76 (Fragment).
 OS Mus musculus (Mouse).
 OS Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eumammalia; Rodentia; Soturognathi; Muridae; Murinae; Mus.
 CN NCBI_TaxID=10090;
 RX [1]

SEQUENCE FROM N.A. PubMed:6251474;
 RA Bernard O. Jacob N.A.
 RT "Nucleotide sequence of immunoglobulin heavy chain joining segments between translocated V_H and J_H constant regions genes."
 CC "Protein coding regions of 33 A.N. 6530-6541(1987) RESIDUES OF THE C-TERMINAL END OF THE SEQUENCE OF THESE JOINING SEGMENTS OF THE C-REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE 1. CORRESPONDING PORTION OF THE MOUSE MOPC 104E M μ CHAIN."
 CC 1. START/ACTIVE CONTAINS 1 Immunoglobulin-like domain.
 CC PIR: P01804 (MUS).
 DR HSP; P0189; IMCP.

DR Interpro: IPR007110; IG-like.
 DR Interpro: IPR003006; IG-MYC.
 DR Pfam: PF00047; Ig_1_5g_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG-LIKE; 1.

FT NON TER 111 111
 FT DOMAIN <1 110 IG-LIKE.
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 12304 MW; 0EDB9BEC7348056A CRC64;

Query March 63.4%; Score 407.5; DB 1; Length 111;
 Best Local Similarity 66.7%; Pred. No. 8.5e-34;
 Matches 78; Conservative 17; Mismatches 15; Indels 7; Gaps 2;

Gy 6 ESQGVIVKSGSLKSCASGFTSTYSNYSKOTPEKLEKLVNMTISGGSTY-TRYPSY 64
 |||||
 Db 1 ESQGVIVQPSGSKSLCVASGFTFSNVMNVSQSPKGLBVAELRLKSGVATVARSV 60
 |||||

Gy 65 RRRFTSRNDIAKNTLYLQMSLSKSEDTANYCTHDGCHGSGSPFYWGQYTLTVS 121
 |||||
 Db 61 KRRFTSRNDIAKNTLYLQMSLSKSEDTANYCTHDGCHGSGSPFYWGQYTLTVS 111
 |||||

Search completed: November 7, 2003, 07:28:08
 Job time : 9.7263 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 18.9025 seconds

782,516 Million cell updates/sec

File: us-09-661-992b-84_copy_1_121

Perfect score: 643 1 EHQVSSGGALVKEKSGSLD.....HGVSSPDVWGQGITLWSS 121

Scoring table: BLOSUM62 Gapex 10.0, Gapexc 0.5

Search: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp. archaea: *
2: sp. bacteria: *
3: sp. fungi: *
4: sp. plants: *
5: sp. invertebrate: *
6: sp. mammal: *
7: sp. mhc: *
8: sp. mhc: *
9: sp. mhc: *
10: sp. plant: *
11: sp. rodent: *
12: sp. virus: *
13: sp. invertebrate: *
14: sp. unclassified: *
15: sp. cytnus: *
16: sp. archaea: *
17: sp. archaea: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	563.5	87.6	487	11	Q93K4	Q93K4 mus musculi
2	540	84.0	119	11	Q92067	Q92067 mus musculi
3	474	73.7	479	11	Q91KPS	Q91KPS mus musculi
4	465.5	72.4	473	11	Q91205	Q91205 mus musculi
5	464.5	72.2	480	11	Q91KX1	Q91KX1 mus musculi
6	462.5	71.5	477	4	Q91K77	Q91K77 homo sapien
7	462.5	71.5	477	4	Q91K77	Q91K77 homo sapien
8	462.5	71.5	477	4	Q91K77	Q91K77 homo sapien
9	452	70.3	116	4	Q92B93	Q92B93 homo sapien
10	448.5	69.8	613	4	Q91KX1	Q91KX1 homo sapien
11	448.5	69.8	613	4	Q91KX1	Q91KX1 homo sapien
12	439.5	68.4	147	4	Q91K77	Q91K77 homo sapien
13	437.5	68.0	118	4	Q91K77	Q91K77 homo sapien
14	437.5	68.0	118	4	Q91K77	Q91K77 homo sapien
15	437.5	68.0	118	4	Q91K77	Q91K77 homo sapien
16	431	67.0	121	4	Q91K77	Q91K77 homo sapien

17	430	66.9	493	4	Q91KX1	Q91KX1 mus musculi
18	427	66.4	493	4	Q91KX1	Q91KX1 mus musculi
19	427	66.4	493	4	Q91KX1	Q91KX1 mus musculi
20	427	66.4	493	4	Q91KX1	Q91KX1 mus musculi
21	426.5	66.3	118	4	Q91K77	Q91K77 homo sapien
22	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
23	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
24	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
25	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
26	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
27	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
28	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
29	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
30	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
31	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
32	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
33	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
34	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
35	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
36	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
37	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
38	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
39	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
40	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
41	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
42	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
43	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
44	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi
45	425.5	66.2	573	4	Q91KX1	Q91KX1 mus musculi

ALIGNMENTS

Result	ID	Query	Length	DB	ID	Description
1	Q93K4	87.6	487	11	Q93K4	Q93K4 mus musculi
2	Q93K4	84.0	119	11	Q92067	Q92067 mus musculi
3	Q93K4	73.7	479	11	Q91KPS	Q91KPS mus musculi
4	Q93K4	72.4	473	11	Q91205	Q91205 mus musculi
5	Q93K4	72.2	480	11	Q91KX1	Q91KX1 mus musculi
6	Q93K4	71.5	477	4	Q91K77	Q91K77 homo sapien
7	Q93K4	71.5	477	4	Q91K77	Q91K77 homo sapien
8	Q93K4	71.5	477	4	Q91K77	Q91K77 homo sapien
9	Q93K4	70.3	116	4	Q92B93	Q92B93 homo sapien
10	Q93K4	69.8	613	4	Q91KX1	Q91KX1 homo sapien
11	Q93K4	69.8	613	4	Q91KX1	Q91KX1 homo sapien
12	Q93K4	68.4	147	4	Q91K77	Q91K77 homo sapien
13	Q93K4	68.0	118	4	Q91K77	Q91K77 homo sapien
14	Q93K4	68.0	118	4	Q91K77	Q91K77 homo sapien
15	Q93K4	68.0	118	4	Q91K77	Q91K77 homo sapien
16	Q93K4	67.0	121	4	Q91K77	Q91K77 homo sapien

OY 118 TVSS 121
DB 140 TVSS 143

RESULT 2

AC 092087 PRELIMINARY; PRT; 119 AA.
DT 01-DEC-2001 (FEBMRL:el. 19, Created)
DT 01-DEC-2001 (FEBMRL:el. 19, Last sequence update)
DT 01-DEC-2001 (FEBMRL:el. 19, Last annotation update)
DE Peptide-attaching anti-idiotypic heavy chain variable region (Fragment).
OS Mus musculus (Mouse).
OC Mus musculus (Mouse); Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mus musculus (Mouse); Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NM NCBI_TaxId=10090;
RM [1]
RT Sequence FROM N.A.

RT Aikin J.D. Taper, J., Jennings I.G., Horvath O., Cotton R.G.H.;
RT "Definition of the idiotope of Peptide-mimicking Antibodies Expressed
RT in Mammalian Cells";
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR Interpro: IPR003596, 19-11ke.
DR Interpro: IPR003596, 19-11ke.
DR Interpro: IPR003596, 19-11ke.
DR SMART: SM00406, IGV 1.
DR PROSITE: PS00835, IG_Like, 1.
FT NON TER 119 119
FT NON TER 119 119
FT NON TER 119 119
SQ SEQUENCE 119 AA; 13025 MW; F6F6940443B1C87C CRC64;

Query Match

Best Local Similarity 84.0%; Score 540; DB 11; Length 119;
Matches 109; Conservative 6; Mismatches 9; Indels 2; Gaps 1;

OY 1 EVOLVSGGGLVKGSGSLKSCAAGRTSTTMSWVQTPKRLKLPWATISGSGSYTY 60
DB 1 EVOLVSGGGLVKGSGSLKSCAAGRTSTTMSWVQTPKRLKLPWATISGSGSYTY 60
OY 61 PSVSGAGFTISDAAATLYLQNSLSLSDTAMVYCTPDGAGVGSFPMVQGITLVS 120
DB 61 PSVSGAGFTISDAAATLYLQNSLSLSDTAMVYCTPDGAGVGSFPMVQGITLVS 118
OY 121 S 121
DB 119 A 119

RESULT 3

AC 091207 PRELIMINARY; PRT; 466 AA.
DT 01-DEC-2001 (FEBMRL:el. 19, Created)
DT 01-DEC-2001 (FEBMRL:el. 19, Last sequence update)
DT 01-DEC-2001 (FEBMRL:el. 19, Last annotation update)
DE Hypothetical 52.7 kDa protein.
OS Mus musculus (Mouse).
OC Bakayofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mus musculus (Mouse); Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NM NCBI_TaxId=10090;
RM [1]
RT Sequence FROM N.A.

RT Aikin J.D. Taper, J., Jennings I.G., Horvath O., Cotton R.G.H.;
RT "Definition of the idiotope of Peptide-mimicking Antibodies Expressed
RT in Mammalian Cells";
RT Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR Interpro: IPR007110, 19-11ke.
DR EMBL: BC010324; AB010324.1; -
DR Interpro: IPR003596, 19-11ke.
DR Interpro: IPR003596, 19-11ke.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D087748584F CRC64;

DR SMART: SM00406, IGV 1.
DR PROSITE: PS00835, IG_Like, 4.
DR PROSITE: PS00835, IG_Like, 2.
SQ SEQUENCE 466 AA; 52682 MW; 4F6F93125DA8708 CRC64;

Query Match

Best Local Similarity 75.9%; Score 488; DB 11; Length 466;
Matches 96; Conservative 10; Mismatches 15; Indels 4; Gaps 2;

OY 1 EVOLVSGGGLVKGSGSLKSCAAGRTSTTMSWVQTPKRLKLPWATISGSGSYTY 60
DB 1 EVOLVSGGGLVKGSGSLKSCAAGRTSTTMSWVQTPKRLKLPWATISGSGSYTY 78
OY 20 EVOLVSGGGLVKGSGSLKSCAAGRTSTTMSWVQTPKRLKLPWATISGSGSYTY 117
DB 20 EVOLVSGGGLVKGSGSLKSCAAGRTSTTMSWVQTPKRLKLPWATISGSGSYTY 118
OY 61 PSVSGAGFTISDAAATLYLQNSLSLSDTAMVYCTPDGAGVGSFPMVQGITLVS 120
DB 61 PSVSGAGFTISDAAATLYLQNSLSLSDTAMVYCTPDGAGVGSFPMVQGITLVS 117
OY 121 S 121
DB 119 TVSS 142

RESULT 4

AC 091205 PRELIMINARY; PRT; 479 AA.
DT 01-DEC-2001 (FEBMRL:el. 19, Created)
DT 01-DEC-2001 (FEBMRL:el. 19, Last sequence update)
DT 01-DEC-2001 (FEBMRL:el. 19, Last annotation update)
DE Hypothetical 51.6 kDa protein.
OS Mus musculus (Mouse).
OC Bakayofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mus musculus (Mouse); Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NM NCBI_TaxId=10090;
RM [1]
RT Sequence FROM N.A.

RT Aikin J.D. Taper, J., Jennings I.G., Horvath O., Cotton R.G.H.;
RT "Definition of the idiotope of Peptide-mimicking Antibodies Expressed
RT in Mammalian Cells";
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC016566; AB016566.1; -
DR Interpro: IPR007110, 19-11ke.
DR Interpro: IPR003596, 19-11ke.
DR Interpro: IPR003596, 19-11ke.
DR SMART: SM00406, IGV 1.
DR PROSITE: PS00835, IG_Like, 4.
DR PROSITE: PS00835, IG_Like, 2.
SQ SEQUENCE 479 AA; 51603 MW; ECB2D087748584F CRC64;

Query Match

Best Local Similarity 75.2%; Score 474; DB 11; Length 479;
Matches 91; Conservative 9; Mismatches 15; Indels 3; Gaps 1;

OY 1 EVOLVSGGGLVKGSGSLKSCAAGRTSTTMSWVQTPKRLKLPWATISGSGSYTY 60
DB 1 EVOLVSGGGLVKGSGSLKSCAAGRTSTTMSWVQTPKRLKLPWATISGSGSYTY 79
OY 61 PSVSGAGFTISDAAATLYLQNSLSLSDTAMVYCTPDGAGVGSFPMVQGITLVS 120
DB 61 PSVSGAGFTISDAAATLYLQNSLSLSDTAMVYCTPDGAGVGSFPMVQGITLVS 113
OY 121 S 121
DB 114 S 134

RESULT 5

AC 091205 PRELIMINARY; PRT; 473 AA.
DT 01-DEC-2001 (FEBMRL:el. 19, Created)
DT 01-DEC-2001 (FEBMRL:el. 19, Last sequence update)
DT 01-DEC-2001 (FEBMRL:el. 19, Last annotation update)
DE Hypothetical 51.6 kDa protein.
OS Mus musculus (Mouse).
OC Bakayofa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Mus musculus (Mouse); Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NM NCBI_TaxId=10090;
RM [1]
RT Sequence FROM N.A.

RN SEQUENCE FROM N.A.
 [1]
 RP TISSUE-Memory gland;
 RA Jorgel T., Oca T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Matsuoka Y., Kikuchi T., Kato Y., Kohara H., Komoto H., Sugawara M.,
 RA Magatani M., Hosoki T., Kaku Y., Kohara H., Komoto H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Nishizawa K., Ono Y., Takibuchi S.,
 RA Matsuda S., Kikuchi K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Nishimura K., Iwayanagi T., Nakamura T., Nagahara K., Masuda Y.,
 RA Nishimura K., Iwayanagi T., Nakamura T., Nagahara K., Masuda Y.,
 RT "NBD human cDNA sequencing project."
 RL Submitted (May-2001) to the BMEI/Genbank/DBJ databases.
 DR BMEI: AK027320.1; BMS07271.1;
 DR Genbank: U000000000.1;
 DR InterPro: IPR003065; 1G_MHC.
 DR InterPro: IPR003596; 1G_V.
 DR Pfam: PF0047; 1G_4.
 DR PROSITE: PS00815; 1G_LIKE; 4.
 DR PROSITE: PS00290; 1G_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 498 AA; 53088 MW; 5ALD7ABEAC6E CRG64;
 Query Match
 Best Local Similarity 70.3%; Score 454.5; DB 4; Length 494;
 Matches 89; Conservative 13; Mismatches 17; Indels 5; Gaps 2;
 QY 1 EVLVSGGGLVGGGSLKICGASGFFSTYTNMVRQTPKRLPMVATISGCSYTY 60
 DB 20 EVLVSGGGLVGGGSLKICGASGFFSTYTNMVRQTPKRLPMVATISGCSYTY 79
 QY 61 PSQVGRFTISNDANRYLYGNSLKSSEBDYNYCTCDGGGSG---YSSGPTWGGQITL 117
 DB 80 PSQVGRFTISNDANRYLYGNSLKSSEBDYNYCTCDGGGSG---YSSGPTWGGQITL 137
 QY 118 TVSS 121
 DB 138 TVSS 141

RESULT 9

ID Q9ULJ3 PRELIMINARY; PRT; 116 AA.
 DT 01-MAR-2002 (TRENBERG; 13, Created)
 DT 01-MAY-2000 (TRENBERG; 23, Last sequence update)
 DT 01-MAR-2003 (TRENBERG; 23, Last annotation update)
 DB 61 PSQVGRFTISNDANRYLYGNSLKSSEBDYNYCTCDGGGSG---YSSGPTWGGQITL 117
 DB 80 PSQVGRFTISNDANRYLYGNSLKSSEBDYNYCTCDGGGSG---YSSGPTWGGQITL 137
 QY 118 TVSS 121
 DB 138 TVSS 141
 SEQUENCE FROM N.A.
 RA Young D.C., Van der Kleve F.J., Kalle R.N., Betney S.M.,
 RT "Hypsin-reactive autoantibodies in rheumatic carditis and normal
 fetus."
 RL Submitted (Immunol) Immunoglobulin, 87:184-192(1998).
 DR BMEI: APO35021; AAD06257.1;
 DR HSBP; P01772; 2F84.
 DR InterPro: IPR007110; 1G_LIKE.
 DR InterPro: IPR003596; 1G_MHC.
 DR Pfam: PF0047; 1G_1.
 DR SWART; SMO046; 1G_V.
 DR SWART; PS00815; 1G_LIKE; 1.
 RT "NBD human cDNA sequencing project."
 RL Submitted (May-2001) to the BMEI/Genbank/DBJ databases.
 DR BMEI: AK027320.1; BMS07271.1;
 DR Genbank: U000000000.1;
 DR InterPro: IPR003065; 1G_MHC.
 DR InterPro: IPR003596; 1G_V.
 DR Pfam: PF0047; 1G_4.
 DR PROSITE: PS00815; 1G_LIKE; 4.
 DR PROSITE: PS00290; 1G_MHC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 498 AA; 53088 MW; 5ALD7ABEAC6E CRG64;
 Query Match
 Best Local Similarity 70.3%; Score 454.5; DB 4; Length 494;
 Matches 89; Conservative 13; Mismatches 17; Indels 5; Gaps 2;
 QY 1 EVLVSGGGLVGGGSLKICGASGFFSTYTNMVRQTPKRLPMVATISGCSYTY 60
 DB 20 EVLVSGGGLVGGGSLKICGASGFFSTYTNMVRQTPKRLPMVATISGCSYTY 79
 QY 61 PSQVGRFTISNDANRYLYGNSLKSSEBDYNYCTCDGGGSG---YSSGPTWGGQITL 117
 DB 80 PSQVGRFTISNDANRYLYGNSLKSSEBDYNYCTCDGGGSG---YSSGPTWGGQITL 137
 QY 118 TVSS 121
 DB 138 TVSS 141

Query Match
 Best Local Similarity 70.3%; Score 452; DB 4; Length 116;
 Matches 89; Conservative 10; Mismatches 18; Indels 4; Gaps 1;
 QY 1 EVLVSGGGLVGGGSLKICGASGFFSTYTNMVRQTPKRLPMVATISGCSYTY 61
 DB 20 EVLVSGGGLVGGGSLKICGASGFFSTYTNMVRQTPKRLPMVATISGCSYTY 79
 QY 61 PSQVGRFTISNDANRYLYGNSLKSSEBDYNYCTCDGGGSG---YSSGPTWGGQITL 117
 DB 80 PSQVGRFTISNDANRYLYGNSLKSSEBDYNYCTCDGGGSG---YSSGPTWGGQITL 137
 QY 118 TVSS 121
 DB 138 TVSS 141

RESULT 10

ID Q96BB9 PRELIMINARY; PRT; 597 AA.
 AC G96BB9; 2001 (TRENBERG; 19, Created)
 DT 01-MAR-2002 (TRENBERG; 20, Last sequence update)
 DT 01-MAR-2003 (TRENBERG; 23, Last annotation update)
 DB 61 PSQVGRFTISNDANRYLYGNSLKSSEBDYNYCTCDGGGSG---YSSGPTWGGQITL 117
 DB 80 PSQVGRFTISNDANRYLYGNSLKSSEBDYNYCTCDGGGSG---YSSGPTWGGQITL 137
 QY 118 TVSS 121
 DB 138 TVSS 141

SEQUENCE FROM N.A.
 RA Strauberg R.,
 RT Submitted (Oct-2001) to the BMEI/Genbank/DBJ databases.
 DR BMEI: AK027320.1; BMS07271.1;
 DR Genbank: U000000000.1;
 DR InterPro: IPR007110; 1G_LIKE.
 DR InterPro: IPR003065; 1G_MHC.
 DR InterPro: IPR003596; 1G_V.
 DR Pfam: PF0047; 1G_1.
 DR SWART; SMO046; 1G_V.
 DR SWART; PS00815; 1G_LIKE; 5.
 DR PROSITE: PS00290; 1G_MHC; 3.
 KW Hypothetical protein.
 SQ SEQUENCE 597 AA; 65039 MW; 4FCALDCECE261D CRG64;
 Query Match
 Best Local Similarity 70.3%; Score 452; DB 4; Length 597;
 Matches 86; Conservative 18; Mismatches 16; Indels 6; Gaps 2;
 QY 1 EVLVSGGGLVGGGSLKICGASGFFSTYTNMVRQTPKRLPMVATISGCSYTY 60
 DB 20 EVLVSGGGLVGGGSLKICGASGFFSTYTNMVRQTPKRLPMVATISGCSYTY 79
 QY 61 PSQVGRFTISNDANRYLYGNSLKSSEBDYNYCTCDGGGSG---YSSGPTWGGQITL 117
 DB 80 PSQVGRFTISNDANRYLYGNSLKSSEBDYNYCTCDGGGSG---YSSGPTWGGQITL 137
 QY 118 TVSS 121
 DB 138 TVSS 144

RESULT 11

ID Q9MUK1 PRELIMINARY; PRT; 613 AA.
 DT 01-MAR-2002 (TRENBERG; 20, Created)
 DT 01-MAR-2002 (TRENBERG; 20, Last sequence update)
 DT 01-MAR-2003 (TRENBERG; 23, Last annotation update)
 DB 61 PSQVGRFTISNDANRYLYGNSLKSSEBDYNYCTCDGGGSG---YSSGPTWGGQITL 117
 DB 80 PSQVGRFTISNDANRYLYGNSLKSSEBDYNYCTCDGGGSG---YSSGPTWGGQITL 137
 QY 118 TVSS 121
 DB 138 TVSS 144
 SEQUENCE FROM N.A.
 RA TISSUE-Fonin;

RA Young D.C.;
 RT Wyo/sin-reactive autoantibodies in rheumatic carditis and normal
 RT Clin. Immunol., Immunopathol. 87:184-192(1998).
 DR HSBP; P01722; 2PB4.
 DR InterPro; IP8007110; 19_11ke.
 DR InterPro; IP8003006; 19_MHC.
 DR Pfam; PF00047; 19_11ke.
 DR SMART; SM00406; 19_11ke.
 DR PROSITE; PS00835; 19_Like; 1.
 FT NON-TER 118 118
 SQ SEQUENCE 118 AA; 12843 MW; D063394F2AC19D CRC64;
 Query Match 68.0%; Score 437.5; DB 4; Length 118;
 Similarity 77.8%; P8007110; 19_11ke; 18;
 Matches 85; Conservative 14; Mismatches 18; Indels 3; Gaps 1;
 QY 1 EVOLVEGCEIIVPGSSILKLSQNSAGTFTSTTMSWVOTPERLEWNTATISGSGSYTY 60
 DB 1 EVOLVEGCEIIVPGSSILKLSQNSAGTFTSTTMSWVOTPERLEWNTATISGSGSYTY 60
 QY 61 PSYVGRFTTSDNANNTLYLQNSGLSEPTTAMTYCTTPODGGYSSPPVWQGTTLTYS 120
 DB 61 ABSYVGRFTTSDNANNTLYLQNSGLSEPTTAMTYCTTPODGGYSSPPVWQGTTLTYS 117
 RESULT 15
 QY 15 PRELIMINARY; PRT; 437 AA.
 ID QSR1A4;
 AC QSR1A4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DT 01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
 DE Gamma1 heavy chain of Mab7 (fragment).
 GN IGh-4.
 OS Mus musculus (mouse)
 OC Eukaryota; Chordata; Eumetazoa; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI TaxId=10090.
 RN SOURCE FROM N.A.
 RA Wride K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
 RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
 RT antibody (Mab 7, its light and heavy chains) and construction of a
 RT Subcloned (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF152372; A040243.1; -.
 DR HSBP; P01842; 7PB3.
 DR NCBI; P21398; 19_11ke.
 DR InterPro; IP8007110; 19_11ke.
 DR InterPro; IP8003006; 19_MHC.
 DR Pfam; PF00447; 19_11ke.
 DR SMART; SM00406; 19_11ke.
 DR PROSITE; PS00835; 19_Like; 1.
 DR PROSITE; PS00290; 19_MHC; 1.
 FT NON-TER 437 437
 SQ SEQUENCE 437 AA; 48142 MW; 5CA7B3E7D697C CRC64;
 Query Match 67.3%; Score 432.5; DB 11; Length 437;
 Similarity 72.5%; P8007110; 19_11ke; 18;
 Matches 87; Conservative 18; Mismatches 20; Indels 7; Gaps 2;
 QY 2 VOLVSGCEIIVPGSSILKLSQNSAGTFTSTTMSWVOTPERLEWNTATISGSGSYTY 61
 DB 2 VOLVSGCEIIVPGSSILKLSQNSAGTFTSTTMSWVOTPERLEWNTATISGSGSYTY 61
 DB 1 VOLVSGCEIIVPGSSILKLSQNSAGTFTSTTMSWVOTPERLEWNTATISGSGSYTY 59
 QY 63 PSYVGRFTTSDNANNTLYLQNSGLSEPTTAMTYCTTPODGGYSSPPVWQGTTLTYS 121
 DB 63 ABSYVGRFTTSDNANNTLYLQNSGLSEPTTAMTYCTTPODGGYSSPPVWQGTTLTYS 121

DB 60 PSYVGRFTTSDNANNTLYLQNSGLSEPTTAMTYCTTPODGGYSSPPVWQGTTLTYS 113

Search completed November 7, 2003, 07:34:35
 Job time : 41.0025 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:17 / Search time 52.1402 Seconds

(without alignments)
368,069 Million calli updates/sec

Title: US-09-661-992b-84_COPY_1_121

RefSeq: 1 EHQVYSGGVLYFGKSSSLK.....HGYSSPDVWGQITLTVSS 121

Sequence: 643

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Total number of hits satisfying chosen parameters: 110763

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	643	100.0	249	22	AA020434
2	552	85.8	140	23	AA076122
3	551	85.7	144	23	AA079730
4	551	85.7	155	24	AA077245
5	551	85.7	155	24	AA077245
6	547	85.1	140	23	AA072814
7	545	84.8	119	23	AA072814
8	545	84.8	119	23	AA065555
9	545	84.8	140	23	AA076133

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
10	545	84.8	249	22	AA072801
11	544.5	84.7	249	22	AA050436
12	544.5	84.7	225	22	AA050436
13	544.5	84.7	225	22	AA050436
14	544.5	84.7	732	22	AA050437
15	542	84.3	123	21	AA01266
16	539	83.8	123	23	AA016426
17	539	83.8	123	23	AA016426
18	535.5	83.5	120	23	AA068393
19	529	82.3	123	19	AA060599
20	529	82.3	138	21	AA012604
21	525	81.8	119	18	AA052946
22	523.5	81.4	118	20	AA059627
23	523.5	81.4	118	20	AA059627
24	523.5	81.4	118	21	AA077602
25	523.5	81.4	118	22	AA063382
26	523.5	81.4	118	22	AA063382
27	523.5	81.4	118	22	AA076880
28	523.5	81.4	118	22	AA076880
29	523.5	81.4	118	22	AA076880
30	523.5	81.4	118	22	AA076880
31	523.5	81.4	118	22	AA076880
32	523.5	81.4	118	22	AA076880
33	523.5	81.4	118	22	AA076880
34	523.5	81.4	118	22	AA076880
35	523.5	81.4	118	22	AA076880
36	523.5	81.4	118	22	AA076880
37	523.5	81.4	118	22	AA076880
38	523.5	81.4	118	22	AA076880
39	523.5	81.4	118	22	AA076880
40	522	81.2	119	23	AA072813
41	522	81.2	119	23	AA072813
42	518.5	80.6	124	22	AA076934
43	517	80.4	125	22	AA076934
44	517	80.4	125	22	AA076934
45	516	80.2	140	24	AA074241

ALIGNMENTS

Result No.	Score	Query Match	Length	ID	Description
1	643	100.0	249	22	AA020434
2	552	85.8	140	23	AA076122
3	551	85.7	144	23	AA079730
4	551	85.7	155	24	AA077245
5	551	85.7	155	24	AA077245
6	547	85.1	140	23	AA072814
7	545	84.8	119	23	AA072814
8	545	84.8	119	23	AA065555
9	545	84.8	140	23	AA076133

Query Match 85.8%; Score 552; DB 23; Length 140;
 Blast Local Similarity 86.0%; Prot. No. 3a-4a; 9; Indels 0; Gaps 0;
 Matches 105; Conservative 0; Mismatches 9

QY 1 EVQLVESGGGLVFRPGSKLKCAASGPTFTTINWVRQTPERKLEAWATISSGSSTYY 60
 DB 20 EVQLVESGGGLVFRPGSKLKCAASGPTFTTINWVRQTPERKLEAWATISSGSSTYY 79
 QY 61 PDVRSKPTISRDNAKNTLYIQGSIKEEDTAWYCTIRGSGHVGSS--SPVYGGGRTL 120
 DB 80 PDVRSKPTISRDNAKNTLYIQGSIKEEDTAWYCTIRGSGHVGAYVYMDWQGSSTV 139
 QY 121 S 121
 DB 140 S 140

RESULT 3
 ABB79730
 ID ABB79730 standard; Protein, 144 AA.
 AC ABB79730;
 DT 29-OCT-2002 (first entry)
 DE Anti-Streptococcus mutans surface antigen MAb SMLA3 VH.
 XX Streptococcus mutans; monoclonal antibody; MAb; mouse;
 XX transgenic animal; carrier; immunotherapy; therapy.
 OS Mus musculus.
 XX US2002060606-A1.
 XX 06-JUN-2002.
 XX 15-JUN-2001; 2001US-0681823.
 XX 20-APR-1999; 99US-0378577.
 XX (SHU)/ SHI Y.
 XX (MORI)/ MORISON S. L.
 XX (TRIN)/ TRIN K.
 XX (WINE)/ WINS L.
 XX (CHEN)/ CHEN L.
 XX (AND)/ ANDERSON M. H.
 XX SHI W, Morrison SL, Trind K, Wines L, Chen L, Anderson MH;
 PI WPI, 2002-55638/60.
 XX N-PSDB; ABB94613.
 XX

PT Treatment and prevention of dental caries in mammals, in particular
 PT humans by orally administering genetically engineered or purified
 PT antibodies that bind to surface antigens of cariogenic organisms -
 XX Claim 14; Fig 3b; 30pp; English.

XX The present sequence is the protein sequence of the heavy chain
 CC variable region (VH) of the murine monoclonal antibody SMLA3 (IgG)
 CC which binds specifically to the surface antigen of cariogenic type
 CC Streptococcus mutans (ATCC 25175). The monoclonal antibody is
 CC produced by SMLA3 (ATCC HB 12538) hybridoma cells. In an example
 CC of the present sequence, the antibody is fused to a chimeric
 CC complementing SMLA3 variable region and human antibody constant
 CC region. Such chimeric monoclonal antibodies can be used to
 CC prevent or treat dental caries in humans. The antibodies engage
 CC the surface antigen of cariogenic organisms, resulting in the chimeric
 CC antibodies may be produced in edible plants, in transgenic animals,
 CC or in chicken eggs for oral ingestion.

XX Sequence 144 AA;
 SQ Query Match 85.7%; Score 551; DB 23; Length 144;
 Blast Local Similarity 84.7%; Prot. No. 3a-4a; 4; Indels 4; Gaps 2;
 Matches 105; Conservative 11; Mismatches 4

QY 1 EVQLVESGGGLVFRPGSKLKCAASGPTFTTINWVRQTPERKLEAWATISSGSSTYY 60
 DB 20 EVQLVESGGGLVFRPGSKLKCAASGPTFTTINWVRQTPERKLEAWATISSGSSTYY 79
 QY 61 PDVRSKPTISRDNAKNTLYIQGSIKEEDTAWYCTIRGSGHVGSS--SPVYGGGRTL 117
 DB 80 PDVRSKPTISRDNAKNTLYIQGSIKEEDTAWYCTIRGSGHVGAYVYMDWQGSSTV 138
 QY 118 TVSS 121
 DB 139 TVSS 142

RESULT 4
 ABB72395
 ID ABB72395 standard; Protein, 155 AA.
 AC ABB72395;
 DT 09-MAY-2003 (first entry)
 DE Chimeric construct comprising dhvart fusion to SMLA3 VH.
 XX Dhvart; SMLA3; antibody; antimicrobial; antibacterial; anticaries.
 XX Unidentified.
 OS Unidentified.
 XX Recp
 XX Peptide 1
 FT /label= Dhvart1
 FT Peptide 15..30
 FT /label= Linker
 FT Protein 32..155
 FT /label= SMLA3_VH
 XX W02003007989-A1.
 XX 30-JAN-2003.
 XX 17-JUL-2002; 2002WO-US22695.
 XX 19-JUL-2001; 2001US-091059.
 XX 14-FEB-2002; 2002US-0077824.
 XX (WASH) WASHINGTON DENTAL SERVICES.
 XX (FDCS) UNITY CALIFORNIA.
 XX SHI W, Morrison SL, Trind K, Wines L, Chen L, Anderson MH, Qi F,
 PI WPI, 2003-205642/22.
 XX N-PSDB; ABB283396.
 XX

PT A composition comprising a targeting moiety and an anti-microbial
 PT peptide moiety, useful for treating microbial infections, e.g. on
 PT proctoco, or parasites
 XX Example 1; Fig 4; 53pp; English.

XX The present sequence is that of a chimeric construct composed of
 CC the antimicrobial peptide dhvart (see also ABB72395) joined via a
 CC a peptide linker to the heavy chain variable region of SMLA3, a
 CC monoclonal antibody made against the cariogenic organism.
 CC The chimeric construct is used to prevent or treat dental caries
 CC activity toward S. mutans strains ATCC 25175, WPI and DM2475, but
 CC not against a range of other oral bacterial strains. It is an

CC example of chimeric constructs of the invention which generally
 CC comprise a targeting moiety that recognizes a target microorganism,
 CC and an antimicrobial peptide. Claimed compositions comprising the
 CC chimeric constructs are useful for treating microbial infections or
 CC diseases, e.g. on mucosal surfaces such as mouth, vagina,
 CC skin, or internal organs, including mouth, vagina,
 CC and internal organs, including mouth, vagina, and internal organs,
 CC such as the lungs, liver, spleen, pancreas, and intestines, by bacteria,
 CC rickettsia, fungi, yeasts, protozoa or parasites.

XX Sequence 165 AA:

Query Match 85.7%; Score 551; DB 24; Length 165;

Best Local Similarity 84.7%; Pred. No. 4,2e-44; Indels 4; Gaps 2;

Matches 105; Conservative 11; Mismatches 4; Indels 4; Gaps 2;

1 EVQVSSGGGLVWPGSGLKSCASGFTFSYTMWVQTPREKRLMWASISSGGSTYY 60

31 DVLVSSGGGLVWPGSGLKSCASGFTFSYTMWVQTPREKRLMWASISSGGSTYY 90

61 PSYNGRFTSRNANKTYLQMSLKSEPTMYCTRCQGHGVS---SPDYGGTTL 117

91 PSYNGRFTSRNANKTYLQMSLKSEPTMYCTRCQGHGVS---SPDYGGTTL 149

XX 118 TWS 121

YY 150 TWS 153

DB 160 TWS 163

RESULT 5

ABP72294

ID ABP72294 standard; Protein; 165 AA.

XX ABP72294:

08-MAY-2003 (first entry)

Chimeric construct comprising histatin 5 fusion to SMUA3 VH.

XX Histatin 5; SMUA3; antibody; antimicrobial; antibacterial;

XX antitoxins.

XX unidentified.

XX Key

XX Location/Qualifiers

XX 1..165 = Histatin 5

XX Peptide

XX 25..40

XX /label= Linker

XX 41..165

XX /label= SMUA3_VH

XX WC0203007989-A1.

XX 30-JAN-2003.

XX 17-JUL-2002; 2002NO-US32695.

XX 19-JUL-2001; 2001US-091938.

XX 14-FEB-2002; 2002US-007624.

XX (WASH.) WASHINGTON DENTAL SERVICE.

XX (WASH.) DENTAL CALIFORNIA.

XX SHI W, Morrison SL, Tish K, Wine L, Chen L, Anderson NH, Qi F;

XX WTI-2003-229542/22.

XX N-7003; AM583571.

XX A composition comprising a targeting moiety and an anti-microbial

XX peptide moiety, useful for treating microbial infections, e.g. on

XX mucosal surfaces such as mouth, vagina, skin, or internal organs,

XX including mouth, vagina, and internal organs, by bacteria,

XX rickettsia, fungi, yeasts, protozoa or parasites.

XX Example 1; Fig 3; 53pp; English.

XX The present sequence is that of a chimeric construct composed of

XX the antimicrobial peptide histatin 5 (see also ABP72294) joined via

XX a peptide linker to the heavy chain variable region of SMUA3, a

XX monoclonal antibody made against a human immunoglobulin G1

XX rickettsia. The chimeric construct is useful for treating microbial

XX activity toward S. mutans strains ATCC 25175, LM7 and OM215, but

XX not against a range of other oral bacterial strains. It is an

XX example of chimeric constructs of the invention which generally

XX comprise a targeting moiety that recognizes a target microorganism,

XX and an antimicrobial peptide. Claimed compositions comprising the

XX chimeric constructs are useful for treating microbial infections or

XX diseases, e.g. on mucosal surfaces such as mouth, vagina,

XX skin, or internal organs, including mouth, vagina, and internal organs,

XX such as the lungs, liver, spleen, pancreas, and intestines, by bacteria,

XX rickettsia, fungi, yeasts, protozoa or parasites.

XX Sequence 165 AA:

Query Match 85.7%; Score 551; DB 24; Length 165;

Best Local Similarity 84.7%; Pred. No. 4,2e-44; Indels 4; Gaps 2;

Matches 105; Conservative 11; Mismatches 4; Indels 4; Gaps 2;

1 EVQVSSGGGLVWPGSGLKSCASGFTFSYTMWVQTPREKRLMWASISSGGSTYY 60

41 DVLVSSGGGLVWPGSGLKSCASGFTFSYTMWVQTPREKRLMWASISSGGSTYY 100

61 PSYNGRFTSRNANKTYLQMSLKSEPTMYCTRCQGHGVS---SPDYGGTTL 117

101 PSYNGRFTSRNANKTYLQMSLKSEPTMYCTRCQGHGVS---SPDYGGTTL 159

XX 118 TWS 121

YY 150 TWS 153

DB 160 TWS 163

RESULT 5

AAU76132

ID AAU76132 standard; Protein; 140 AA.

XX AAU76132:

08-MAY-2002 (first entry)

Mouse mAb 26-2F heavy chain variable region mutant M1007.

XX Mouse; angiotensin; angiotensin; tumour; cancer; retinopathy;

XX ocular neovascular disease; vitamin A deficiency; myelitis;

XX Kaposi's sarcoma; rheumatoid arthritis; macular degeneration;

XX rheumatoid arthritis; graft versus host disease; autoimmune disease;

XX type I diabetes; multiple sclerosis; systemic lupus erythematosus;

XX myasthenia gravis; mutant; murine; monoclonal antibody; 26-2F;

XX heavy chain variable region; M1007.

XX Mut sp.

XX Synthetic.

XX Key

XX Location/Qualifiers

XX 1..139

XX Peptide

XX 20..140

XX /label= Signal_peptide

XX Protein

XX 140

XX /label= Mature_VH

XX Misc-difference 100

XX /note= "Wild-type Met substituted by Tyr"

XX US0200201030-A1.

XX 24-JAN-2002.

XX 05-APR-1999; 9905-0286240.

XX 05-APR-1999; 9905-0286240.

CC The antibody or its fragment is useful for inhibiting the angiogenic
CC activity of angiotensin. The antibody is useful for treating a tumour in
CC patients, or inhibiting the ability of circulating tumour cells to form a
CC growth, or inhibiting the ability of circulating tumour cells to form a
CC vasculatured tumour mass. The antibody is useful for treating a tumour
CC with abnormal or unwanted angiogenesis, including cancer, and other
CC diseases mediated by angiogenesis, including ocular neovascular disease,
CC rejection, neovascular glaucoma and retrolental fibroplasia and other
CC diseases associated with corneal neovascularization, including epidemic
CC keratoconjunctivitis, vitamin A deficiency, contact lens overwear,
CC infections, lipid degeneration, chemical burns, bacterial ulcers
CC fungal ulcers, herpes simplex infections, herpes zoster infections,
CC proctosan infections, Kaposi's sarcoma, Koenen ulcer, rheumatoid
CC Seven Johnson's disease, and corneal neovascularization include macular
CC degeneration, sickle cell anaemia, sarcoid, Paget's disease,
CC mycobacterial infections, Behcet's disease, trauma, osteoarthritis,
CC rejection, autoimmune diseases such as type 1 diabetes, multiple
CC sclerosis, systemic lupus erythematosus, and myasthenia gravis. The
CC present sequence represents the B99 mutant of the mouse monoclonal
CC antibody. The present sequence is not shown in the specification but was
CC created by the indexer using the sequence appearing as AAU76122 and the
CC information in the claims.

CC Sequence 140 AA:

Query Match 84.8%; Score 545; DB 23; Length 140;
Best Local Similarity 85.1%; Pval: No. 1,4e-43;

Matches 109; Conservative 8; Mismatches 10; Indels 0; Gaps 0;
CC 1 EVQLVESGGGLVQPGGSLRLCSAASGFTSTTYSNWVRQPPKRLRWMTISGGSYTY 60

DB 20 EYVLVESGGGLVQPGGSLRLCSAASGFTSTTYSNWVRQPPKRLRWMTISGGSYTY 79

CC 61 PSYVGRFTISDNANTLYLQMSLSKEDTAMVYCTCDGSGVGSFPMQGGITLVIS 120

DB 80 PSYVGRFTISDNANTLYLQMSLSKEDTAMVYCTCDGSGVGSFPMQGGITLVIS 139

CC 121 S 121

CC 140 S 140

RESULT 10

AAU72801

AAU72801 standard; Protein: 464 AA.

CC AAU72801;

CC 26-FEB-2002 (first entry)

CC TRA-8 heavy chain.

CC Tumour necrosis factor-related apoptosis-inducing ligand receptor;
CC TNF-related apoptosis-inducing ligand (TRAIL) receptor; TNF-related
CC autoimmune disease; systemic lupus erythematosus; Hashimoto's
CC rheumatoid arthritis; Sjogren's syndrome; Chro'n's disease; anaemia;
CC Addison disease; scleroderma; Goodpasture's syndrome; sterility;
CC allergy; arteriosclerosis; myocardiitis; Basen's disease; diabetes;
CC glomerular nephritis; cancer; antibody; chromosome Bp21-22; TRA-8.

CC Mus musculus.

CC W020018150-A1.

CC 06-NOV-2001.

CC XX

PF 02-MAY-2001; 2001MO-US14151.

CC 02-MAY-2001; 2000MO-20134AP.

CC (UABR-) UNB RES FOUND.

CC Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;

CC WPI; 2002-04338/06.

CC N-PSBP; A897082.

CC Novel antibody specific for tumour necrosis factor-related

CC apoptosis-inducing ligand, useful for inhibiting cell proliferation in

CC cancer.

CC Claim 26; Page 198-199; 229pp; English.

CC The invention describes a novel antibody which recognizes a tumour

CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor

CC b25 (located on chromosome Bp21-22). The antibody has apoptosis-inducing

CC activity to a cell expressing b25 in vivo. It is also useful for

CC dysregulating cells, and for inhibiting cell proliferation in a cell,

CC preferably a human breast, ovary, colon, haematopoietic, prostate,

CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may

CC antibody is used to treat autoimmune disease or cancer.

CC erythematosus, Hashimoto's disease, rheumatoid arthritis, lupus

CC graft-versus-host disease, Sjogren's syndrome, Chro'n's disease,

CC pruritus anaemia, Addison disease, scleroderma, Goodpasture's syndrome,

CC sclerosis, Basen's disease, insulin-dependent diabetes mellitus,

CC allergy, atopic disease, arteriosclerosis, myocardiitis, cardiomyopathy,

CC glomerular nephritis, hypoplastic anaemia, rejection after organ

CC ovary, lymphatic or breast tissue. The antibodies used in the assay for

CC isolating heavy and light chain cDNA of the mouse TRAIL (AAU72801 and

CC AAU72802), TRA-8 are shown in AAU72799 and AAU72800.

CC Sequence 464 AA:

Query Match 84.8%; Score 545; DB 23; Length 464;
Best Local Similarity 87.6%; Pval: No. 5.3e-43;

Matches 106; Conservative 4; Mismatches 9; Indels 1; Gaps 1;
CC 1 EVQLVESGGGLVQPGGSLRLCSAASGFTSTTYSNWVRQPPKRLRWMTISGGSYTY 60

DB 20 EYVLVESGGGLVQPGGSLRLCSAASGFTSTTYSNWVRQPPKRLRWMTISGGSYTY 79

CC 61 PSYVGRFTISDNANTLYLQMSLSKEDTAMVYCTCDGSGVGSFPMQGGITLVIS 120

DB 80 PSYVGRFTISDNANTLYLQMSLSKEDTAMVYCTCDGSGVGSFPMQGGITLVIS 137

CC 121 S 121

CC 138 S 138

RESULT 11

AAU20436

AAU20436 standard; Protein: 249 AA.

CC AAU20436;

CC 21-JUN-2001 (first entry)

CC Anti-FIX/PRX antibody 198/Al actv.

CC Factor IX; FIX; Factor IXa; FIXa; actv; antibody; procoagulant;

CC haemorrhagic diathesis; haemostatic; antibody; therapy; mouse.

CC Chimeric - Mus musculus.

CC 06-NOV-2001.

CC XX

CC Chimeric - Synthetic.
 PH Key Location/Qualifiers
 FT Protein 1..122
 FT 1/label1 VH
 FT Region 9..111
 FT Peptide 123..136
 FT 1/label4 Linker
 FT 1/label5 VL
 FT Region 230..238
 FT Misc-difference 1/label1 CDR3
 FT 1/label2 CDR3
 FT 1/label3 CDR3
 FT Misc-difference 224
 FT /note= "encoded by GCM"
 FT /note= "encoded by GCM"
 FT /note= "encoded by GCM"
 PD 22-MAR-2001.
 PD 13-SEP-2000, 2000NOV-EP08936.
 PD 14-SEP-1999, 99AAT-0001576.
 XX (BAXT) BAXTER AG.
 PI Schefflinger F, Kerschbaum R, Falkner F, Dornier F,
 XX HPF 2001-290358/30.
 XX M-PSDB; AAF30726.
 XX
 PT New factor IX/factor IXa antibodies and their derivatives useful for
 PT increasing antithrombotic activity of factor IXa, and for treating blood
 PT coagulation disorders such as haemophilia A and haemorrhagic diatheses
 PS Example 10; Fig 17; 138pp; English.
 XX
 CC The present sequence is that of a single chain Fv (scFv) derivative
 CC of antibody 198/Al comprising the heavy (VH) and light (VL) chain
 CC variable regions of 198/Al joined by an artificial, flexible linker
 CC peptide. The scFv was obtained by PCR amplification of cDNAs for
 CC 198/Al VH and VL regions. Factor IXa (scFv)/activated Factor IXa (FIXa)
 CC antibodies of the invention. Anti-FIX/FIXa and their derivatives,
 CC including scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor
 CC activity or FIXa activating activity. Administration leads to an
 CC increase in the activity of Factor IXa. The antibodies of the invention
 CC in the absence of FVIII or FVIIIa, and in the case of FVIII
 CC inhibitor patients. The antibodies and derivatives are used in a
 CC method of increasing the activity of Factor IXa, and in the treatment of
 CC coagulation disorders, especially haemophilia A and haemorrhagic
 CC diatheses.
 CC
 XX Sequence 249 Aa.
 SQ
 Query Match 84.7%; Score 544.5; DB 22; Length 249;
 Best Local Similarity 87.7%; Freq. No. 2,9e+43;
 Matches 107; Conservative 5; Mismatches 9; Indels 1; Gaps 1;
 QY 1 EVQLVESGGIGLVKPGASVKQLCKASGFTFSITYSWVRQPEKELRWNISSGSIYY 60
 DB 1 EVQLVESGGIGLVKPGASVKQLCKASGFTFSITYSWVRQPEKELRWNISSGSIYY 60
 QY 61 PDVYKAGFTSGSGLVVRQASVKLVDSGPDNATNYCTPRGGGVRGS-SFVYVQGITLAV 119
 DB 61 PDVYKAGFTSGSGLVVRQASVKLVDSGPDNATNYCTPRGGGVRGS-SFVYVQGITLAV 119
 QY 120 SS 121
 QY 121 SS 122
 DB 121 SS 122

RESULT 12
 AAB20442 standard; Protein, 294 Aa.
 AAB20442;
 XX
 AC AAB20442;
 XX
 FT 21-JUN-2001 (first entry)
 DE Anti-FIX/FIXa antibody 198/B1-myc-tag fusion.
 DE
 XX Factor IX; FIX. Factor IXa; FIXa; scFv; antibody; procoagulant;
 XX Factor IXa; FIXa. Factor IXa; FIXa; scFv; antibody; procoagulant;
 XX haemorrhagic diathesis, haemostatic, antithrombotic, therapy; mouse;
 XX myc-tag.
 XX
 CC Chimeric - Nucleus.
 CC Chimeric - Synthetic.
 CC Chimeric - Receptor.
 PH Key Location/Qualifiers
 FT Peptide 1/label1 Signal_Peptide
 FT Protein 23..294 Mature_Protein
 FT 1/label1 Mature_Protein
 FT 1/label1 scFv
 FT Region 23..144
 FT 1/label1 VH
 FT Misc-difference 1/label1 CDR3
 FT 1/label2 CDR3
 FT 1/label3 CDR3
 FT Misc-difference 224
 FT /note= "encoded by GCM"
 FT /note= "encoded by GCM"
 FT /note= "encoded by GCM"
 PD 22-MAR-2001.
 PD 13-SEP-2000, 2000NOV-EP08936.
 PD 14-SEP-1999, 99AAT-0001576.
 XX (BAXT) BAXTER AG.
 PI Schefflinger F, Kerschbaum R, Falkner F, Dornier F,
 XX HPF 2001-290358/30.
 XX M-PSDB; AAF30732.
 XX
 PT New factor IX/factor IXa antibodies and their derivatives useful for
 PT increasing antithrombotic activity of factor IXa, and for treating blood
 PT coagulation disorders such as haemophilia A and haemorrhagic diatheses
 PS Example 18; Fig 34; 138pp; English.
 XX
 CC The present sequence is that of a fusion protein comprising a Fe18
 CC leader, a single chain Fv (scFv) derivative of antibody 198/B1
 CC comprising the heavy (VH) and light (VL) chain variable regions of
 CC antibody 198/B1, and a C-terminal His affinity tag.
 CC a myc-tag peptide, a spacer, and a C-terminal His affinity tag.
 CC 198/B1 is an example of anti-human factor IX (FIX)/activated Factor
 CC IX (FIXa) antibodies of the invention. Anti-FIX/FIXa antibodies and

CC their derivatives, including scfv fragments, have FvIIIA cofactor
 CC activity or FIXa activating activity. Administration leads to an
 CC increase in the procoagulant activity of FIXa, even in the presence
 CC of anti-FIXa antibodies. The antibodies and derivatives are used in
 CC the absence of FvIII or FvIIIA, and in the case of FvIII inhibitor
 CC patients. The antibodies and derivatives are used in a claimed
 CC pharmaceutical composition for treating patients with blood
 CC coagulation disorders, especially haemophilia A and haemorrhagic
 CC diseases. The expression of a fusion protein comprising a FIXa
 CC exhibited FvIII-like activity.

Sequence 294 AA:

Query Match 86.7%; Score 544.5; DB 22; Length 294;

Best Local Similarity 86.7%; Pred. No. 3.5e-43; Mismatches 5; Indels 3; Gaps 2;

Matches 100; Conservative 9; Mismatches 5; Indels 3; Gaps 2;

1 EVQLVDSGGGVLPFGSGSLSCAASGFFSTFTSMWRCQPERKRLMWNTISSGSSTYY 60

23 EVKLVSQGGGVLPFGSGSLSCAASGFFSTFTSMWRCQPERKRLMWNTISSGSSTYY 82

61 PSVNGRFTIRDNNAKNTLYLQMSLKSEEDTMYTCRGGGKQSS--PVMQGGITLL 118

83 PSVNGRFTIRDNNAKNTLYLQMSLKSEEDTMYTCRGGGKQSS--PVMQGGITLL 141

119 VSS 121

142 VSS 144

AA820438 standard; Protein: 325 AA.

AA820438;

21-UN-2001 (first entry)

Anti-FIX/FIXa antibody 198/B1 bivalent miniantibody.

Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;

Factor VIII cofactor; blood coagulation disorder; haemophilia A;

bivalent antibody; patient; p21-198a2102;

Chimeric - Mus musculus.

Chimeric - Synthetic.

Chimeric - Bacteriophage coli.

Key Location/Qualifiers

Peptide 1..32; signal peptide

Protein 23..325; /note="Pdb leader"

Protein 23..325; /label="Mature Protein"

Region 23..144; scfv

Misc-difference 76; /label="VA"

Peptide 145..159; /note="encoded by GGN"

Region 150..271; /label="Linker"

Misc-difference 166; /note="VL"

Misc-difference 181; /note="encoded by TWT"

Peptide 272..274; /label="Spacer"

Protein 275..284; /label="Hinge"

Protein 285..319
 /label="Helix
 Peptide 310..325
 /label="His_tag"

MO20019992-A2.

22-MAR-2001.

13-SEP-2000; 000M00-EP08936.

14-SEP-1999; 99AT-0001576.

(BAXT) BAXTER AG.

Schellfinger F, Kerschhauer R, Palmer F, Dörner F;

WPI.1-01-29055/70.

N-58B; AA820437.

New factor IX/factor IXa antibodies and their derivatives useful for

coagulation disorders such as haemophilia A and haemorrhagic diseases

Example 16; Fig 26; 13pp; English.

The present sequence is that of a bivalent miniantibody comprising
 a Fab leader peptide, the single chain Fv (scfv) fragment of
 antibody 198/B1 (subclone A82), an amphipathic helical structure
 and a C-terminal His tag. The protein was expressed in
 a baculovirus system using a baculovirus vector (BAXT0728).
 Antibody 198/B1 is an example of anti-Factor IX (FIX).
 CC (FIX)/activated Factor IX (FIXa) antibodies of the invention.

Anti-FIX/FIXa antibodies and their derivatives have FvIIIA cofactor
 activity or FIXa activating activity. Administration leads to an
 increase in the procoagulant activity of FIXa, even in the presence
 of FvIII inhibitors. This allows for rapid blood coagulation even
 in the absence of FvIII or FvIIIA, and in the case of FvIII
 inhibitor patients. The antibodies and derivatives are used in a
 claimed pharmaceutical composition for treating patients with blood
 coagulation disorders, especially haemophilia A and haemorrhagic
 diseases. The bivalent miniantibody exhibited FvIII-like
 activity.

Sequence 325 AA;

Query Match 86.7%; Score 544.5; DB 22; Length 325;

Best Local Similarity 86.7%; Pred. No. 3.5e-43; Mismatches 5; Indels 3; Gaps 2;

Matches 100; Conservative 9; Mismatches 5; Indels 3; Gaps 2;

1 EVQLVDSGGGVLPFGSGSLSCAASGFFSTFTSMWRCQPERKRLMWNTISSGSSTYY 60

23 EVKLVSQGGGVLPFGSGSLSCAASGFFSTFTSMWRCQPERKRLMWNTISSGSSTYY 82

61 PSVNGRFTIRDNNAKNTLYLQMSLKSEEDTMYTCRGGGKQSS--PVMQGGITLL 118

83 PSVNGRFTIRDNNAKNTLYLQMSLKSEEDTMYTCRGGGKQSS--PVMQGGITLL 141

119 VSS 121

142 VSS 144

AA820437 standard; Protein: 732 AA.

AA820437;

21-UN-2001 (first entry)

Anti-FIX/FIXa antibody 198/B1-alkaline phosphatase fusion.

Fri Nov 7 09:40:20 2003

us-09-661-992b-84_copy_1_121.rag

Page 11

DB 121 VSS 123

Search completed: November 7, 2003, 07:27:02
Job time : 53.1802 secs

GenCode version 5.1.6
Copyright (c) 1995 - 2003 Comagen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 07:30:13 / Search time 106.138 seconds
(without alignments)

195.799 Million cells updates/sec

Title: US-09-661-992b-84_COPY_1_121

RefSeq score: 643 EHVJUSGGGVGVSGSLVFCSSSLAT.....HOYSSPDVWGQITLVSS 121

Sequence:

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/prodata/2/pubpa/ECT_NEW_PUB.pep.*
3: /cgn2_6/prodata/2/pubpa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/2/pubpa/US07_NEW_PUB.pep.*
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6: /cgn2_6/prodata/2/pubpa/ECTUS_PUBCOMB.pep.*
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11: /cgn2_6/prodata/2/pubpa/US09C_PUBCOMB.pep.*
12: /cgn2_6/prodata/2/pubpa/US09C_NEW_PUB.pep.*
13: /cgn2_6/prodata/2/pubpa/US10B_PUBCOMB.pep.*
14: /cgn2_6/prodata/2/pubpa/US10B_PUBCOMB.pep.*
15: /cgn2_6/prodata/2/pubpa/US10C_PUBCOMB.pep.*
16: /cgn2_6/prodata/2/pubpa/US10C_NEW_PUB.pep.*
17: /cgn2_6/prodata/2/pubpa/US10C_NEW_PUB.pep.*
18: /cgn2_6/prodata/2/pubpa/US06_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
sequence similarity to the sequence of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	552	85.9	140	US-09-286-240-4	Sequence 4, App1
2	551	85.7	155	US-10-077-624-7	Sequence 12, App1
3	551	85.7	155	US-10-077-624-7	Sequence 4, App1
4	551	85.7	155	US-10-077-624-7	Sequence 4, App1
5	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
6	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
7	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
8	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
9	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
10	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
11	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
12	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
13	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
14	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
15	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
16	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
17	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
18	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
19	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
20	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
21	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
22	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
23	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
24	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
25	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
26	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
27	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
28	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
29	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
30	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
31	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
32	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
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35	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
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37	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
38	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
39	545	84.8	119	US-10-281-479A-61	Sequence 61, App1
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16	523.5	81.4	118	US-10-169-003-46	Sequence 46, App1
17	523.5	81.4	137	US-09-423-800-76	Sequence 76, App1
18	523.5	81.4	137	US-10-371-961-76	Sequence 76, App1
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41	523.5	81.4	137	US-10-371-961-76	Sequence 76, App1
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45	523.5	81.4	137	US-10-371-961-76	Sequence 76, App1

ALIGNMENTS

RESULT 1
US-09-286-240-4
Sequence 4, Application US/09286240
Patient No. US01020010320M1
Applicant: Pelti-Jones W
TITLE REFERENCE: 10498/74073 US/09/286_240
CURRENT FILING DATE: 1998-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 140
TYPE: PRT
ORGANISM: Mus musculus
US-09-286-240-4

Query Match 85.8%; Score 552; DB 9; Length 140;
Best Local Similarity 86.0%; Pred. No. 8.6e-44;

Matches 104; Consecutive 8; Mismatches 9; Indels 0; Gaps 0;

1 EHVJUSGGGVGVSGSLVFCSSSLAT.....HOYSSPDVWGQITLVSS 121
US-09-661-992b-84_COPY_1_121
61 PHTVGGVGGGVGVSGSLVFCSSSLAT.....HOYSSPDVWGQITLVSS 120
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US-09-661-992b-84_COPY_1_121
140 S 140

US-09-661-992b-84_COPY_1_121
Sequence 12, Application US/09681823


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/ APPLICANT: Oshumi, Jun
/ APPLICANT: Lobbaum, Albert S.
/ APPLICANT: Buchsbaum, Donald J.
/ TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
/ RELATED AND RELATED ARTS-RELATED ARTS-INDUCING LIGAND RECEPTOR AND OTHER THEM
/ TITLE OF INVENTION: AGENTS
/ FILE REFERENCE: 21085,002906
/ CURRENT APPLICATION NUMBER: US/10/281,479A
/ PRIOR APPLICATION NUMBER: US/09/38
/ PRIOR FILING DATE: 2001-06-24/38,1,478
/ PRIOR FILING DATE: 2002-06-24/38,1,478
/ PRIOR APPLICATION NUMBER: 60/346,402
/ PRIOR FILING DATE: 2001-11-02/USO/14151
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: 60/201,344
/ PRIOR FILING DATE: 2000-05-02
/ PRIOR APPLICATION NUMBER: 60/138
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 23
/ LENGTH: 462
/ TYPE: NUCLEIC ACID SEQUENCE
/ OTHER INFORMATION: Description of Artificial Sequence./No. US2003013932A1e = Synthe
/
Query Match
/ Sequence 23, Application US/10286132A
/ Best Local Similarity: 84.8%; DB 12; Length 462;
/ Matches 106; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
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QY 1 EVOLVSSGGLVKGSGSLKCAAGGFFSTTSMVNRQTPKRLBMAVNTSSGGSTTY 60
DB 20 EWLWSSGGLVKGSGSLKCAAGGFFSTTSMVNRQTPKRLBMAVNTSSGGSTTY 79
QY 61 PSVWGRFTISDPAKNTLYLQNSLSSEDTMYCTCDGAGSGSPWVGQGITLVS 120
DB 80 PSVWGRFTISDPAKNTLYLQNSLSSEDTMYCTCDGAGSGSPWVGQGITLVS 137
QY 121 S 121
DB 138 S 138
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RESULT 9
/ US-10-286-132A-23
/ Sequence 23, Application US/10286132A
/ GENERAL INFORMATION: US/09/319837A1
/ APPLICANT: Zhou, Tong
/ APPLICANT: Kimbely, Robert P.
/ APPLICANT: Koppman, William J.
/ APPLICANT: Buchsbaum, Donald J.
/ TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
/ RELATED AND RELATED ARTS-RELATED ARTS-INDUCING LIGAND RECEPTOR AND USBS THEROP
/ CURRENT APPLICATION NUMBER: US/10/286,132A
/ CURRENT FILING DATE: 2003-01-22
/ PRIOR APPLICATION NUMBER: US 60/346,402
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: PCT/US01/14151
/ PRIOR FILING DATE: 2001-05-02
/ PRIOR APPLICATION NUMBER: US 60/201,344
/ NUMBER OF SEQ ID NOS: 09-02
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 23
/ LENGTH: 462
/ TYPE: NUCLEIC ACID SEQUENCE
/ OTHER INFORMATION: Description of Artificial Sequence./No. US2003013932A1e = Synthe
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OTHER INFORMATION: Description of Artificial Sequence./No. US2003013932A1e = Synthe

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/ US-10-286-132A-23
/ Query Match
/ Best Local Similarity: 84.8%; DB 12; Length 462;
/ Matches 106; Conservative 4; Mismatches 9; Indels 2; Gaps 1;
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DB 20 EWLWSSGGLVKGSGSLKCAAGGFFSTTSMVNRQTPKRLBMAVNTSSGGSTTY 79
QY 61 PSVWGRFTISDPAKNTLYLQNSLSSEDTMYCTCDGAGSGSPWVGQGITLVS 120
DB 80 PSVWGRFTISDPAKNTLYLQNSLSSEDTMYCTCDGAGSGSPWVGQGITLVS 137
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DB 138 S 138
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/ US-10-275-180A-23
/ Sequence 23, Application US/10275180A
/ GENERAL INFORMATION: US/09/3190687A1
/ APPLICANT: The Uab Research Foundation
/ APPLICANT: Zhou, Tong
/ APPLICANT: Koppman, William J.
/ APPLICANT: Kimbely, Robert P.
/ APPLICANT: Buchsbaum, Donald J.
/ TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
/ RELATED AND RELATED ARTS-RELATED ARTS-INDUCING LIGAND RECEPTOR AND USBS THEROP
/ CURRENT APPLICATION NUMBER: US/10/275,180A
/ CURRENT FILING DATE: 2002-10-31
/ NUMBER OF SEQ ID NOS: 102
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 23
/ LENGTH: 464
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/ OTHER INFORMATION: Synthetic Construct
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OTHER INFORMATION: Synthetic Construct
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DB 20 EWLWSSGGLVKGSGSLKCAAGGFFSTTSMVNRQTPKRLBMAVNTSSGGSTTY 79
QY 61 PSVWGRFTISDPAKNTLYLQNSLSSEDTMYCTCDGAGSGSPWVGQGITLVS 120
DB 80 PSVWGRFTISDPAKNTLYLQNSLSSEDTMYCTCDGAGSGSPWVGQGITLVS 137
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DB 138 S 138
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RESULT 11
/ US-09-144-886-63
/ Sequence 63, Application US/09144886
/ GENERAL INFORMATION: US/09/319511A1
/ APPLICANT: Marks, James D
/ APPLICANT: Amersdorfer, Peter
/ TITLE OF INVENTION: Immunologic Monoclonal Antibodies That Neutralize
/ RELATED AND RELATED ARTS-RELATED ARTS-INDUCING LIGAND RECEPTOR AND USBS THEROP
/ CURRENT APPLICATION NUMBER: US/09/144,886

```


CORRESPONDENCE ADDRESSES:
 ADDRESSES: Townsend and Townsend and Crew
 STREET: One Market Plaza, Stewart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 MEDIUM SIZE: 3.5" (1.4 MB)
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: 09/05/93, 378A
 FILING DATE: 27-DEC-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA: US 09/160,074
 FILING DATE: 30-NOV-1993
 PRIOR APPLICATION DATA: US 07/983,946
 APPLICATION NUMBER: US 07/983,946
 FILING DATE: 1-DEC-1992
 PRIOR APPLICATION DATA: EP 95112895.8
 APPLICATION NUMBER: EP 95112895.8
 FILING DATE: 17-AUG-1995
 PRIOR APPLICATION DATA: EP 95114696.8
 APPLICATION NUMBER: EP 95114696.8
 FILING DATE: 19-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Liebschuetz, Joe O.
 ADDRESS: 11000 Wilshire Blvd., Suite 1000
 TELEPHONE: 415-326-2400
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: 11823-002220
 TELEPHONE: 415-326-2400
 IMPROVEMENT FOR SEQ TO NO: 16;
 SEQUENCE CHARACTERISTICS: 16;
 LENGTH: 135 amino acids
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-579-378A-16
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 Best Local Similarity: 82.7%; Score 531.5; DB 3; Length 135;
 Matched 103; Conservative 7; Mismatches 6; Indels 5; Gaps 2;
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 Db 20 EVQVSSGGLVPGSGKLSGASGFTPTMTSPROTREGLFVMAVATSSGSYTY 78
 Oy 61 PSYKERTISRDNAKTYLQMSLSKSPRYMTCT-PROGSGSSPDVQCTITV 120
 Db 79 PSYKERTISRDNAKTYLQMSLSKSPRYMTCT-PROGSGSSPDVQCTITV 134
 Oy 121 S 121
 Db 135 S 135
 RESULT 3
 US-08-075-674A-1
 Sequence 1, Application US/08075674A
 Patent No. 6572857
 ADDRESSES: Townsend and Townsend and Crew
 STREET: One Market Plaza, Stewart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 MEDIUM SIZE: 3.5" (1.4 MB)
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: 09/05/93, 378A
 FILING DATE: 27-DEC-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA: US 09/160,074
 FILING DATE: 30-NOV-1993
 PRIOR APPLICATION DATA: US 07/983,946
 APPLICATION NUMBER: US 07/983,946
 FILING DATE: 1-DEC-1992
 PRIOR APPLICATION DATA: EP 95112895.8
 APPLICATION NUMBER: EP 95112895.8
 FILING DATE: 17-AUG-1995
 PRIOR APPLICATION DATA: EP 95114696.8
 APPLICATION NUMBER: EP 95114696.8
 FILING DATE: 19-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Liebschuetz, Joe O.
 ADDRESS: 11000 Wilshire Blvd., Suite 1000
 TELEPHONE: 415-326-2400
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: 11823-002220
 TELEPHONE: 415-326-2400
 IMPROVEMENT FOR SEQ TO NO: 16;
 SEQUENCE CHARACTERISTICS: 16;
 LENGTH: 135 amino acids
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-579-378A-16

ADDRESSES: Liebschuetz, Siegel Marullo Atkinson & Greenpan, P.C.
 STREET: One Chase Road
 CITY: Scarsdale
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10583
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk 3.5" (1.4 MB)
 MEDIUM SIZE: 3.5" (1.4 MB)
 OPERATING SYSTEM: PC IBM (0405, 8 M Ram).
 SOFTWARE: Word Perfect 5.0 for Windows 95.
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/875, 674A
 FILING DATE: 17-JULY-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: ECT/03/6/00004
 FILING DATE: 31-NOV-1996
 NAME: HENRY A. MARULLO JR.
 REGISTRATION NUMBER: 20,910
 REFERENCE/DOCKET NUMBER: P-12
 TELEPHONE: (914) 723-4300
 TELEFAX: (914) 723-4301
 INFORMATION FOR SEQ TO NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 113 amino acid residues.
 TYPE: Amino acid.
 TOPOLOGY: unknown.
 MOLECULE TYPE: protein.
 HYDROTHERMAL: No
 ANTI-SENSE: No
 FRAGMENT TYPE: N Terminal fragment.
 ORGANISM: Mouse BALB/c
 INDIVIDUAL ISOLATE: 10r CIA
 TISSUE TYPE: Maxilla hybridoma
 INCLON: sub-clone for CIA
 PRIMER:
 IDENTIFICATION METHOD: Experimental.
 OTHER INFORMATION: Sequence corresponding to the variable region
 of the heavy chain of the monoclonal antibody recogn
 OTHER INFORMATION: designated as sub-clone for CIA.
 US-08-875-674A-1
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 Best Local Similarity: 81.8%; Score 526; DB 4; Length 119;
 Matched 105; Conservative 2; Mismatches 11; Indels 4; Gaps 2;
 Oy 1 EVQVSSGGLVPGSGKLSGASGFTPTMTSPROTREGLFVMAVATSSGSYTY 60
 Db 1 EVQVSSGGLVPGSGKLSGASGFTPTMTSPROTREGLFVMAVATSSGSYTY 60
 Oy 61 PSYKERTISRDNAKTYLQMSLSKSPRYMTCT-PROGSGSSPDVQCTITV 119
 Db 61 PSYKERTISRDNAKTYLQMSLSKSPRYMTCT-PROGSGSSPDVQCTITV 117
 Oy 120 S 121
 Db 118 S 119
 RESULT 4
 US-08-435-516-3
 Sequence 3, Application US/08435516
 Patent No. 6500511
 ADDRESSES: Townsend and Townsend and Crew
 STREET: One Market Plaza, Stewart Tower, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk 3.5" (1.4 MB)
 MEDIUM SIZE: 3.5" (1.4 MB)
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: 09/05/93, 378A
 FILING DATE: 27-DEC-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA: US 09/160,074
 FILING DATE: 30-NOV-1993
 PRIOR APPLICATION DATA: US 07/983,946
 APPLICATION NUMBER: US 07/983,946
 FILING DATE: 1-DEC-1992
 PRIOR APPLICATION DATA: EP 95112895.8
 APPLICATION NUMBER: EP 95112895.8
 FILING DATE: 17-AUG-1995
 PRIOR APPLICATION DATA: EP 95114696.8
 APPLICATION NUMBER: EP 95114696.8
 FILING DATE: 19-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Liebschuetz, Joe O.
 ADDRESS: 11000 Wilshire Blvd., Suite 1000
 TELEPHONE: 415-326-2400
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: 11823-002220
 TELEPHONE: 415-326-2400
 IMPROVEMENT FOR SEQ TO NO: 16;
 SEQUENCE CHARACTERISTICS: 16;
 LENGTH: 135 amino acids
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-579-378A-16

CLASSIFICATION: C12N5/20
CLASSIFICATION: G01N33/574
CLASSIFICATION: C07K16/00
CLASSIFICATION: A61K39/295
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM929000457
FILING DATE: 17-JUN-1992
PRIORITY DATE: 17-JUN-1992
APPLICATION NUMBER: NO PCT/EP93/0533
FILING DATE: 16-JUN-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,731
REFERENCE/DOCKET NUMBER: 118-9040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 503-8007
TELEX: 240867
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 119
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-356-272-3

Query Match
Best Local Similarity: 79.4%; Score 510.5; DB 1; Length 123;
Matches 103 Conservative 6 Mismatches 11; Indels 3; Gaps 3;

Df Yq 1 EVLVRESGGLVLR-PESIKISQALGGVETSGTSMWVGPEPRKELEVWATISSGAGTY 59
Db 1 QVLQSSGVGLVLRDPSKLSLQASLGFTSTGSMWVGPEPRKELEVWATISSGAGTY 60

Yq 60 PEVSREFTSIRPNANIVLLQSSSLASESDMYTCDDG-AQGSSEPDWVAQTILE 118
Db 60 PEYSRKFSTSRKANILVQLSSSLASESDMYCANAPRRRY-SNPAMWGQITVT 119

I11 VSS 121
I11 VSS 122

Db 120 VSS 122

RESULT 6
PCT-US94-07659-2
GENERAL INFORMATION
PC/TUS94/07659
APPPLICANT: Young, Peter
APPPLICANT: Grose, Mitchell
APPPLICANT: Jonek, Zenka L.
APPPLICANT: Wessely, Timothy
APPPLICANT: Harte, Mark
APPPLICANT: Jackson, Jeffrey R.
TITLE OF INVENTION: Recombinant and Humanized I1-1 beta
TITLE OR INVENTION: Directed Treatment of I1-1 Mediated Inflammatory
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESS: SmithKline Beecham Corporation - Corp.
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/Ms-DOS
SOFTWARE: PatentIn Release 11.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: PCT/US94/07659

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/090,534
 FILING DATE: 09-JUL-1993
 INVENTOR: ARTHUR J. KATZ
 NAME: ARTHUR J. KATZ
 REGISTRATION NUMBER: 931,028
 REFERENCE/DOCKET NUMBER: P90171-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 270-5090
 TELEFAX: (610) 270-5090
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FCT-0691-07653-2

Query Match 78.8%; Score 507; DB 5; Length 247;
 Best Local Similarity 82.0%; Pred. No. 5.3e-46;
 Matches 100; Conservative 6; Mismatches 12; Indels 4; Gaps 2;

QY 1 EVLVESGGGLVYFGGSLKSCASGSGFTSTYTWNRQFPEKRLMVAITISGSGITY 60
 DB 20 EVLVESGGGLVYFGGSLKSCASGSGFTSTYTWNRQFPEKRLMVAITISGSGITY 79
 QY 61 PSYRGFTSRNNKNTLYLQNSKSEETWYCYTRCG-CHGSGSPFYWGCGITLY 119
 DB 80 PSYRGFTSRNNKNTLYLQNSKSEETWYCYTRCG-CHGSGSPFYWGCGITLY 136
 QY 120 SS 121
 DB 117 SS 138

RESULT 7
 US-08-653-402b-2
 Sequence 2 Application US/08653402b
 GENERAL INFORMATION:
 APPLICANT: CARCELLER, Ana
 APPLICANT: ROSELI, Elisabeth
 APPLICANT: ROSELI, Elisabeth
 APPLICANT: ADON, Jaime
 APPLICANT: PIJUAN, Jaime
 TITLE OF INVENTION: Anti-Idiotypic antibodies which induce an
 NUMBER OF SEQUENCES: 4
 TITLE OF INVENTION: Immune response against epidermal growth factor receptor.
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Milten, White, Zalano & Brangan, P. C.
 ADDRESS: 2200 Clarendon Boulevard, Suite 1400
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 CITY: 22201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/653,402b
 FILING DATE: 24-MAY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95107667.2
 FILING DATE: 26-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 37,067
 REFERENCE/DOCKET NUMBER: WERCK 1761
 TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-243-4333
 TELEFAX: 703-243-4610
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 159 amino acids
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-653-402b-2

Query Match 76.6%; Score 505.5; DB 2; Length 159;
 Best Local Similarity 77.3%; Pred. No. 4.4e-46;
 Matches 99; Conservative 7; Mismatches 13; Indels 9; Gaps 2;

QY 1 EVLVESGGGLVYFGGSLKSCASGSGFTSTYTWNRQFPEKRLMVAITISGSGITY 60
 DB 20 EVLVESGGGLVYFGGSLKSCASGSGFTSTYTWNRQFPEKRLMVAITISGSGITY 79
 QY 61 PSYRGFTSRNNKNTLYLQNSKSEETWYCYTRCG-CHGSGSPFYWGCGITLY 119
 DB 80 PSYRGFTSRNNKNTLYLQNSKSEETWYCYTRCG-CHGSGSPFYWGCGITLY 137
 QY 114 TRTVSS 121
 DB 118 TRTVSS 145

RESULT 8
 US-08-675-674b-3
 Sequence 3 Application US/08675674b
 GENERAL INFORMATION:
 PATENT NO. 6,579,857
 APPLICANT: MONTERO CASIMIRO, J. E.
 APPLICANT: LOMBARDERO VILLALBA, J.
 APPLICANT: PEREZ RODRIGUEZ, R.
 APPLICANT: PEREZ RODRIGUEZ, R.
 APPLICANT: TORO REAYO, B. R.
 TITLE OF INVENTION: Anti-CD8 monoclonal antibodies and their uses
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Word Perfect 5.0 for Windows 95
 ADDRESS: One Chase Road
 STREET: One Chase Road
 CITY: Scarsdale
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10583
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).
 OPERATING SYSTEM: Windows 95 (60486, 8 M Ram).
 SOFTWARE: Word Perfect 5.0 for Windows 95.
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/675,674b
 FILING DATE: 1997-1997
 PRIOR APPLICATION DATA:
 CLASSIFICATION: 530
 APPLICATION NUMBER: PCT/US96/00004
 ATTORNEY/AGENT INFORMATION:
 NAME: HENRY A. MARZULLO, JR.
 REGISTRATION NUMBER: 20,910
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (914) 723-4300
 INFORMATION FOR SEQ ID NO: 3:
 LENGTH: 119 amino acid residues.
 TYPE: Amino acid.
 STRANDEDNESS: Unknown.
 MOLECULE TYPE: Protein
 HYPOTHETICAL: NO

```

1 12345 070-5010
2 INFORMATION FOR SEQ ID NO: 10:
3 SEQUENCE CHARACTERISTICS:

```


LENGTH: 118 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-08435-10

Query Match 78.3%; Score 503.5; DB 5; Length 118;
Best Local Similarity 80.5%; Pred. No. 5e-46;

Matches 95; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 5 LEEGGGLVYKGSGLKLSGASGFFSTYSWVWQTPKRLKLVWATISGSGSYTY 64
DB 1 LEEGGGLVYKGSGLKLSGASGFFSTYSWVWQTPKRLKLVWATISGSGSYTY 60
QY 63 RGFPTISDMMATNTLYLWMSLSGSDPMYVCTCRDGGVY-GSGPFWQGGITLV 121
DB 61 TGFPTISDMMATNTLYLWMSLSGSDPMYVCTCRDGGVY-GSGPFWQGGITLV 118

RESULT 11

US-08-339-582-2 Application US/08339582

SEQUENCE 2, Application US/08339582

Patent No. 583651

GENERAL INFORMATION:

APPLICANT: Bismar, Darrell D.

APPLICANT: Zalusky, Michael R.

APPLICANT: Zalusky, Michael R.

TITLE OF INVENTION: METHOD OF TREATMENT

CORRESPONDENCE ADDRESS: 4

STREET: P.O. Drawer 34009

CITY: Charlotte

STATE: No. 5558524th Carolina

ZIP CODE: 28234

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

SOFTWARE: IBM PC compatible

SOFTWARE: Patientin Release #1.0, Version #1.25

CURRENT APPLICATION DATA: US/08/339,582

APPLICATION NUMBER: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/033,864

ATTORNEY/AGENT INFORMATION:

NMME: Sibley, Kenneth D.

REGISTRATION NUMBER: 31,665

REFERENCE/DOCKET NUMBER: 5405-89

TELEPHONE: 919-420-2200

TELEFAX: 919-881-3175

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

LENGTH: 121 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-339-582-2

Query Match 78.2%; Score 503; DB 1; Length 121;

Best Local Similarity 83.3%; Pred. No. 8e-46;

Matches 101; Conservative 67; Mismatches 10; Indels 4; Gaps 2;

QY 1 EYQVLESGGLVYKGSGLKLSGASGFFSTYSWVWQTPKRLKLVWATISGSGSYTY 60
DB 1 EYQVLESGGLVYKGSGLKLSGASGFFSTYSWVWQTPKRLKLVWATISGSGSYTY 63
QY 63 RGFPTISDMMATNTLYLWMSLSGSDPMYVCTCRDGGVY-GSGPFWQGGITLV 120
DB 61 TGFPTISDMMATNTLYLWMSLSGSDPMYVCTCRDGGVY-GSGPFWQGGITLV 120

DB 64 POSYKGFRTISDMMATNTLYLWMSLSGSDPMYVCTCRDGGVY-GSGPFWQGGITLV 120
QY 121 S 121
DB 121 S 121

RESULT 12 378A-20 Application US/0837878A
Patent No. 6210671

GENERAL INFORMATION:

APPLICANT: Co. Man Sung

APPLICANT: Co. Man Sung

TITLE OF INVENTION: Shuffled Antibodies Reactive with

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSER: Townsend and Townsend and Crew

CITY: San Francisco

STATE: California

COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

SOFTWARE: IBM PC compatible

SOFTWARE: Patientin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/579,378A

FLING DATE: 27-DEC-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/160,074

FLING DATE: 30-NOV-1993

PRIOR APPLICATION DATA: US 07/983,946

FLING DATE: 01-DEC-1992

APPLICATION NUMBER: EP 95112895.8

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 95114696.8

FLING DATE: 13-SEP-1995

ATTORNEY/AGENT INFORMATION:

NMME: Liebschultz, Joe O.

REGISTRATION NUMBER: 37,505

REFERENCE/DOCKET NUMBER: 11823-002220

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

LENGTH: 121 amino acids

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-579-378A-20

Query Match 78.1%; Score 502.5; DB 3; Length 125;

Best Local Similarity 80.2%; Pred. No. 7.5e-46;

Matches 97; Conservative 107; Mismatches 9; Indels 5; Gaps 2;

QY 1 EYQVLESGGLVYKGSGLKLSGASGFFSTYSWVWQTPKRLKLVWATISGSGSYTY 60
DB 20 EYQVLESGGLVYKGSGLKLSGASGFFSTYSWVWQTPKRLKLVWATISGSGSYTY 78
QY 79 POSYKGFRTISDMMATNTLYLWMSLSGSDPMYVCTCRDGGVY-GSGPFWQGGITLV 120
DB 79 POSYKGFRTISDMMATNTLYLWMSLSGSDPMYVCTCRDGGVY-GSGPFWQGGITLV 134

Db 135 S 135

RESULT 13

Sequence 4, Application PC/T09613152
GENERAL INFORMATION: Ulrich, et al
TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fail
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: Ulrich
ADDRESSER: Alvin Norman D. Hanson
CITY: New York
STREET: 805 Third Avenue
COUNTRY: U.S.A.
ZIP: 10022-5, N.Y.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Computer Disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
FILING DATE: PCT/US96/13152
CLASSIFICATION:
PRIORITY APPLICATION DATA:
PRIORITY NUMBER: 08/570,953
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 112 895,8
FILING DATE: 17-Aug-95
APPLICATION NUMBER: EP 95 114 969,9
ATTORNEY/AGENT INFORMATION:
NAME: Norman D. Hanson
REGISTRATION NUMBER: 30,946
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-9200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 443 characters
TYPE: amino acid
STANDARDNESS: double
MOLCULE TYPE: protein
PCT-US96-13152-4

Query Match

Best Local Similarity: 82.4% Seq. ID: 499, Mismatches: 49, Indels: 5, Gaps: 2

Db 1 EVOLVESGGGLVPGSSKLSQASGPTFTTINMRCPTPERLRLMVAIISGSGSYTY 60
Db 1 EVOLVESGGGLVPGSSKLSQASGPTFTTINMRCPTPERLRLMVAIISGSGSYTY 60
QY 61 PDSVGGFTTSDNAAKNTLYLQNSLSLSDTANYCTCDGNGYGSFPMWQGGTTLVS 120
Db 60 PDSVGGFTTSDNAAKNTLYLQNSLSLSDTANYCTCDGNGYGSFPMWQGGTTLVS 115
QY 121 S 121
Db 116 S 116

RESULT 14

Sequence 2, Application US/0832362
Patent No. 5730981
GENERAL INFORMATION:
APPLICANT: Bostel, Klaus

APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
TITLE OF INVENTION: Its Preparation and Use as a Therapeutic Agent
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSER: Finnegan, Henderson, Peabody, Garrett &
CITY: Washington
STREET: N.W., Suite 700
COUNTRY: USA
ZIP: 20005-3115
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
CURRENT APPLICATION DATA:
FILING DATE: US/08/326,362
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
PRIORITY NUMBER: US 08/032,863
FILING DATE: 17-MAR-1993
APPLICATION NUMBER: DS P 42 08 795.3
ATTORNEY/AGENT INFORMATION:
NAME: Binandt, Carol P.
REGISTRATION NUMBER: 32,120
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acids
TYPE: amino acid
MOLCULE TYPE: linear

Query Match

Best Local Similarity: 77.8% Score 500.5; DB 1, Length 118;

Seq. ID: 10145, Mismatches: 12, Indels: 3, Gaps: 2;

Db 1 EVOLVESGGGLVPGSSKLSQASGPTFTTINMRCPTPERLRLMVAIISGSGSYTY 60
Db 1 EVOLVESGGGLVPGSSKLSQASGPTFTTINMRCPTPERLRLMVAIISGSGSYTY 60
QY 61 PDSVGGFTTSDNAAKNTLYLQNSLSLSDTANYCTCDGNGYGSFPMWQGGTTLVS 120
Db 61 PDSVGGFTTSDNAAKNTLYLQNSLSLSDTANYCTCDGNGYGSFPMWQGGTTLVS 117
QY 121 S 121
Db 118 S 118

RESULT 15

US-08-379-057-14
Patent No. 5676933
GENERAL INFORMATION:
APPLICANT: Sasaki, Anthony W.
TITLE OF INVENTION: Biotinylated, Diamine L-
APPLICANT: Gordon, Marcia L.
APPLICANT: Bagatich, Jungun
TITLE OF INVENTION: Antibodies Specific For
TITLE OF INVENTION: Different Epitopes of Human SP39 and Methods For Their
TITLE OF INVENTION: In Diagnosis and Therapy

NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Bristol-Myers Squibb Company
 STREET: 3005 First Avenue
 CITY: New York
 STATE: Washington
 COUNTRY: USA
 ZIP: 98121
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 APPLICATION NUMBER: US/08/379,057
 FILING DATE: 26-JAN-1995
 CLASSIFICATION: 435
 ATOM/SCAT INFORMATION:
 NAME: POOL Brian W
 REGISTRATION NUMBER: 32,928
 REFERENCE/DOCKET NUMBER: ONO133-
 TELEPHONE/CATION INFORMATION:
 TELEFAX: (206) 727-3601
 TELEPHONE: (206) 727-5770
 INFORMATION FOR SEQ ID NO: 14:
 SOURCE CHARACTERISTICS:
 LENGTH: 138
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Protein
 SEQUENCE TYPE: N-terminal
 US-08-379-057-14

Query Match 77.1%; Score 496; DS 2; Length 138;
 Identicality 70.3%; Pct. Matches 71; Indels 4; Gaps 3;
 Mismatches 98; Conservative 9; Mismatches 11; Indels 4; Gaps 3;
 QY 1 EVQIVSSGZSLVPEGSGLKSCASPTFTWSPQTEPGLKLVATISSGSYYTY 60
 DB 20 EYVIVSGGZSLVPEGSGLKSCASPTFTWSPQTEPGLKLVATISSGSYYTY 78
 QY 61 PPSYRGRFTISRDNAKXLYLQMSGLKSEPTFAMVYCTROQHGYS-SEPMQQTITLY 119
 DB 79 EDSYRGRFTISRDNAKXLYLQMSGLKSEPTFAMVYCTROQHGYS-SEPMQQTITLY 136
 QY 120 SS 121
 DB 137 SS 138

Search completed: November 7, 2003, 07:30:10
 Job time : 18.7704 secs

C/Accession: P70159
 R/Sherman, R.; Kistner, G.; Turken, A.; Papazian, L.; Diamond, B.
 J. Exp. Med. 173, 287-296, 1991
 A/Title: A novel class of anti-DNA antibodies identified in BALB/c mice.
 A/Accession: P70159; MIMD:91108325; PMID:1986536
 A/Accession: P70159
 A/Molecule type: mRNA

A/Residues: 1-118 <SHB>
 A/Experimental source: strain BALB/c
 A/Accession: P70159; MIMD:91108325; PMID:1986536
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F/15-98/Domain: immunoglobulin homology <IMB>

Query Match 32.94% Score 541; DB 2; Length 118;
 Best Local Similarity 91.14% Pred. No. 7.1e-43;
 Matches 102; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 IVLTGSHLPLVSLDQDQSGISGSGSSGIVSHSNNTLYLWYLOKQSGPKLLIYVNSRFS 61
 DB 5 VVMTGSLPLVSLDQDQSGISGSGSSGIVSHSNNTLYLWYLOKQSGPKLLIYVNSRFS 64
 QY 62 GVPEPSSGSGGDTPLTKISRYEADLVYFCGSGIVHVPFGGQTKLEIK 113
 DB 65 GVPEPSSGSGGDTPLTKISRYEADLVYFCGSGIVHVPFGGQTKLEIK 116

RESULT 8
 538719
 19 light chain V region - mouse

C/Spectrum: Mus musculus (house mouse)
 C/Date: 27-Jul-1990 Sequence revision 06-Jan-1995 flex_change 20-Jun-2000
 C/Accession: 538719
 R/Chenais, A.Y.
 submitted to the EMBL Data Library, November 1993

A/Accession: 538719
 A/Molecule type: mRNA
 A/Status: preliminary
 A/Accession: 538719
 A/Accession: 538719
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F/15-98/Domain: immunoglobulin homology <IMB>

Query Match 92.44% Score 548; DB 2; Length 112;
 Best Local Similarity 91.74% Pred. No. 1.3e-43;
 Matches 104; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IVLTGSHLPLVSLDQDQSGISGSGSSGIVSHSNNTLYLWYLOKQSGPKLLIYVNSRFS 61
 DB 2 IVLTGSHLPLVSLDQDQSGISGSGSSGIVSHSNNTLYLWYLOKQSGPKLLIYVNSRFS 61
 QY 62 GVPEPSSGSGGDTPLTKISRYEADLVYFCGSGIVHVPFGGQTKLEIK 112
 DB 62 GVPEPSSGSGGDTPLTKISRYEADLVYFCGSGIVHVPFGGQTKLEIK 112

RESULT 9

A23673 chain V-11 region TE33 - mouse

C/Spectrum: Mus musculus (house mouse)
 C/Date: 23-Jan-1990 Sequence revision 29-Jan-1990 flex_change 21-Jan-2000
 C/Accession: A23673
 R/Schwarz, O.; Scherf, F.; Lewitz, M.; Engelstaler, J.
 Biochemistry 28, 1168-1175, 1989
 A/Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, predicted heterocenterization, immunoglobulin homology
 A/Reference number: A23673; MIMD:9005406; PMID:2810959
 A/Accession: A23673
 A/Molecule type: mRNA

A/Residues: 1-114 <LEV>
 A/Experimental source: strain A23673
 A/Accession: A23673; MIMD:9005406; PMID:2810959
 C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Accession: P70159
 R/Sherman, R.; Kistner, G.; Turken, A.; Papazian, L.; Diamond, B.
 J. Exp. Med. 173, 287-296, 1991
 A/Title: A novel class of anti-DNA antibodies identified in BALB/c mice.
 A/Accession: P70159; MIMD:91108325; PMID:1986536
 A/Accession: P70159
 A/Molecule type: mRNA

A/Residues: 1-118 <SHB>
 A/Experimental source: strain BALB/c
 A/Accession: P70159; MIMD:91108325; PMID:1986536
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F/15-98/Domain: immunoglobulin homology <IMB>

Query Match 32.94% Score 541; DB 2; Length 118;
 Best Local Similarity 91.14% Pred. No. 7.1e-43;
 Matches 102; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 IVLTGSHLPLVSLDQDQSGISGSGSSGIVSHSNNTLYLWYLOKQSGPKLLIYVNSRFS 61
 DB 5 VVMTGSLPLVSLDQDQSGISGSGSSGIVSHSNNTLYLWYLOKQSGPKLLIYVNSRFS 64
 QY 62 GVPEPSSGSGGDTPLTKISRYEADLVYFCGSGIVHVPFGGQTKLEIK 113
 DB 65 GVPEPSSGSGGDTPLTKISRYEADLVYFCGSGIVHVPFGGQTKLEIK 116

RESULT 10
 538719
 19 kappa chain precursor V region (12-40 and 5-14) - mouse

C/Spectrum: Mus musculus (house mouse)
 C/Date: 27-Jul-1990 Sequence revision 27-Jul-1990 flex_change 21-Jul-2000
 R/Sherman, R.; Kistner, G.; Turken, A.; Papazian, L.; Diamond, B.
 J. Exp. Med. 173, 287-296, 1991
 A/Title: Active site structure and antigen binding properties of idiotypically
 A/Reference number: A23673; MIMD:9005406; PMID:2810959
 A/Accession: A23673
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA

A/Residues: 1-118 <SHB>
 A/Experimental source: strain A23673
 A/Accession: A23673; MIMD:9005406; PMID:2810959
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F/15-114/Domain: immunoglobulin homology <IMB>

Query Match 92.14% Score 546; DB 2; Length 131;
 Best Local Similarity 91.04% Pred. No. 2.3e-43;
 Matches 101; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 IVLTGSHLPLVSLDQDQSGISGSGSSGIVSHSNNTLYLWYLOKQSGPKLLIYVNSRFS 61
 DB 2 IVLTGSHLPLVSLDQDQSGISGSGSSGIVSHSNNTLYLWYLOKQSGPKLLIYVNSRFS 61
 QY 62 GVPEPSSGSGGDTPLTKISRYEADLVYFCGSGIVHVPFGGQTKLEIK 112
 DB 62 GVPEPSSGSGGDTPLTKISRYEADLVYFCGSGIVHVPFGGQTKLEIK 112

RESULT 11

B31485
 19 kappa chain V region (14-20) - mouse (tegment)

C/Spectrum: Mus musculus (house mouse)
 C/Date: 31-Jul-1989 Sequence revision 31-Jul-1989 flex_change 21-Jan-2000
 C/Accession: B31485
 R/Bedley, N.D.; Johnson, L.S.; Rocard, G.S.; Voss Jr., E.W.
 J. Biol. Chem. 265, 133-138, 1990
 A/Title: Active site structure and antigen binding properties of idiotypically
 A/Reference number: B31485; MIMD:8910167; PMID:2492278
 A/Accession: B31485
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: protein

A/Residues: 1-112 <SHD>
 A/Experimental source: strain B31485
 A/Accession: B31485; MIMD:8910167; PMID:2492278
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 F/15-99/Domain: immunoglobulin homology <IMB>

Query Match 91.67% Score 543; DB 2; Length 112;
 Best Local Similarity 90.11% Pred. No. 3.6e-43;
 Matches 100; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 IVLTGSHLPLVSLDQDQSGISGSGSSGIVSHSNNTLYLWYLOKQSGPKLLIYVNSRFS 61
 DB 2 IVLTGSHLPLVSLDQDQSGISGSGSSGIVSHSNNTLYLWYLOKQSGPKLLIYVNSRFS 61

RESULT 12

19 kappa chain V region (H1C5-401) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Dec-1988 #sequence_revision: 15-Dec-1988 #text_change: 21-Jan-2000
 C/Accession: F73887
 B/Seq: 157-1587, 1966
 B/ID: U. 5.1577-1587, 1966
 A/R: Structural and functional implications of a restricted antibody response to a d
 A/Reference number: A31043; PMID:8630658; PMID:2427335
 A/Molecule type: RNA
 A/Status: preliminary
 A/Residues: 1-112 <CMT>
 A/Experimental source: Strain Balb/c
 A/Note: this sequence was determined from the germline gene
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/16-95/Domain: immunoglobulin homology <IM>

Query Match

Best Local Similarity 91.4%; Score 541; DB 2; Length 112;
 Matched 102; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

1 IVLTGSPSPSPGADGASISCRSSGSIYHNSNNTYLTWYLTQFGSPFLTYKNSRFS 61
 2 VVMTGTPSPSPGADGASISCRSSGSIYHNSNNTYLTWYLTQFGSPFLTYKNSRFS 61
 62 GVPRFSSSGSDTPTLKISRVARDGVYFCGTHVYFGQTRLEIK 112
 63 GVPRFSSSGSDTPTLKISRVARDGVYFCGTHVYFGQTRLEIK 112

RESULT 13

19 kappa chain precursor V region (J3-24) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 27-Jul-1990 #sequence_revision: 27-Jul-1990 #text_change: 21-Jan-2000
 C/Accession: C34904; J31455
 B/Seq: 265, 133-138, 1990
 B/ID: J. 265, 133-138, 1990
 A/R: Structural and functional implications of a restricted antibody response
 A/Reference number: A31409; PMID:9009487; PMID:2106617
 A/Accession: C34904
 A/Molecule type: RNA
 A/Status: preliminary; not compared with conceptual translation
 A/Residues: 1-131 <EBD>

19 kappa chain V region (H37-60) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Dec-1988 #sequence_revision: 15-Dec-1988 #text_change: 21-Jan-2000
 C/Accession: A27887
 B/Seq: 157-1587, 1966
 B/ID: J. 5.1577-1587, 1966
 A/R: Structural and functional implications of a restricted antibody response
 A/Reference number: A31043; PMID:8630658; PMID:2427335
 A/Accession: A27887
 A/Molecule type: RNA
 A/Status: preliminary

19 kappa chain V region (H37-60) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Dec-1988 #sequence_revision: 15-Dec-1988 #text_change: 21-Jan-2000
 C/Accession: A27887
 B/Seq: 157-1587, 1966
 B/ID: J. 5.1577-1587, 1966
 A/R: Structural and functional implications of a restricted antibody response
 A/Reference number: A31043; PMID:8630658; PMID:2427335
 A/Accession: A27887
 A/Molecule type: RNA
 A/Status: preliminary

19 kappa chain V region (H37-60) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Dec-1988 #sequence_revision: 15-Dec-1988 #text_change: 21-Jan-2000
 C/Accession: A27887
 B/Seq: 157-1587, 1966
 B/ID: J. 5.1577-1587, 1966
 A/R: Structural and functional implications of a restricted antibody response
 A/Reference number: A31043; PMID:8630658; PMID:2427335
 A/Accession: A27887
 A/Molecule type: RNA
 A/Status: preliminary

19 kappa chain V region (H37-60) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Dec-1988 #sequence_revision: 15-Dec-1988 #text_change: 21-Jan-2000
 C/Accession: A27887
 B/Seq: 157-1587, 1966
 B/ID: J. 5.1577-1587, 1966
 A/R: Structural and functional implications of a restricted antibody response
 A/Reference number: A31043; PMID:8630658; PMID:2427335
 A/Accession: A27887
 A/Molecule type: RNA
 A/Status: preliminary

19 kappa chain V region (H37-60) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Dec-1988 #sequence_revision: 15-Dec-1988 #text_change: 21-Jan-2000
 C/Accession: A27887
 B/Seq: 157-1587, 1966
 B/ID: J. 5.1577-1587, 1966
 A/R: Structural and functional implications of a restricted antibody response
 A/Reference number: A31043; PMID:8630658; PMID:2427335
 A/Accession: A27887
 A/Molecule type: RNA
 A/Status: preliminary

RESULT 14

19 kappa chain V region (G2a) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Dec-1988 #sequence_revision: 15-Dec-1988 #text_change: 21-Jan-2000
 C/Accession: S16112
 B/Seq: 157-1587, 1966
 B/ID: J. 5.1577-1587, 1966
 A/R: Structural and functional implications of a restricted antibody response
 A/Reference number: A31043; PMID:8630658; PMID:2427335
 A/Accession: S16112
 A/Molecule type: RNA
 A/Status: preliminary
 A/Experimental source: Strain Balb/c
 A/Note: this sequence was determined from the germline gene
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotrimer; immunoglobulin
 F/16-95/Domain: immunoglobulin homology <IM>

Query Match

Best Local Similarity 91.2%; Score 541; DB 2; Length 219;
 Matched 100; Conservative 10; Mismatches 2; Indels 0; Gaps 0;

1 IVLTGSPSPSPGADGASISCRSSGSIYHNSNNTYLTWYLTQFGSPFLTYKNSRFS 61
 2 VVMTGTPSPSPGADGASISCRSSGSIYHNSNNTYLTWYLTQFGSPFLTYKNSRFS 61
 62 GVPRFSSSGSDTPTLKISRVARDGVYFCGTHVYFGQTRLEIK 113
 63 GVPRFSSSGSDTPTLKISRVARDGVYFCGTHVYFGQTRLEIK 113

RESULT 15

19 kappa chain V region (H37-60) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Dec-1988 #sequence_revision: 15-Dec-1988 #text_change: 21-Jan-2000
 C/Accession: A27887
 B/Seq: 157-1587, 1966
 B/ID: J. 5.1577-1587, 1966
 A/R: Structural and functional implications of a restricted antibody response
 A/Reference number: A31043; PMID:8630658; PMID:2427335
 A/Accession: A27887
 A/Molecule type: RNA
 A/Status: preliminary

19 kappa chain V region (H37-60) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Dec-1988 #sequence_revision: 15-Dec-1988 #text_change: 21-Jan-2000
 C/Accession: A27887
 B/Seq: 157-1587, 1966
 B/ID: J. 5.1577-1587, 1966
 A/R: Structural and functional implications of a restricted antibody response
 A/Reference number: A31043; PMID:8630658; PMID:2427335
 A/Accession: A27887
 A/Molecule type: RNA
 A/Status: preliminary

19 kappa chain V region (H37-60) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Dec-1988 #sequence_revision: 15-Dec-1988 #text_change: 21-Jan-2000
 C/Accession: A27887
 B/Seq: 157-1587, 1966
 B/ID: J. 5.1577-1587, 1966
 A/R: Structural and functional implications of a restricted antibody response
 A/Reference number: A31043; PMID:8630658; PMID:2427335
 A/Accession: A27887
 A/Molecule type: RNA
 A/Status: preliminary

19 kappa chain V region (H37-60) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Dec-1988 #sequence_revision: 15-Dec-1988 #text_change: 21-Jan-2000
 C/Accession: A27887
 B/Seq: 157-1587, 1966
 B/ID: J. 5.1577-1587, 1966
 A/R: Structural and functional implications of a restricted antibody response
 A/Reference number: A31043; PMID:8630658; PMID:2427335
 A/Accession: A27887
 A/Molecule type: RNA
 A/Status: preliminary

19 kappa chain V region (H37-60) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Dec-1988 #sequence_revision: 15-Dec-1988 #text_change: 21-Jan-2000
 C/Accession: A27887
 B/Seq: 157-1587, 1966
 B/ID: J. 5.1577-1587, 1966
 A/R: Structural and functional implications of a restricted antibody response
 A/Reference number: A31043; PMID:8630658; PMID:2427335
 A/Accession: A27887
 A/Molecule type: RNA
 A/Status: preliminary

19 kappa chain V region (H37-60) - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Dec-1988 #sequence_revision: 15-Dec-1988 #text_change: 21-Jan-2000
 C/Accession: A27887
 B/Seq: 157-1587, 1966
 B/ID: J. 5.1577-1587, 1966
 A/R: Structural and functional implications of a restricted antibody response
 A/Reference number: A31043; PMID:8630658; PMID:2427335
 A/Accession: A27887
 A/Molecule type: RNA
 A/Status: preliminary

Search completed: November 7, 2003, 07:36:19
 Old time: 14:7342 secs

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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 8.1686 seconds

(without alignments)

Title: US-09-661-992B-84_COPY_137_249

Sequence: 593 BLOSIN62
1 QIVTQSTSLPVSADQAS.....FGSHVPTFGGKLEIKR 113

Scoring table: Gapco 10.0, Gapexc 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Swissprot_41.*

Pred. No. is the number of results predicted by chance to have a
score as high as the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	625	88.5	113	KV2Z_MOUSE	P01631 mus musc
2	457	77.1	117	KV2Z_HUMAN	P06310 homo sapien
3	457	76.2	113	KV2Z_HUMAN	P01617 homo sapien
4	439	74.0	113	KV2Z_HUMAN	P01617 homo sapien
5	439	73.4	113	KV2Z_MOUSE	P03976 mus musc
6	439.5	72.4	112	KV2Z_HUMAN	P01616 homo sapien
7	439.5	72.4	112	KV2Z_HUMAN	P01630 mus musc
8	419	70.7	113	KV2Z_MOUSE	P01629 mus musc
9	416	70.2	112	KV2Z_MOUSE	P06313 homo sapien
10	397.5	64.9	133	KV4B_HUMAN	P01628 mus musc
11	384	64.8	113	KV4B_HUMAN	P01628 mus musc
12	384	64.8	113	KV4B_HUMAN	P01628 mus musc
13	384	64.8	113	KV4B_HUMAN	P01628 mus musc
14	384	64.8	113	KV4B_HUMAN	P01628 mus musc
15	376.5	63.5	111	KV3O_MOUSE	P01651 mus musc
16	376.5	63.5	111	KV3O_MOUSE	P01651 mus musc
17	376.5	63.5	111	KV3O_MOUSE	P01651 mus musc
18	374.5	63.2	108	KV1_CANFA	P01651 mus musc
19	374.5	63.2	108	KV1_MOUSE	P01651 mus musc
20	372.5	62.8	111	KV3I_MOUSE	P01651 mus musc
21	370.5	62.5	111	KV3I_MOUSE	P01651 mus musc
22	370.5	62.5	111	KV3I_MOUSE	P01651 mus musc
23	370.5	62.5	111	KV3I_MOUSE	P01651 mus musc
24	369.5	62.3	111	KV3I_MOUSE	P01651 mus musc
25	369.5	62.3	111	KV3I_MOUSE	P01651 mus musc
26	369.5	62.3	111	KV3I_MOUSE	P01651 mus musc
27	369.5	62.3	111	KV3I_MOUSE	P01651 mus musc
28	369.5	62.3	111	KV3I_MOUSE	P01651 mus musc
29	366.5	61.8	111	KV3I_MOUSE	P01651 mus musc
30	366.5	61.3	111	KV3I_MOUSE	P01651 mus musc
31	361.5	61.0	111	KV3I_MOUSE	P01651 mus musc
32	359	60.5	109	KV3O_MOUSE	P01630 mus musc
33	359	60.5	109	KV3O_MOUSE	P01630 mus musc

ALIGNMENTS

RESULT 1
KV2Z_MOUSE STANDARD; PRT, 113 AA.

ID KV2Z_MOUSE STANDARD; PRT, 113 AA.

DC P01631_1986 (Ref. 01, Created)

DT 21-JUN-1986 (Ref. 01, Last sequence update)

DR 15-JUN-1999 (Ref. 36, Last annotation update)

DE 15 kDpa chain V-II region 26-10.

OC Burkholderia (Bioss Cordelia; Gramella; Verticillium; Bacteroides; Mammalia; Bacteria; Rodentia; Scutigerella; Muridae; Muridae; Mus).

OX NCBI_TaxID=10990.

PS NCBI_TaxID=10990.

PC STRAIN-A/71

RE MEDLINE=83178921; PubMed=6404396;

RA Novotny J., Margolis M.N.,

RT The sequence of the 118th chain variable region from a mouse

BL Biochemistry 22:1153-1158(1983).

CC -1. MISCELLANEOUS. THIS CHAIN WAS ISOLATED FROM AN IGGA2 HYBRIDOMA

CC PIR, PROTEIN THR BINDS DIOXIN.

DR HSBP, P80362, 1976.

DR Inspec, IP8007110, 19-11k.

DR Inspec, IP800006, 19-11k.

DR Pflm, PFO0047, 19-11k.

DR SNAAT, SMO0406, 10-1.

DR PROSIT, P850835, 10 LIMS, 1.

DR Immunoglobulin V region; Monoclonal antibody; Hybridoma.

FT DOMAIN 24 39

FT DOMAIN 24 39

FT DOMAIN 24 39

FT DOMAIN 24 39

FT DOMAIN 24 39

FT DOMAIN 24 39

FT DISULFID 23 93

SEQUENCE 113 AA, 1273 MM, P939C9A9A6C2A CR64.

Query Match 88.5% Score 525, DB 1, Length 113;

Accession 59, Complementarity 5, Indels 0, Gaps 0;

RESULT 2

DB 62 QVDPFSGSGSGTPTLIRSEVEDLGVYTCQGSNHWYVGGKTKLEIKR 113

62 QVDPFSGSGSGTPTLIRSEVEDLGVYTCQGSNHWYVGGKTKLEIKR 113

KX2E HUMAN STANDARD; PRT; 133 AA.
 AC P06137-1988 (Rel. 06, Created)
 DT 01-JUN-1988 (Rel. 06, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE 19 kappa chain V-II region RPT 6410 precursor.
 CC Homo sapiens (human)
 CC Bacteria; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Carnivora; Homidae; Homo.
 NCBI_TaxId=9606;
 RX MEDLINE=4431506; PubMed=6425927;
 RA Kloeck H.G., Solomon A., Zachau H.G.;
 EL human immunoglobulin kappa light chain genes of subgroups II and
 EL Nucleic Acids Res. 11:6499-6513(1983)
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 or send an email to license@embl.ch)
 CC EMBL; 200020; CNA7315.1;
 PR PIR: A01890; K2HNP.
 DR GO: G0:0005576; C:cytoregulatory; NS.
 DR GO: G0:0005823; F:antigen binding activity; NS.
 DR GO: G0:0006955; F:immune response; NS.
 DR Interpro: IPR003066; 19 MC.
 DR Interpro: IPR003596; 19 V.
 PR Pfam: PF00047; 19.1.
 DR SMART: SM00405; 19.1.
 DR PROSITE: PS00835; 19 LITE; 1.
 EL immunoglobulin V region; signal.
 FT SIGNAL 1 20
 FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPT 6410.
 FT DOMAIN 22 133 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 44 59 FRAMENOR-2.
 FT DOMAIN 60 74 FRAMENOR-3.
 FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 112 113 FRAMENOR-4.
 FT DOMAIN 123 133 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 113 BY SIMILARITY.
 FT NON TER 117 117
 SE SEQUENCE 133 AA; 14907 MW; 5130CAF363009EE CRC64;
 Query Match 80.9%; Score 48; DB 1; Length 133;
 Best Local Similarity 79.5%; Pred. No. 58-45;
 Matches 89; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
 Oy 2 IYVDSPTSLPVSIGDQAGISCSGSSQSVHSNNTLYLTQFGSGPELLIVYSNRF 61
 Db 22 VYHNGPSLTPVTLKIKSYVADLVGYVFGSGHVPFPGGGLTETIR 113
 Oy 62 GPVDFKSSGSSGSDTFLKIKSYVADLVGYVFGSGHVPFPGGGLTETIR 113
 Db 62 GPVDFKSSGSSGSDTFLKIKSYVADLVGYVFGSGHVPFPGGGLTETIR 113
 DB 62 GPVDFKSSGSSGSDTFLKIKSYVADLVGYVFGSGHVPFPGGGLTETIR 113
 RESULT 3
 KX2E HUMAN STANDARD; PRT; 117 AA.
 AC P06509;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 15-JUN-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE 19 kappa chain V-II region RPT 6410 precursor.
 CC Homo sapiens (human)
 CC Bacteria; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Carnivora; Homidae; Homo.
 NCBI_TaxId=9606;

DE 19 kappa chain V-II region OK607 precursor (fragment).
 CC Homo sapiens (human)
 CC Bacteria; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Carnivora; Homidae; Homo.
 NCBI_TaxId=9606;
 RX MEDLINE=4431506; PubMed=6425927;
 RA Kloeck H.G., Solomon A., Zachau H.G.;
 EL human immunoglobulin kappa light chain genes of subgroups II and
 EL Nucleic Acids Res. 11:6499-6513(1983)
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 entities requires a license agreement (see <http://www.1ab-sb.ch/annouce/>
 or send an email to license@embl.ch)
 CC EMBL; 200009; NOT ANNOTATED CDS.
 PR PIR: A01890; K2HNP.
 DR GO: G0:0005576; C:cytoregulatory; NS.
 DR GO: G0:0005823; F:antigen binding activity; NS.
 DR Interpro: IPR003066; 19 MC.
 DR Interpro: IPR003596; 19 V.
 PR Pfam: PF00047; 19.1.
 DR SMART: SM00405; 19.1.
 DR PROSITE: PS00835; 19 LITE; 1.
 EL immunoglobulin V region; signal.
 FT SIGNAL 1 1
 FT CHAIN 2 117
 FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 44 58 FRAMENOR-2.
 FT DOMAIN 66 97 FRAMENOR-3.
 FT DOMAIN 98 106 FRAMENOR-4.
 FT DISULFID 107 116 BY SIMILARITY.
 FT NON TER 117 117
 SE SEQUENCE 117 AA; 12664 MW; 92C57C719B58B1 CRC64;
 Query Match 72.4%; Score 457; DB 1; Length 117;
 Best Local Similarity 78.8%; Pred. No. 48-44;
 Matches 88; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
 Oy 2 IYVDSPTSLPVSIGDQAGISCSGSSQSVHSNNTLYLTQFGSGPELLIVYSNRF 61
 Db 6 IYVDSPTSLPVSIGDQAGISCSGSSQSVHSNNTLYLTQFGSGPELLIVYSNRF 65
 Oy 62 GPVDFKSSGSSGSDTFLKIKSYVADLVGYVFGSGHVPFPGGGLTETIR 113
 Db 66 GPVDFKSSGSSGSDTFLKIKSYVADLVGYVFGSGHVPFPGGGLTETIR 117
 DB 66 GPVDFKSSGSSGSDTFLKIKSYVADLVGYVFGSGHVPFPGGGLTETIR 117
 RESULT 4
 KX2D HUMAN STANDARD; PRT; 113 AA.
 AC P06137-1988 (Rel. 01, Created)
 DT 21-JUN-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-1999 (Rel. 38, Last annotation update)
 DE 19 kappa chain V-II region YW.
 CC Homo sapiens (human)
 CC Bacteria; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Carnivora; Homidae; Homo.
 NCBI_TaxId=9606;

[illegible]

OY 2 IVTQSPFSLPVSIGADQKASISCSGSGIVSHSNQNTYLYLQKQFQSGFLTKLYKVSNNRS 15
 DB 22 VVMTLTLTSLVYTGQPAISISCSGSGIVSHSNQNTYLYLQKQFQSGFLTKLYKVSNNRS 81
 OY 62 GVPDFSGSGSGTDFPLTKISVRVADGVYTCGSHVPPYTCGQTKLETR 113
 DB 82 GVPDFSGSGSGTDFPLTKISVRVADGVYTCGSHVPPYTCGQTKLETR 133

RESULT 9
 Q98K122 PRELIMINARY; PRT; 148 AA.

DR 08K122
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DB 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DB Mus musculus (Mouse)
 DB Mus musculus (Mouse)
 DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DB Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 DB taxid=10090;

SEQUENCE FROM N.A.
 PE TISSUE=salivary gland;
 KA Strimberg R.; (2002) to the EMBL/GenBank/DBS databases.
 DB BMM; NC028922; AAB2925.1;
 DB InterPro; IPR003599; IG_1
 DB InterPro; IPR007110; IG_1LKG
 DB InterPro; IPR003596; IG_1LKG
 DB Pfam; PF00047; IG_1
 DB SMART; SM00409; IG_1
 DB PROSITE; PS00835; IG_LIKE; 1.
 DB Hypothetical protein
 SEQUENCE 148 AA; 16345 MW; 183920BED9P3B21 CCK64;

Query Match 64.6%; Score 383; DB 11; Length 148;
 Best Local Similarity 71.7%; Pctd. No. 1.1e-33;
 Matches 71; Conservative 15; Mismatches 13; Indels 0; Gaps 0;
 OY 2 IVTQSPFSLPVSIGADQKASISCSGSGIVSHSNQNTYLYLQKQFQSGFLTKLYKVSNNRS 61
 DB 21 VVMTLTLTSLVYTGQPAISISCSGSGIVSHSNQNTYLYLQKQFQSGFLTKLYKVSNNRS 80
 OY 62 GVPDFSGSGSGTDFPLTKISVRVADGVYTCGSHVPPYTCGQTKLETR 100
 DB 81 GVPDFSGSGSGTDFPLTKISVRVADGVYTCGSHVPPYTCGQTKLETR 119

RESULT 10
 Q920B9 PRELIMINARY; PRT; 111 AA.

DR 0920B9
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 23, Last sequence update)
 DB 01-DEC-2001 (TREMBLrel. 23, Last sequence update)
 DB Protein-Matching anti-Idiotope kappa chain variable region
 DB Mus musculus (Mouse)
 DB Mus musculus (Mouse)
 DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DB Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 DB taxid=10090;
 SEQUENCE FROM N.A.

RA Acklin J.D., Iipe A., Jennings I.G., Horvath O., Cotton R.G.H.;
 RA Identification of the Idiotope of Protein-Matching Antibodies Expressed
 RA in Murine B-Cell Hybridomas
 RA Submitted (SEP-2000) to the EMBL/GenBank/DBS databases.
 DB EMBL; AF307935; AAL09419.1;
 DB InterPro; IPR007110; IG_1LKG.

DR InterPro; IPR003596; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_1;
 DR SMART; SM00406; IG_1;
 DR NCBI; P50835; IG_LIKE; 1.
 DR NON TER
 PT NON TER
 SEQUENCE 111 AA; 12046 MW; 1B4698A4685826 CCK64;

Query Match 62.1%; Score 368.5; DB 11; Length 111;
 Best Local Similarity 66.7%; Pctd. No. 2.6e-32;
 Matches 74; Conservative 11; Mismatches 25; Indels 1; Gaps 1;

OY 2 IVTQSPFSLPVSIGADQKASISCSGSGIVSHSNQNTYLYLQKQFQSGFLTKLYKVSNNRS 61
 DB 21 VVMTLTLTSLVYTGQPAISISCSGSGIVSHSNQNTYLYLQKQFQSGFLTKLYKVSNNRS 80
 OY 62 GVPDFSGSGSGTDFPLTKISVRVADGVYTCGSHVPPYTCGQTKLETR 112
 DB 61 GVPDFSGSGSGTDFPLTKISVRVADGVYTCGSHVPPYTCGQTKLETR 111

RESULT 11
 Q9U7U8 PRELIMINARY; PRT; 109 AA.

DR 09U7U8
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DB 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DB Myosin-reactive immunoglobulin light chain variable region
 DB (fragment)
 DB Mus musculus (Human)
 DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DB Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 DB taxid=9606;
 SEQUENCE FROM N.A.
 PE MEDLINE=86277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Werf P.L., Kallis N.N., Berry S.M.,
 RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RA fetus".
 RA Clin. Immunol. Immunopathol. 87:184-192(1998).
 DB 1035206; AAD56272.1;
 DB HSPB; IPR007110; IG_1LKG
 DB InterPro; IPR003065; IG_1LKG
 DB InterPro; IPR003596; IG_V.
 DB SMART; SM00406; IG_1
 DB PROSITE; PS00835; IG_LIKE; 1.

DR NON TER
 PT NON TER
 SEQUENCE 109 AA; 11646 MW; 5F67053E07BE197 CCK64;
 Query Match 62.1%; Score 368; DB 4; Length 109;
 Best Local Similarity 62.8%; Pctd. No. 3.1e-32;
 Matches 74; Conservative 15; Mismatches 13; Indels 4; Gaps 1;

OY 1 QIVTQSPFSLPVSIGADQKASISCSGSGIVSHSNQNTYLYLQKQFQSGFLTKLYKVSNNRS 60
 DB 1 EVVMTLTLTSLVYTGQPAISISCSGSGIVSHSNQNTYLYLQKQFQSGFLTKLYKVSNNRS 86
 OY 61 GVPDFSGSGSGTDFPLTKISVRVADGVYTCGSHVPPYTCGQTKLETR 113
 DB 57 FQIDPFGSGSGTDFPLTKISVRVADGVYTCGSHVPPYTCGQTKLETR 109

RESULT 12
 Q9U7U7 PRELIMINARY; PRT; 108 AA.
 AC 09U7U7
 DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DB MEDLINE-96277139, PubMed-9614934;
 DR Myosin-reactive immunoglobulin light chain variable region
 (Fragment)
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Euteleostomi; Actinopterygii; Clupeiformes; Clupeidae; Homo.
 NX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RA MEDLINE-96277139, PubMed-9614934;
 RA Young D.C., Van der Merwe F.L., Kalls N.N., Berner S.M.,
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 cells."
 DR EMBL: A035037, A056273.1;
 DR HSB: P01607, IAB5273.1;
 DR InterPro: IP000710, I9_1like.
 DR InterPro: IP000306, I9_MHC.
 DR Pfam: PF00047, I9_1_1g_v.
 DR SMART, SM00406, IGV_1.
 DR PROSITE, PS00835, I9_LIKE, 1.
 FT NON_TER
 SQ SEQUENCE 108 AA; 11738 MW; C0668116C4D16F3 CRC64;
 Query Match 57.3% Score 339.5, DB 4; Length 108;
 Best Local Similarity 50.9% Evid. NC 6.7e-26; Indels 5; Gaps 1;
 Matches 66; Conservative 15; Mismatches 22; Indels 5; Gaps 1;
 Oy 2 IVTVTSPFLVPLVGLQDAISISCSGSGSYHNSNNYLTETLQVPCQSPFLLYKNSRG 61
 Db 2 IONTGSPISLVSDVDVITTCASQSI-----SYLVNQKQSDVRLNASSD 56
 Oy 62 GVPKFGSSGSGTDPFLKIRVQAEADLVYTCQGSHPVFGGQTELEIK 113
 Db 57 GVPKFGSSGSGTDPFLKIRVQAEADLVYTCQGSHPVFGGQTELEIK 108
 RESULT 13
 Q9UL60 PRELIMINARY; PRT, 103 AA.
 AC Q9UL60 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DR 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Anti-myosin immunoglobulin light chain variable region
 (Fragment)
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Euteleostomi; Actinopterygii; Clupeiformes; Clupeidae; Homo.
 NX NCBI_TaxID=10930;
 RP SEQUENCE FROM N.A.
 RA MEDLINE-9044912, PubMed-1092489;
 RA Walker S., Liao L., Cunningham M.M., Diamond B.,
 RT "Antibodies to the epitope of the dominant epitope of
 with cardiac myosin."
 DR HSB: P06362, IAB5924.1;
 DR InterPro: IP000710, I9_1like.
 DR InterPro: IP000306, I9_MHC.
 DR Pfam: PF00047, I9_1_1g_v.
 DR SMART, SM00406, IGV_1.
 DR PROSITE, PS00835, I9_LIKE, 1.
 FT NON_TER
 SQ SEQUENCE 103 AA; 1103 MW; 4B843EC5B877F16 CRC64;

SQ SEQUENCE 103 AA; 11224 MW; EC87D653DB3AB21 CRC64;
 Query Match 53.1% Score 338.5, DB 11; Length 103;
 Best Local Similarity 43.1% Evid. NC 1.5e-29; Indels 1; Gaps 1;
 Matches 66; Conservative 15; Mismatches 22; Indels 1; Gaps 1;
 Oy 10 SIPVSPFLKISVADLVYTCQGSHPVFGGQTELEIK 112
 Db 2 IONTGSPISLVSDVDVITTCASQSI-----SYLVNQKQSDVRLNASSD 56
 Oy 70 SSGTDPFLKIRVQAEADLVYTCQGSHPVFGGQTELEIK 112
 Db 61 SSGTDPFLKIRVQAEADLVYTCQGSHPVFGGQTELEIK 103
 RESULT 14
 Q96S39 PRELIMINARY; PRT, 107 AA.
 AC Q96S39 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DR 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Anti-myosin immunoglobulin kappa light chain
 variable region (Fragment)
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Euteleostomi; Actinopterygii; Clupeiformes; Clupeidae; Homo.
 NX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RA MEDLINE-8715893, PubMed-8712075;
 RA Addelman R., Bressan K.E., Cunningham M.M.,
 RT "Molecular analysis of polyclonal monoclonal antibodies from
 rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
 antibody region genes." (1998).
 DR EMBL: U96396, IAB5785.1;
 DR InterPro: IP000710, I9_1like.
 DR InterPro: IP000306, I9_MHC.
 DR Pfam: PF00047, I9_1_1g_v.
 DR SMART, SM00406, IGV_1.
 DR PROSITE, PS00835, I9_LIKE, 1.
 FT NON_TER
 SQ SEQUENCE 107 AA; 11550 MW; 4B843EC5B877F16 CRC64;
 Query Match 56.8% Score 337, DB 4; Length 107;
 Best Local Similarity 40.7% Evid. NC 6.7e-29; Indels 6; Gaps 2;
 Matches 68; Conservative 16; Mismatches 22; Indels 6; Gaps 2;
 Oy 2 IVTVTSPFLVPLVGLQDAISISCSGSGSYHNSNNYLTETLQVPCQSPFLLYKNSRG 61
 Db 2 IONTGSPISLVSDVDVITTCASQSI-----SYLVNQKQSDVRLNASSD 56
 Oy 62 GVPKFGSSGSGTDPFLKIRVQAEADLVYTCQGSHPVFGGQTELEIK 113
 Db 57 GVPKFGSSGSGTDPFLKIRVQAEADLVYTCQGSHPVFGGQTELEIK 107
 RESULT 15
 Q9UL66 PRELIMINARY; PRT, 109 AA.
 AC Q9UL66 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DR 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE Myosin-reactive immunoglobulin kappa chain variable region
 (Fragment)
 OS Homo sapiens (human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 NC Euteleostomi; Actinopterygii; Clupeiformes; Clupeidae; Homo.
 NX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:9827139; PubMed:9614934;
RA M.X., Jan B., Van der Werf P.L., Kalle N.N., Berny S.M.,
RB Vanden Berghe P.
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
RD PubMed:9827139; PubMed:9614934;
DR HSBP; P00462; IWL.
DR HSBP; P00462; IWL.
DR Interpro; IPR007110; Ig_Like.
DR Interpro; IPR003006; Ig_Like.
DR Interpro; IPR003096; Ig_V.
DR Pfam; PF004713; Ig_Like.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; Ig_Like; 1.
DR NON_TER
FT NON_TER
FT NON_TER
SQ SEQUENCE 109 aa; 11928 MW; 2433572CDAC83 CRC64;

Query Match 56.88; Score 337; DB 4; Length 109;
Query: Local Similarity 56.88; Percent Identical 22; Indels 4; Gaps 1;
Matches 66; Conservative 21; Mismatches 45

```

```

Oy 1 QVLTSTPLSLPVLADQASISCSQSIVHNSGNTLYEVLQRFQSPKLLIYVSNRF 60
Db 1 EIVLISGSLILSPFKNVILSDNLSGV---SSILNMQQLQDQPHLLIYSSSSA 56
Oy 61 SGEVDPFGSGSGDPFTLLISRVPAHLGVYVCFQGSNVMWTFEGTKLEIK 113
Db 57 KQIDHFGSGSISDPLILSHHSEDRNVLICQVCGSIFTFQGTANDLHK 109

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Search completed: November 7, 2003, 07:34:34
Job time : 38.3614 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:17 / Search time 48 7703 seconds

(without alignments)
368.069 Million cell updates/sec

US-09-661-992b-84_copy_137_249

Perfect score: 593
Sequence: 1 QIVTQSGSLPVSIGDQAS.....FGSHWPTGGDTLSIKR 113

Scoring table: BLOSUM62
Gap: 10.0, Gapext: 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

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1: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1180.DAT.*
2: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1181.DAT.*
3: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1182.DAT.*
4: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1183.DAT.*
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7: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1186.DAT.*
8: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1187.DAT.*
9: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1188.DAT.*
10: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1189.DAT.*
11: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1190.DAT.*
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13: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1192.DAT.*
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17: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1196.DAT.*
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21: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1200.DAT.*
22: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1201.DAT.*
23: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1202.DAT.*
24: /SIBS1/gcgcata/geneseq/geneseq-emb1/AA1203.DAT.*

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Prod. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	593	100	AA1203.4	Chimeric - Nucleus
2	570	96.1	AA1203.4	Chimeric - Nucleus
3	567	95.6	AA1203.4	Chimeric - Nucleus
4	567	95.6	AA1203.4	Chimeric - Nucleus
5	565	95.3	AA1203.4	Chimeric - Nucleus
6	563	94.9	AA1203.4	Chimeric - Nucleus
7	563	94.9	AA1203.4	Chimeric - Nucleus
8	562	94.8	AA1203.4	Chimeric - Nucleus

10	561	94.6	149	20	AA1203.4	Chimeric - Nucleus
11	561	94.6	149	20	AA1203.4	Chimeric - Nucleus
12	558	94.1	249	20	AA1203.4	Chimeric - Nucleus
13	558	94.1	249	20	AA1203.4	Chimeric - Nucleus
14	555	93.6	112	20	AA1203.4	Chimeric - Nucleus
15	555	93.6	112	20	AA1203.4	Chimeric - Nucleus
16	554	93.4	238	20	AA1203.4	Chimeric - Nucleus
17	554	93.4	238	20	AA1203.4	Chimeric - Nucleus
18	552	93.1	112	16	AA1203.4	Chimeric - Nucleus
19	552	93.1	112	16	AA1203.4	Chimeric - Nucleus
20	552	93.1	112	16	AA1203.4	Chimeric - Nucleus
21	552	93.1	249	14	AA1203.4	Chimeric - Nucleus
22	552	93.1	249	14	AA1203.4	Chimeric - Nucleus
23	551	92.9	112	13	AA1203.4	Chimeric - Nucleus
24	551	92.9	112	13	AA1203.4	Chimeric - Nucleus
25	550	92.7	112	16	AA1203.4	Chimeric - Nucleus
26	550	92.7	112	16	AA1203.4	Chimeric - Nucleus
27	550	92.7	112	16	AA1203.4	Chimeric - Nucleus
28	549	92.6	112	13	AA1203.4	Chimeric - Nucleus
29	549	92.6	112	13	AA1203.4	Chimeric - Nucleus
30	547	92.2	111	15	AA1203.4	Chimeric - Nucleus
31	547	92.2	111	15	AA1203.4	Chimeric - Nucleus
32	547	92.2	111	15	AA1203.4	Chimeric - Nucleus
33	547	92.2	111	15	AA1203.4	Chimeric - Nucleus
34	547	92.2	111	15	AA1203.4	Chimeric - Nucleus
35	545	91.9	122	20	AA1203.4	Chimeric - Nucleus
36	545	91.9	122	20	AA1203.4	Chimeric - Nucleus
37	546	92.1	111	14	AA1203.4	Chimeric - Nucleus
38	546	92.1	111	14	AA1203.4	Chimeric - Nucleus
39	545	91.9	122	20	AA1203.4	Chimeric - Nucleus
40	545	91.9	122	20	AA1203.4	Chimeric - Nucleus
41	543	91.6	109	23	AA1203.4	Chimeric - Nucleus
42	543	91.6	109	23	AA1203.4	Chimeric - Nucleus
43	543	91.6	112	20	AA1203.4	Chimeric - Nucleus
44	543	91.6	112	20	AA1203.4	Chimeric - Nucleus
45	543	91.6	238	15	AA1203.4	Chimeric - Nucleus

ALIGNMENTS

Result	Query Match Length	ID	Description
1	100	AA1203.4	Chimeric - Nucleus
2	96.1	AA1203.4	Chimeric - Nucleus
3	95.6	AA1203.4	Chimeric - Nucleus
4	95.6	AA1203.4	Chimeric - Nucleus
5	95.3	AA1203.4	Chimeric - Nucleus
6	94.9	AA1203.4	Chimeric - Nucleus
7	94.9	AA1203.4	Chimeric - Nucleus
8	94.8	AA1203.4	Chimeric - Nucleus

XX 13-SEP-2000; 2000MO-BP09936.
 XX 14-SEP-1999; 99AT-0001576.
 XX (BAXT) BAXTER AG.
 XX Schellinger F, Kerschbaurer R, Falkner F, Dornier F,
 XX WPI, 2001-280158/30.
 XX N-PDB; AMF0724.
 XX
 XX New factor IX/factor IXa antibodies and their derivatives useful for
 XX increasing antithrombotic activity of factor IXa and for treating blood
 XX coagulation disorders such as hemophilia A and haemorrhagic diathesis -
 XX Claim 10; Fig 15; 13pp; English.
 XX
 XX The present sequence is that of a single chain (scFv) derivative
 XX of antibody 193/K2, comprising the heavy (VH) and light (VL) chain
 XX variable regions of 193/K2 joined by an artificial, flexible linker
 XX peptide. The scFv was obtained by PCR amplification of cDNAs for
 XX heavy and light chain regions and cloning in vector pM2.2.19/K2.193/K2
 XX as a single and anti-idiotype antibody. The scFv is a derivative of
 XX antibodies of the invention. Anti-FX/FIXa and their derivatives,
 XX including scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor
 XX activity and are useful for the treatment of haemophilia A and other
 XX bleeding disorders. This allows for rapid blood coagulation even
 XX in the absence of FVIII or FVIIIa, and in the case of FVIII
 XX inhibitor patients. The antibodies and derivatives are used in a
 XX coagulation disorders, especially haemophilia A and haemorrhagic
 XX diathesis.
 XX
 XX Sequence 249 AA:
 XX
 XX Query Match 100.0%; Score 593; DB 22; Length 249;
 XX Best Local Similarity 100.0%; Pred. NO. 1.5e-44;
 XX Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 QIVLTGSPLESLVGLDQASISCRSSQIVNSNMYLWYKQPGSRKLLIYVNSRF 60
 XX DB 137 QIVLTGSPLESLVGLDQASISCRSSQIVNSNMYLWYKQPGSRKLLIYVNSRF 196
 XX 61 SGVPVFGSGSGDTPLKISRVNARDELQVYTCQSHVWPFPGGCTLEIKR 113
 XX DB 197 SGVPVFGSGSGDTPLKISRVNARDELQVYTCQSHVWPFPGGCTLEIKR 249

XX 21-MAY-1987; 87DS-0052800.
 XX (CREA-) CREATIVE BIOMOLECULES INC.
 XX Hueton JS, Oppermann R,
 XX WPI; 1988-353928/49.
 XX N-PDB; AAB0180.
 XX Recombinant multifunctional protein - having antibody binding site and a
 XX solid support. Biological activity, ion sequestering or binding to a
 XX solid support.
 XX Disclosure; Page 7; 15pp; English.
 XX
 XX The biosynthetic antibody binding site forms part of a recombinant
 XX multifunctional protein which also comprises an effector protein, an AA
 XX acid sequence capable of sequestering an ion, or a sequence capable of
 XX binding to a solid support. The RAS comprises the framework region from
 XX CC and the complementarity determining region from G1-loop-1 heavy chain
 XX variable region and has lysozyme specificity. The effector protein is an
 XX enzyme, toxin, receptor, binding site, growth factor, cytokine, is
 XX calmodulin or metallothionein. The sequence capable of binding to solid
 XX support is streptavidin or a protein A fragment. The protein may be used
 XX for, eg specific binding assays, affinity purification, bioassays, drug
 XX screening, or as a model for the study of protein structure and function.
 XX diseases. The protein offers fast and easy cloning and expression, and
 XX proteolytic enzymes and have improved stability. They reach target organs
 XX rapidly and are cleared quickly from the body. They also have reduced
 XX immunogenicity.
 XX (updated on 31-OCT-2002 to add missing OS field.)
 XX
 XX Sequence 249 AA:
 XX
 XX Query Match 96.1%; Score 570; DB 9; Length 249;
 XX Best Local Similarity 94.6%; Pred. NO. 1.6e-42;
 XX Matches 106; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 2 IVTNGSPSLRLDQASISCRSSQIVNSNMYLWYKQPGSRKLLIYVNSRF 61
 XX DB 136 IVTNGSPSLRLDQASISCRSSQIVNSNMYLWYKQPGSRKLLIYVNSRF 195
 XX 62 GVPVFGSGSGDTPLKISRVNARDELQVYTCQSHVWPFPGGCTLEIKR 113
 XX DB 196 GVPVFGSGSGDTPLKISRVNARDELQVYTCQSHVWPFPGGCTLEIKR 247

XX (CDB-) CREATIVE BIOMOLECULES INC.
 XX Huston JS, Oppermann H;
 XX WPI, 1988-353928/43.
 XX N-PSDB; AAB50173.
 XX
 XX Recombinant multifunctional protein - having antibody binding site and a
 XX sequence for biological activity, ion sequestering or binding to a solid
 XX support.
 XX Disclosure: Page 7; 15pp; English.
 XX
 XX The light chain variable domain comprises complementarily determining
 XX regions from murine anti-dioxin monoclonal
 XX 25-10. The domain forms part of a
 XX biophoretic protein. The protein also comprises an effector molecule
 XX with biological activity (eg an enzyme, receptor binding site, growth
 XX factor, chemokine, cytokine or antimetabolite), an amino acid sequence
 XX capable of forming a stable complex with a target antigen, a
 XX amino acid sequence capable of selective binding to a solid support or an
 XX streptavidin or a fragment of protein A). The protein can be used for
 XX specific binding assays, affinity purification, bioassays, drug targeting,
 XX immunodiagnosis, immunotherapy, immunovaccination, immunotoxic diseases,
 XX it offers fewer cleavage sites to circulating proteolytic enzymes,
 XX improved stability. It reaches target tissues rapidly and is quickly
 XX cleared from the body. It also has reduced immunogenicity and its design
 XX allows binding to other molecules in drug targeting and imaging
 XX applications
 XX (Updated on 31-OCT-2002 to add missing OS field.)
 XX
 XX Sequence 115 AA;
 XX
 XX Query Match 95.6%; Score 567; DB 9; Length 115;
 XX Best Local Similarity 93.8%; Pred. No. 1.3e-42;
 XX Matches 105; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 2 IYLGSPFLSPVSLDQASICRSGSYVNSGNTYLTMYLQKPGSPPLLYIKYNSRS 63
 XX 4 VVMTQPLSLVSLDQASICRSGSYVNSGNTYLTMYLQKPGSPPLLYIKYNSRS 63
 XX 62 GVPKRSQSGSGCDPLFLKLSIVKAEADGIYFCQSHVPTFGCGTLEIKR 113
 XX 64 GVPKRSQSGSGCDPLFLKLSIVKAEADGIYFCQSHVPTFGCGTLEIKR 115
 XX
 XX RESULT 4
 XX AAB62301
 XX ID AAB62301 standard; Protein; 115 AA.
 XX AC AAB62301;
 XX DT 29-JUN-2001 (first entry)
 XX
 XX Chimeric Fv (FMS) light chain variable domain.
 XX
 XX Bioanalytic; antibody binding site; binding assay; drug targeting;
 XX bioassays; imaging; affinity purification; immunological; oncogenic;
 XX immunodiagnosis; immunotherapy; immunovaccination; immunotoxic;
 XX antimicrobial; monoclonal; 9p-4; anti-lysozyme; dimeric.
 XX
 XX Mus sp.
 XX
 XX US6207404-B1.
 XX
 XX 27-MAR-2001.
 XX
 XX 18-DEC-1995; 95US-0675724.
 XX
 XX 21-MAY-1987; 87US-0052800.
 XX 21-MAY-1987; 87US-0052800.
 XX 19-OCT-1992; 93US-019901.
 XX

PR 30-JUN-1998; 98US-0213671.
 XX
 XX (CDB-) CDB INC.
 XX Huston JS, Oppermann H;
 XX WPI, 2001-280767/29.
 XX N-PSDB; AAB57658.
 XX
 XX Novel biosynthetic antibody binding site having chimeric polypeptide
 XX Fv which defines selective antigen binding region and has CDR and
 XX framework amino acid sequences homologous to different immunoglobulin
 XX molecules
 XX
 XX Disclosure: Pgs 4b; 26pp; English.
 XX
 XX The invention relates to a biosynthetic antibody binding site that
 XX defines a binding region for an antigen. The binding site region comprises
 XX defining single, complete antigen (Ag) binding site region (CDR) and
 XX polypeptide domain having sets of complementarily determining regions
 XX (CDR) and framework (FR) amino acid sequences homologous to first and
 XX second immunoglobulin (Ig) chains. The biosynthetic antibody binding
 XX site are used in specific binding assays, immunodiagnosis, immunotherapy,
 XX bioassays, drug targeting, imaging immunological treatment of various
 XX oncogenic and infectious diseases. The present sequence represents the
 XX light chain variable domain of a chimeric Fv (FMS) comprising the CDRs
 XX 26-10 (anti-lysozyme) and FRs of murine monoclonal
 XX
 XX Sequence 115 AA;
 XX
 XX Query Match 95.6%; Score 567; DB 22; Length 115;
 XX Best Local Similarity 93.8%; Pred. No. 1.3e-42;
 XX Matches 105; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 XX
 XX 2 IYLGSPFLSPVSLDQASICRSGSYVNSGNTYLTMYLQKPGSPPLLYIKYNSRS 63
 XX 4 VVMTQPLSLVSLDQASICRSGSYVNSGNTYLTMYLQKPGSPPLLYIKYNSRS 63
 XX 62 GVPKRSQSGSGCDPLFLKLSIVKAEADGIYFCQSHVPTFGCGTLEIKR 113
 XX 64 GVPKRSQSGSGCDPLFLKLSIVKAEADGIYFCQSHVPTFGCGTLEIKR 115
 XX
 XX RESULT 5
 XX AAB21262
 XX ID AAB21262 standard; Protein; 249 AA.
 XX AC AAB21262;
 XX DT 21-MAY-1992 (first entry)
 XX
 XX pcepNO21 encoding anti-coxalzone antibody.
 XX
 XX Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
 XX pIII; gP; binding; adsorption; gene VIII; diverse repertoire;
 XX immunoglobulin; etc.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 XX FT 1..118
 XX FT Protein /label = VH
 XX FT Peptide /119..138 linker
 XX FT 139..249
 XX FT Protein /label = VL
 XX
 XX WO201047-A.
 XX
 XX 23-JUN-1992.
 XX

PF 10-JUN-1991; 91MO-GB01134.
 XX 15-MAY-1991; 91GB-0010549.
 PR 19-OCT-1990; 90GB-0012248.
 PR 12-NOV-1990; 90GB-0014503.
 PR 06-MAR-1991; 91GB-0004744.
 XX (CMM-) CAMBRIDGE ANTIBODY.
 PA (MMD-) MED RES COUNCIL.
 XX Mc Cafferty J, Pope AR, Johnson KS, Hogenboom HNJ, Griffiths AD;
 PI 1992-01-01, 1992-01-01, 1992-01-01, 1992-01-01, 1992-01-01;
 PI Winter GP, Bonnett TP;
 XX WPI: 1392-056862/07.
 XX N-DBP; AA021098.
 PT Producing members of specific binding pairs - by expression in
 PT recombinant host cells with a secreting replicable genetic
 PT display package.
 RS Example 9; Fig 13: 209pp; English.
 CC Oxalotone is a hapten used for studying the immune response and the
 CC immune response to oxalotone. Oxalotone is a derivative of oxalotone
 CC Penwell, and C. Milstien, NJ Immunol. 1992; 67: 60. Oxalotone is
 CC by inserting the BclII/SacI fragment of pSPD-3 myc (nucleotides
 CC pSPD-3 myc (nucleotides 1-1000) into the BclII/SacI fragment of
 CC pSPD-3 myc (nucleotides 1-1000) to generate pSPD-3 myc (nucleotides
 CC pSPD-3 myc (nucleotides 1-1000) to generate pSPD-3 myc (nucleotides
 CC of pSPD-3 myc (nucleotides 1-1000) to generate pSPD-3 myc (nucleotides
 CC see also AA021260-307, 309-311; AA021450, 565-581.
 XX Sequence 249 AA:
 50
 Query Match: 95.68; Score 567; DB 13; Length 249;
 Matches 108; Conservative 5; Pct. No. 1.9e-42; Indels 0; Gaps 0;
 DB 2 1VLDSHSLPVLSDIDASISCRSSQSVNSNNTLYLMTLQFGQSPKLLTYKNSRF 61
 138 ILCTQPLSLPVLSDIDASISCRSSQSVNSNNTLYLMTLQFGQSPKLLTYKNSRF 197
 62 GVPDPFSSGSGTPTLKISRYEADLVGYTCGSHVPTFGGCTALAI 113
 198 GVPDPFSSGSGTPTLKISRYEADLVGYTCGSHVPTFGGCTALAI 249
 DB
 RESULT 6
 AA0215704
 ID AA0215704 standard; Protein; 112 AA.
 XX AA0215704;
 XX 12-MAR-2002 (first entry)
 DB Mouse monoclonal antibody alpha 340 light chain variable (VK) region.
 XX Mouse; humanised form; monoclonal antibody alpha 340, gene therapy;
 KW epidermal growth factor receptor; EGF; cancer; colorectal; lung; breast;
 KW gastric; ovarian; immune response; cytotoxic; cell growth; apoptosis;
 XX Inhibitor.
 OS Mus sp.
 PH Key
 PI Location/Qualifiers
 PI Region
 PI /label: CBR1
 PI /note= "Complementarity determining region 1"
 XX Region
 XX 55..68
 XX /label: CDR2

PF /note= "Complementarity determining region 2"
 XX 95..102
 PF /label: CDR3
 XX /note= "Complementarity determining region 3"
 DB NO02018813b-AA1.
 XX 22-NOV-2001.
 XX 21-MAY-2001; 2001NO-GB02226.
 XX 19-MAY-2000; 2000GB-0011931.
 XX 24-AUG-2000; 2000GB-0020794.
 XX (SCN-) SCONECELL LTD.
 XX Ellis JM, Durrant LG;
 XX WPI: 2002-05384/08.
 XX N-DBP; AA025247.
 XX New humanised form of mouse monoclonal antibody 340 which binds to
 XX epidermal growth factor receptor, and inhibits binding of growth factor,
 XX useful for treating colorectal, lung, breast, gastric and ovarian
 XX cancer.
 XX Claim 6; Fig 2; 53pp; English.
 CC The present invention relates to a humanised form of the antibody 340 (a
 CC mouse monoclonal antibody which binds to epidermal growth factor (EGF)
 CC receptor and inhibits binding of EGF), obtainable from the cell line
 CC form of the antibody 340 is useful in gene therapy, medicine and as a
 CC manufacture of a medicament for treatment or prophylaxis of cancer. The
 CC invention is useful for treating colorectal, lung, breast, gastric or
 CC initial treatment or surgery. The invention also relates to a recombinant
 CC a protective immune response against cancer by optimised immunisation
 CC schedules. The humanised form of the antibody 340 has reduced
 CC receptor binding to the epidermal growth factor receptor, thereby
 CC inhibit the cell growth of EGF receptor expressing cells. The invention is
 CC used as cell growth and apoptosis inhibitor. The present sequence is
 CC is mouse monoclonal antibody alpha 340 light chain variable (VK) region.
 XX Sequence 112 AA:
 50
 Query Match: 95.34; Score 555; DB 23; Length 112;
 Matches 104; Conservative 6; Pct. No. 1.9e-42; Indels 0; Gaps 0;
 DB 2 1VLDSHSLPVLSDIDASISCRSSQSVNSNNTLYLMTLQFGQSPKLLTYKNSRF 61
 2 1VLDSHSLPVLSDIDASISCRSSQSVNSNNTLYLMTLQFGQSPKLLTYKNSRF 61
 62 GVPDPFSSGSGTPTLKISRYEADLVGYTCGSHVPTFGGCTALAI 111
 62 GVPDPFSSGSGTPTLKISRYEADLVGYTCGSHVPTFGGCTALAI 111
 DB
 RESULT 7
 AA021599
 ID AA021599 standard; Protein; 149 AA.
 XX AA021599;
 XX 25-MAR-2003 (updated)
 XX 26-FEB-1997 (first entry)
 DB Anti-Idotype monoclonal antibody 1A7 variable light chain.
 XX Murine; mouse; anti-Idotype; monoclonal antibody; MH; 1A7;
 XX variable light chain; ganglioside 2; GD2; 1A7a; neuroblastoma;


```

OS      Mas sp.
XX      Key
XX      Peptide
XX      Location/Qualifiers
XX      1..29
XX      /label: signal
XX      20..238
XX      /label: immunoglobulin E light chain
XX      EP02189-A1.
XX
XX      PD      09-JUN-1999.
XX      PF      13-NOV-1998; 98EB-0309040.
XX      PR      14-NOV-1997; 9709-0313589.
XX      PA      (SNV) SANKYO CO LTD.
XX      PA      (TOKM) TOKYO METROPOLITAN INST MEDICAL SCI.
XX      KA      Katsunuma H, Matsushita K, Taya C, Yonemura H;
XX      WP1: 1999-315604/27.
XX      DR      N-PSDB, A061085.
XX      TS      Transgenic non-human animal allergy models
XX      CL      Claim 28; Page 30-32; 42BP: English.
XX
XX      The present invention describes a transgenic, non-human animal with the
XX      gene that can produce and constitutively express an antigen having constant
XX      region which can bind an IgE receptor on mast cells in the animals, the
XX      molecule having an immunoglobulin structure and being further capable of
XX      specifically binding a protease-inhibiting antigen. The transgenic animal is
XX      used to study the mechanism of allergic reaction, and the transgenic animal is
XX      substances, e.g. with antiallergic activity, to affect any allergic
XX      reaction caused in the animal by the administration of the antigen to
XX      the animal, and applying the substance to be evaluated. The present
XX      invention is immunoglobulin B (IgB) light chain, given in
XX      XX
XX      Sequence 238 Aa:
XX
XX      Query Match      93.6%; Score 555; DB 20; Length 238;
XX      Blast Local Similarity 92.9%; Pval. No. 3.2e-11;
XX      Matches 104; Conservative; G; Mismatches 27; Indels 0; Gaps 0
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XX      2  VVATGSSGSSGTPFLTISRATDAGVYICGASGAPVPGGATLLETR 113
XX      21 VVATGSSGSSGTPFLTISRATDAGVYICGASGAPVPGGATLLETR 113
XX      62 GPRGSSGSSGTPFLTISRATDAGVYICGASGAPVPGGATLLETR 113
XX      DB      81 GPRGSSGSSGTPFLTISRATDAGVYICGASGAPVPGGATLLETR 113
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XX      Search completed: November 7, 2003, 07:27:01
XX      Job time : 49.7303 secs

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OM protein - protein search, using sw model

Run on:

November 7, 2003, 07:30:13

Search time 99.120 seconds

(Without alignment updates/sec)

195.739 Million cell updates/sec

US-09-661-992b-84_COPY_137_249

Perfect score: 593

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Scoring table: BLOSUM62

Gap: 10.0, Gapext: 0.5

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Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Minimum Match of

Post-processing: Minimum Match 10%

Maximum Match 100%

Listing filter 45 summaries

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18: /cgm2_6/prodata/2/pubpa/US06_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
sequence identical to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	524	112	11	US-09-995-529-10	Sequence 10, Appl
2	524	96.3	11	US-09-995-529-10	Sequence 2, Appl
3	564	94.6	149	US-10-153-401-2	Sequence 2, Appl
4	558	94.1	263	US-10-153-401-6	Sequence 16, Appl
5	555	93.6	112	US-10-153-401-15	Sequence 15, Appl
6	541	92.2	114	US-09-917-563-15	Sequence 15, Appl
7	541	92.2	114	US-09-917-563-15	Sequence 15, Appl
8	541	91.2	10	US-09-341-894-4	Sequence 4, Appl
9	535	90.2	132	US-09-796-744-16	Sequence 4, Appl
10	535	90.2	132	US-10-231-452-64	Sequence 64, Appl
11	533	90.2	132	US-10-231-452-64	Sequence 64, Appl
12	531	89.5	111	US-09-948-049-24	Sequence 4, Appl
13	526	88.7	112	US-09-518-737-4	Sequence 4, Appl
14	525	88.5	121	US-09-947-839-55	Sequence 55, Appl
15	525	88.5	252	US-09-887-853-4	Sequence 4, Appl

16	523	88.2	113	12	US-10-277-471-6	Sequence 6, Appl
17	523	88.2	113	12	US-10-277-471-6	Sequence 6, Appl
18	522	88.0	271	15	US-10-138-505-6	Sequence 6, Appl
19	522	88.0	271	15	US-10-138-505-6	Sequence 6, Appl
20	522	88.0	271	15	US-10-138-505-6	Sequence 6, Appl
21	521	87.9	285	5	US-09-883-752-46	Sequence 26, Appl
22	519	87.5	131	5	US-10-138-505-10	Sequence 10, Appl
23	519	87.5	245	15	US-10-138-505-14	Sequence 40, Appl
24	519	87.5	271	15	US-10-138-505-34	Sequence 34, Appl
25	519	87.5	271	15	US-10-138-505-34	Sequence 34, Appl
26	516	87.0	131	12	US-09-947-839-11	Sequence 11, Appl
27	516	87.0	131	12	US-09-947-839-11	Sequence 11, Appl
28	512.5	86.8	474	15	US-10-270-555-3	Sequence 3, Appl
29	512.5	86.8	474	15	US-10-270-555-3	Sequence 3, Appl
30	512.5	86.8	474	15	US-10-270-555-3	Sequence 3, Appl
31	512	86.3	112	10	US-09-982-929-4	Sequence 45, Appl
32	512	86.3	112	10	US-09-982-929-4	Sequence 45, Appl
33	512	86.3	112	10	US-09-982-929-4	Sequence 45, Appl
34	512	86.3	112	10	US-09-982-929-4	Sequence 45, Appl
35	507	85.5	112	12	US-10-231-452-12	Sequence 8, Appl
36	505	85.2	112	12	US-10-231-452-12	Sequence 8, Appl
37	504	85.0	112	12	US-10-231-452-14	Sequence 14, Appl
38	504	85.0	112	12	US-10-231-452-14	Sequence 14, Appl
39	502	84.7	116	9	US-09-753-436-66	Sequence 46, Appl
40	502	84.7	116	9	US-10-153-992-66	Sequence 66, Appl
41	500	84.3	100	10	US-09-640-459-26	Sequence 26, Appl
42	499.5	83.4	114	15	US-10-794-523-119	Sequence 119, Appl
43	499.5	83.4	114	15	US-10-794-523-119	Sequence 119, Appl
44	487	82.1	100	10	US-09-840-459-25	Sequence 25, Appl
45	484	81.6	138	9	US-09-748-960-8	Sequence 9, Appl

ALIGNMENTS

```

RESULT 1
/ Sequence 10, Application US/0995529
/ Publication No. US2003095655A1
/ Applicant: Maltin, Jeffrey D.
/ Applicant: Huse, William D.
/ APPICONT: Tsue, Ying
/ TITLE OF INVENTION: Humanized Collagen Antibodies and
/ TITLE REFERENCE: P. IX 4376
/ CURRENT FILING DATE: 2001-11-26
/ CURRENT APPLICATION NUMBER: US/0995_529
/ NUMBER OF SEQUENCES: 2
/ SOFTWARE: Fastcd for Windows Version 4.0
/ SEQ ID NO 10
/ LENSRT: 112
/ ORGANISM: Mus musculus
US-09-995-529-10
Query Match 86.34; Score 571; DB 11; Length 112;
Best local Similarity 96.34; Score 571; DB 11; Length 112;
Matches 106; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 2 IVTSGSLDPLVSGDQASISKSSGSIHNSNNTLVETVOKPQSPKLLIVNSNPF 61
2 VVDTGSLDPLVSGDQASISKSSGSIHNSNNTLVETVOKPQSPKLLIVNSNPF 61
DB 2 VVDTGSLDPLVSGDQASISKSSGSIHNSNNTLVETVOKPQSPKLLIVNSNPF 61
QY 62 GPPEPSSGSGSDPTLTKIKIRNEDLDGVYCCQSSIVPFGSKTLKIR 112
62 GPPEPSSGSGSDPTLTKIKIRNEDLDGVYCCQSSIVPFGSKTLKIR 112
DB 62 QIVTSGSLDPLVSGDQASISKSSGSIHNSNNTLVETVOKPQSPKLLIVNSNPF 61
62 QIVTSGSLDPLVSGDQASISKSSGSIHNSNNTLVETVOKPQSPKLLIVNSNPF 61
RESULT 2
US-09-990-205-2
/ Sequence 2, Application US/0990205
/ Patent No. US20020150572A1

```

GENERAL INFORMATION:
 APPLICANT: POON, Kenneth A.
 APPLICANT: CHATTERJEE, MALAYA
 TITLE OF INVENTION: ANTIBODY AND COMPOSITIONS FOR THE TREATMENT OF PSORIASIS
 FILE REFERENCE: US 01420050
 CURRENT APPLICATION NUMBER: US/09/390,205
 PRIOR APPLICATION NUMBER: U.S. 09/192,838
 PRIOR FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: U.S. 60/065,774
 PRIOR FILING DATE: 1997-11-17
 NUMBER OF SEQ ID NOS: 5
 SEQ ID NO: 2
 LENGTH: 149
 TYPE: PRT Mus Musculus
 US-09-390-205.2

Query Match 94.9%; Score 563; DB 10; Length 149;
 Best Local Similarity 93.8%; Pred. No. 1.7e-48;
 Matches 105; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Db 2 IVTQSPFSLSPVLDQDAISCSGSSQSVHSNCKYTLNRYLQKQSPFLITVPSNRS 61
 21 VPMQPSFSLSPVLDQDAISCSGSSQSVHSNCKYTLNRYLQKQSPFLITVPSNRS 80
 62 GVPRSSGSSGDTPTLKSIVNADLVYTCQSHVWFGGDTLEIR 113
 DB 81 GVPRSSGSSGDTPTLKSIVNADLVYTCQSHVWFGGDTLEIR 132

RESULT 3
 US-10-153-401-2
 Sequence 66: Application US/10153401
 Publication No. US20030143981
 GENERAL INFORMATION:
 APPLICANT: Chatterjee, Malaya
 APPLICANT: Chatterjee, Sunil K.
 TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESS: MORRISON & FORSTER
 STREET: 755 PINE MILL ROAD
 CITY: PALO ALTO
 STATE: CALIF. 94304-1018
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/153,401
 FILING DATE: 27-Aug-2002
 CLASSIFICATION: unknown
 PRIOR APPLICATION NUMBER: US 09/293,533
 FILING DATE: 1999-04-15
 APPLICATION NUMBER: US 08/372,676
 FILING DATE: 1999-01-17
 FILING DATE: 1996-01-16
 ATTORNEY/AGENT INFORMATION:
 NAME: Catherine M. Polizzi
 FIRM: POLITZ & ASSOCIATES, P.C.
 TELEPHONE: (415) 813-5600
 TELECOMMUNICATION INFORMATION: 30442000202
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792

TELEX: 706141
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 149 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-153-401-2

Query Match 94.8%; Score 561; DB 15; Length 149;
 Best Local Similarity 93.8%; Pred. No. 2.6e-48;
 Matches 105; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Db 2 IVTQSPFSLSPVLDQDAISCSGSSQSVHSNCKYTLNRYLQKQSPFLITVPSNRS 61
 21 VPMQPSFSLSPVLDQDAISCSGSSQSVHSNCKYTLNRYLQKQSPFLITVPSNRS 80
 62 GVPRSSGSSGDTPTLKSIVNADLVYTCQSHVWFGGDTLEIR 113
 DB 81 GVPRSSGSSGDTPTLKSIVNADLVYTCQSHVWFGGDTLEIR 132

RESULT 4
 US-10-153-401-66
 Sequence 66: Application US/10153401
 Publication No. US20030143981
 GENERAL INFORMATION:
 APPLICANT: Chatterjee, Malaya
 APPLICANT: Poon, Kenneth A.
 TITLE OF INVENTION: ANTIBODY 1A7 AND USE FOR THE
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESS: MORRISON & FORSTER
 STREET: 755 PINE MILL ROAD
 CITY: PALO ALTO
 STATE: CALIF. 94304-1018
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/153,401
 FILING DATE: 27-Aug-2002
 CLASSIFICATION: unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/293,533
 FILING DATE: 1999-04-15
 APPLICATION NUMBER: US 08/372,676
 FILING DATE: 1999-01-17
 FILING DATE: 1996-01-16
 ATTORNEY/AGENT INFORMATION:
 NAME: Catherine M. Polizzi
 FIRM: POLITZ & ASSOCIATES, P.C.
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 INFORMATION FOR SEQ ID NO: 66:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 265 amino acids
 TYPE: amino acid
 MOLECULE TYPE: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 66:
 US-10-153-401-66

Query Match 94.18; Score 558; DB 15; Length 263;
Best Local Similarity 93.78; Pred. No. 9-96-48;
Matches 104; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 IVTGTGPTSLPVLPGDQASISCSGSGSYVNSNDYTLVWYLOKQKQKPKLLTYKNSRF 61
DB 153 VMTGTGPTSLPVLPGDQASISCSGSGSYVNSNDYTLVWYLOKQKQKPKLLTYKNSRF 212
QY 62 GVDPRFGSSGSGTDFLTKISRVADLVGYTCQSHVPAKCGQTKLEIK 112
DB 213 GVDPRFGSSGSGTDFLTKISRVADLVGYTCQSHVPAKCGQTKLEIK 263

RESULT 5
US-10-153-401-15
Sequence 15, Application US/10153401
Publication No. US20010135841
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
Room, Kenneth A.
TITLE OF INVENTION: ANTIBODY 1A7 AND USE FOR THE
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
STREET: 755 PINE MILL ROAD
CITY: PALO ALTO
STATE: CA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,401
CLASSIFICATION: chmnom-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/293,533
FILING DATE: 1995-01-17
APPLICATION NUMBER: US 08/732,676
APPLICATION NUMBER: US 08/591,196
ATTORNEY/AGENT INFORMATION:
NAME: Catherine M. Polizzi
REGISTRATION NUMBER: 40,130
TELEPHONE: (415) 813-5600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
INFORMATION FOR SEQ ID NO. 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO. 15:
US-10-153-401-15

Query Match 93.64; Score 555; DB 15; Length 112;
Best Local Similarity 93.44; Pred. No. 9-96-48;
Matches 104; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 IVTGTGPTSLPVLPGDQASISCSGSGSYVNSNDYTLVWYLOKQKQKPKLLTYKNSRF 61
DB 213 VMTGTGPTSLPVLPGDQASISCSGSGSYVNSNDYTLVWYLOKQKQKPKLLTYKNSRF 61

QY 62 GVDPRFGSSGSGTDFLTKISRVADLVGYTCQSHVPAKCGQTKLEIK 112
DB 62 GVDPRFGSSGSGTDFLTKISRVADLVGYTCQSHVPAKCGQTKLEIK 112

RESULT 6
US-10-006-773-15
Sequence 15, Application US/10006773
Publication No. US200129536X
GENERAL INFORMATION:
APPLICANT: Jungmans, Richard P.
TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against T
CURRENT APPLICATION NUMBER: US/10/006,773
CURRENT FILING DATE: 2001-12-10
PRIOR FILING DATE: 2000-11-30
MEDIUM TYPE: floppy disk
SOFTWARE: Patent Invention 3.1
SEQ ID NO 15
LENGTH: 112
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: Dedicated amino acid sequence of VK of murine R3 antibody
US-09-217-2688-27

Query Match 92.94; Score 551; DB 16; Length 123;
Best Local Similarity 92.04; Pred. No. 2-36-47;
Matches 103; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 2 IVTGTGPTSLPVLPGDQASISCSGSGSYVNSNDYTLVWYLOKQKQKPKLLTYKNSRF 61
DB 21 VMTGTGPTSLPVLPGDQASISCSGSGSYVNSNDYTLVWYLOKQKQKPKLLTYKNSRF 80
QY 62 GVDPRFGSSGSGTDFLTKISRVADLVGYTCQSHVPAKCGQTKLEIK 113
DB 81 GVDPRFGSSGSGTDFLTKISRVADLVGYTCQSHVPAKCGQTKLEIK 132

RESULT 7
US-09-217-2688-27
Sequence 27, Application US/092172688
Publication No. US20020065398A1
GENERAL INFORMATION:
APPLICANT: Meco de Acosta del Rio, Christina M
APPLICANT: Rodriguez, Rolando P
APPLICANT: Farias, Ernesto M
TITLE OF INVENTION: Chimeric Antigen and Chimeric Monoclonal Antibodies That Recogni
FILE REFERENCE: 2720, IUS
CURRENT APPLICATION NUMBER: US/09/217,2688
CURRENT FILING DATE: 2000-12-21
MEDIUM TYPE: floppy disk
SOFTWARE: Patent Invention 3.1
SEQ ID NO 27
LENGTH: 114
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: Murine R3 antibody
US-09-217-2688-27

Query Match 91.24; Score 541; DB 3; Length 114;
Best Local Similarity 90.24; Pred. No. 9-96-46;
Matches 101; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 2 IVTGTGPTSLPVLPGDQASISCSGSGSYVNSNDYTLVWYLOKQKQKPKLLTYKNSRF 61
DB 2 VMTGTGPTSLPVLPGDQASISCSGSGSYVNSNDYTLVWYLOKQKQKPKLLTYKNSRF 61
QY 62 GVDPRFGSSGSGTDFLTKISRVADLVGYTCQSHVPAKCGQTKLEIK 113

Db 62 GVPBPGSSGGTDTPLKISVBAEDLVYTCYCSHWPTGGQTLTKIR 113

RESULT 8

Sequence 4, Application US/09341894

Patent No. US020016833921

GENERAL INFORMATION:

TITLE OF INVENTION: Biological material for creating a mammal by antibody gene trans

FILE REFERENCE: 1994-002

CURRENT FILING DATE: 1999-12-15

PRIOR FILING DATE: 1997-01-20

SOFTWARE: Patent version 3.1

SEQ ID NO 4

LENGTH: 140

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: misc:feature

OTHER INFORMATION: a1n

Query Match 81.28; Score 541; DB 10; Length 140;

Best Local Similarity 90.28; Pred. No. 2,46-46;

Matches 101; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Db 21 VMTQPLSLPVLSDQASISCRSSGSIYNSNGTYLEWYLCQSGPILLYVNSRF 61

Db 81 GVPBPGSSGGTDTPLKISVBAEDLVYTCYCSHWPTGGQTLTKIR 113

RESULT 9

Sequence 16, Application US/0976744

Patent No. US020098527A1

GENERAL INFORMATION:

TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

FILE REFERENCE: EIM-002

CURRENT FILING DATE: 2000-03-03

PRIOR FILING DATE: 2000-03-03

SOFTWARE: Patent ver. 2.1

SEQ ID NO 16

LENGTH: 132

ORGANISM: Mus musculus

Query Match 90.28; Score 535; DB 12; Length 132;

Best Local Similarity 87.58; Pred. No. 8,86-46; Mismatches 2; Indels 0; Gaps 0;

Matches 98; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

Db 62 GVPBPGSSGGTDTPLKISVBAEDLVYTCYCSHWPTGGQTLTKIR 113

Db 81 GVPBPGSSGGTDTPLKISVBAEDLVYTCYCSHWPTGGQTLTKIR 132

RESULT 10

Sequence 64, Application US/10231452

Publication No. US2003017527A1

GENERAL INFORMATION:

TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

FILE REFERENCE: 249-273

CURRENT FILING DATE: 2003-04-18

PRIOR FILING DATE: 2001-08-31

SOFTWARE: Patent ver. 2.1

SEQ ID NO 78

LENGTH: 132

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: misc:feature

Query Match 90.28; Score 535; DB 12; Length 132;

Best Local Similarity 87.58; Pred. No. 8,86-46; Mismatches 2; Indels 0; Gaps 0;

Matches 98; Conservative 12; Mismatches 2; Indels 0; Gaps 0;

Db 62 GVPBPGSSGGTDTPLKISVBAEDLVYTCYCSHWPTGGQTLTKIR 113

Db 81 GVPBPGSSGGTDTPLKISVBAEDLVYTCYCSHWPTGGQTLTKIR 132

RESULT 11

Sequence 14, Application US/1001942B

Patent No. US020016833921

GENERAL INFORMATION:

TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE

FILE REFERENCE: EIM-002

CURRENT FILING DATE: 2000-12-06

PRIOR FILING DATE: 2000-12-06

SOFTWARE: Patent ver. 2.1

SEQ ID NO 14

LENGTH: 131

ORGANISM: Mus musculus

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? LOCATION: 11... (19)
US-10-010-942B-14
Query Match
Best Local Similarity 90.1%; Score 534; DB 12; Length 131;
Matches 97; Conservative 11; Mismatches 3; Indels 0; Gaps 0;
OY 2 IVTQPSLSPVSLADQASISGSSGSIYHNSNGNTLYLWYLFKQPSGPKLLIYKNSRFS 61
DB 21 VMTQPSLSPVSLADQASISGSSGSIYHNSNGNTLYLWYLFKQPSGPKLLIYKNSRFS 80
OY 62 GVPKRSSSGSDTPTLKISVYKADQAVYVFCOSHVPPVFCGGTLEIK 112
DB 81 GVPKRSSSGSDTPTLKISVYKADQAVYVFCOSHVPPVFCGGTLEIK 131

RESULT 12
US-09-946-049-2
Sequence 2, Application US/09948049
Score 534; DB 12; Length 131;
GENERAL INFORMATION:
APPLICANT: NICOLAI, Yves Claude
TITLE OF INVENTION: Methods and Compositions for Diseases Associated with Amyloidosis
REFERENCE: 1472, 0112 4005-7261163
CURRENT FILING DATE: 2001-09-06/946,049
PRIOR APPLICATION NUMBER: US 60/255,033
PRIOR FILING DATE: 2000-12-12/60,250,391
PRIOR APPLICATION NUMBER: US 60/255,033
PRIOR FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patent version 3.1
LENGTH: 111
SEQUENCE TYPE: DNA
ORGANISM: Murinae gen. sp.
US-09-946-049-2

Query Match
Best Local Similarity 89.5%; Score 531; DB 10; Length 111;
Matches 97; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
OY 2 IVTQPSLSPVSLADQASISGSSGSIYHNSNGNTLYLWYLFKQPSGPKLLIYKNSRFS 61
DB 3 VMTQPSLSPVSLADQASISGSSGSIYHNSNGNTLYLWYLFKQPSGPKLLIYKNSRFS 62
OY 62 GVPKRSSSGSDTPTLKISVYKADQAVYVFCOSHVPPVFCGGTLEIK 110
DB 63 GVPKRSSSGSDTPTLKISVYKADQAVYVFCOSHVPPVFCGGTLEIK 111

RESULT 13
US-09-518-737-4
Sequence 1, Application US/09518737
Score 525; DB 12; Length 131;
GENERAL INFORMATION:
APPLICANT: FUKUI, YASUHIKA
APPLICANT: NAGATA, SATOSHI
APPLICANT: SATO, KIOKAHI
APPLICANT: SATO, KIOKAHI
TITLE OF INVENTION: MONOCLONAL ANTIBODY RECOGNIZING
REFERENCE: 565/19616
CURRENT FILING DATE: 2000-03-03
CURRENT FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: JP 1999-250209
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2, 1
SOFTWARE: Patent ver. 2.1
SEQ ID NO: 4
LENGTH: 112
SEQUENCE TYPE: DNA
ORGANISM: Mus musculus

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US-09-518-737-4
Query Match
Best Local Similarity 88.7%; Score 526; DB 11; Length 112;
Matches 96; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
OY 2 IVTQPSLSPVSLADQASISGSSGSIYHNSNGNTLYLWYLFKQPSGPKLLIYKNSRFS 61
DB 2 VMTQPSLSPVSLADQASISGSSGSIYHNSNGNTLYLWYLFKQPSGPKLLIYKNSRFS 61
OY 62 GVPKRSSSGSDTPTLKISVYKADQAVYVFCOSHVPPVFCGGTLEIK 112
DB 62 GVPKRSSSGSDTPTLKISVYKADQAVYVFCOSHVPPVFCGGTLEIK 112

RESULT 14
US-09-947-839-95
Sequence 2, Application US/09947839
Score 526; DB 11; Length 112;
GENERAL INFORMATION:
APPLICANT: do Couto Dr., Fernando J.R.
APPLICANT: Cariani Dr., Roberto L.
APPLICANT: Padlan Dr., Eduardo A.
TITLE OF INVENTION: Analogue Peptides With Broad
Anticancer Specificity, and Kit and
Therapeutic Methods
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
STRESSIA, PREVEY, Schroeder & Poplawski
CITY: Los Angeles
STATE: California
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SOFTWARE: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/947,839
FILING DATE: 06-09-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/976,288
FILING DATE: unknown/077,656
FILING DATE: 08/976,288
FILING DATE: 08/976,288
ATTORNEY/AGENT INFORMATION:
NAME: Vlachas Angel Ph.D.
REFERENCE/DOCKET INFORMATION:
TELEPHONE: (213) 622-7700
TELEPHONE: (213) 489-4210
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
MOLECULE TYPE: peptide
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-09-947-839-95

Query Match
Best Local Similarity 87.4%; Score 525; DB 12; Length 131;
Matches 97; Conservative 11; Mismatches 3; Indels 0; Gaps 0;
OY 2 IVTQPSLSPVSLADQASISGSSGSIYHNSNGNTLYLWYLFKQPSGPKLLIYKNSRFS 61

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Db 21 VMTQTPSLPVTGPGPASIICSSSSGSIYHNSNNTYLMYLAKPGQSPQLIYKYSIRFS 80
QY 62 GVPDKESGSSGSDTFTLKISRVAEDLGVYCFQGSHPWTFPGGATLEIR 112
81 GVPDKESGSSGSDTFTLKISRVAEDLGVYCFQGSHPWTFPGGATLEIR 131

RESULT 15

US-09-661-992b-84
Sequence 4, Application US/0987/853
Patent No. US20020168375A1

GENERAL INFORMATION:

APPLICANT: Huseon, James S.
Huseon, L. L.
Huston, L. L.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
Huseon, L. L.
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESS: Testa, Rutz & Thibault/Patent Department
CITY: Boston
STATE: Massachusetts
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PC DOS/MS-DOS
SOFTWARE VERSION: Release 8.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/887,853
FILING DATE: 21-Jun-2001
PRIORITY DATE: <unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/133,804

ATTORNEY/AGENT INFORMATION:

NAME: <unknown>
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-246-7100
TELEFAX: 617-246-7100

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 132
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-687-853-4

Query Match 88.5%; Score 525; DB 10; Length 252;
Local Similarity 88.4%; Read No. 18e-45;
Matches 59; Conservative 5; Indels 0; Gaps 0;

QY 2 IVTOSPLSPVSLDQASIRCSGSIYHNSNNTYLMYLAKPGQSPQLIYKYSIRFS 61
DB 135 VMTQTPSLPVTGPGPASIICSSSSGSIYHNSNNTYLMYLAKPGQSPQLIYKYSIRFS 194

QY 62 GVPDKESGSSGSDTFTLKISRVAEDLGVYCFQGSHPWTFPGGATLEIR 113
DB 135 GVPDKESGSSGSDTFTLKISRVAEDLGVYCFQGSHPWTFPGGATLEIR 246

Search completed: November 7, 2003, 08:16:52
CPU time: 100.12 sec

GenCode version 5.1.6
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OM protein - protein search, using sw model

Run on:

November 7, 2003, 07:21:18 / Search time 16.5955 Seconds
286,098 Million csl1 updates/sec

Title:

US-09-661-992b-84_COPY_137_249

Perfect score:

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Sequence:

BL0S0962

Scoring table:

Gapop 10.0, Gapext 0.5

Searched:

328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
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2: /cgn2_6/prodata/1/aa/5B_COHB.pap.*
3: /cgn2_6/prodata/1/aa/5C_COHB.pap.*
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6: /cgn2_6/prodata/1/aa/5F_COHB.pap.*

SUMMARIES

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1	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
2	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
3	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
4	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
5	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
6	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
7	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
8	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
9	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
10	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
11	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
12	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
13	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
14	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
15	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
16	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
17	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
18	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
19	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
20	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
21	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
22	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
23	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
24	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
25	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
26	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	
27	563	94.9	149	4	US-08-324-191-2	Sequence 2, Appl	

Prod. No. is the number of results predicted by chance to have a
score equal to or greater than the score being printed,
and is derived by analysis of the local score distribution.

28	560	92.7	112	2	US-08-859-648-29	Sequence 29, Appl
29	550	92.7	112	4	US-08-207-861-29	Sequence 19, Appl
30	550	92.7	112	4	US-08-207-861-29	Sequence 19, Appl
31	550	92.7	112	4	US-08-859-648-19	Sequence 19, Appl
32	550	92.7	112	4	US-08-859-648-19	Sequence 19, Appl
33	550	92.7	112	4	US-08-859-648-19	Sequence 19, Appl
34	550	92.7	112	4	US-08-859-648-19	Sequence 19, Appl
35	548	92.4	114	2	US-08-560-5588-27	Sequence 27, Appl
36	548	92.4	114	2	US-08-560-5588-27	Sequence 27, Appl
37	548	92.4	114	2	US-08-560-5588-27	Sequence 27, Appl
38	543	91.6	238	2	US-08-392-3388-12	Sequence 12, Appl
39	543	91.6	238	2	US-08-392-3388-12	Sequence 12, Appl
40	543	91.6	238	2	US-08-392-3388-12	Sequence 12, Appl
41	543	91.6	238	2	US-08-392-3388-12	Sequence 12, Appl
42	543	91.6	238	2	US-08-392-3388-12	Sequence 12, Appl
43	543	91.6	238	3	US-09-166-093-21	Sequence 21, Appl
44	543	91.6	238	3	US-09-166-093-21	Sequence 21, Appl
45	543	91.6	238	3	US-09-166-093-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-192-838B-2
Sequence 2, Appl
Query Match 94.8%; Pred. No. 1.1e+47
Matches 105; Conservative 2; Indels 0; Gaps 0
GENERAL INFORMATION:
APPLICANT: FOUN KENNETH A.
APPLICANT: UNIVERSITY OF KENTUCKY
FILE REFERENCE: 3044200500
CURRENT APPLICATION NUMBER: US/09/192.838B
CURRENT FILING DATE: 1998-01-16
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
TYPER: PAT
LENGTH: 149
ORGANISM: Mus Musculus
US-09-192-838B-2
Query Match 94.8%; Score 563; DB 4; Length 149;
Result Local Similarity 94.8%; Pred. No. 1.1e+47;
Matches 105; Conservative 2; Indels 0; Gaps 0
GENERAL INFORMATION:
APPLICANT: FOUN KENNETH A.
APPLICANT: UNIVERSITY OF KENTUCKY
FILE REFERENCE: 3044200500 US/09/192.838B
CURRENT FILING DATE: 1998-01-16
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
US-09-324-191-2
Sequence 2, Appl
Query Match 94.8%; Score 563; DB 4; Length 149;
Result Local Similarity 94.8%; Pred. No. 1.1e+47;
Matches 105; Conservative 2; Indels 0; Gaps 0
GENERAL INFORMATION:
APPLICANT: FOUN KENNETH A.
APPLICANT: UNIVERSITY OF KENTUCKY
FILE REFERENCE: 3044200500 US/09/192.838B
CURRENT FILING DATE: 1998-01-16
PRIOR FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0

Qy 2 IVTGGPSTLPSVIGLQKASISGSSGSIYHNNQTVLWYLOKQGGPGLLYVYNSRRS 61
 Db 2 VLVTPFLSLVPSLVLQKASISGSSGSIYHNNQTVLWYLOKQGGPGLLYVYNSRRS 61
 Qy 62 GVPFSSGSGGTPDLTKISRVKEDLVYVCGQSSVWMPFGCTKLEK 113
 Db 62 GVPFSSGSGGTPDLTKISRVKEDLVYVCGQSSVWMPFGCTKLEK 113

RESULT 5
 US-08-759-804A-66
 Sequence 66, Application US/0875980A4
 Patent No. 5391286
 GENERAL INFORMATION:
 APPLICANT: Pasten, Ira
 APPLICANT: Hilligheim, Mark J.
 APPLICANT: Fitzgerald, David J.
 APPLICANT: Fink, David
 APPLICANT: Peli, Lee
 TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
 TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA: Version #1.0
 APPLICATION NUMBER: US/08/759,804A
 FILING DATE: 03-DEC-1996
 CLASSIFICATION: 526
 PRIOR APPLICATION NUMBER: 08/331,398
 FILING DATE: 28-OCT-1994
 PRIOR APPLICATION DATA: US 07/767,331
 FILING DATE: 30-SEP-1991
 PRIOR APPLICATION DATA: US 07/596,289
 APPLICATION NUMBER: US 07/596,289
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen L.
 REGISTRATION NUMBER: 32,762
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 IMPRESSIONS: 66
 SEQUENCE CHARACTERISTICS:
 LENGTH: 125 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURES:
 NAME/KEY: Region
 LOCATION: 113
 OTHER INFORMATION: /note="Mouse monoclonal antibody B5 FV
 Light chain region"
 US-08-759-804A-66

Query Match 94.8%; Score 562; DB 2; Length 125;
 Best Local Similarity 94.8%; Pred. No. 1,2e-47;
 Matches 106; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 2 IVTGGPSTLPSVIGLQKASISGSSGSIYHNNQTVLWYLOKQGGPGLLYVYNSRRS 61

Db 2 VLVTPFLSLVPSLVLQKASISGSSGSIYHNNQTVLWYLOKQGGPGLLYVYNSRRS 61
 Qy 62 GVPFSSGSGGTPDLTKISRVKEDLVYVCGQSSVWMPFGCTKLEK 113
 Db 62 GVPFSSGSGGTPDLTKISRVKEDLVYVCGQSSVWMPFGCTKLEK 113

RESULT 6
 US-08-521-196-2
 Sequence 2, Application US/08752844
 Patent No. 5315921
 GENERAL INFORMATION:
 APPLICANT: Foon, Kenneth A.
 APPLICANT: Foon, Kenneth A.
 APPLICANT: Chatterjee, Swati K.
 TITLE OF INVENTION: MONOCLONAL ANTIBODY LAY AND USE FOR THE
 TREATMENT OF METASTASIS OF MELANOMA AND SMALL CELL CARCINOMA
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FORSTER
 STREET: 1000 WILK ROAD
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1219
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA: Version #1.30
 APPLICATION NUMBER: US/08/752,844
 FILING DATE: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Schiff, J. Michael
 REGISTRATION NUMBER: 40,253
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 IMPRESSIONS: 21
 SEQUENCE CHARACTERISTICS:
 LENGTH: 149 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-752-844-2

Query Match 94.8%; Score 561; DB 2; Length 149;
 Best Local Similarity 93.8%; Pred. No. 1.8e-47;
 Matches 105; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 2 IVTGGPSTLPSVIGLQKASISGSSGSIYHNNQTVLWYLOKQGGPGLLYVYNSRRS 61
 Db 21 VLVTPFLSLVPSLVLQKASISGSSGSIYHNNQTVLWYLOKQGGPGLLYVYNSRRS 80
 Qy 62 GVPFSSGSGGTPDLTKISRVKEDLVYVCGQSSVWMPFGCTKLEK 113
 Db 62 GVPFSSGSGGTPDLTKISRVKEDLVYVCGQSSVWMPFGCTKLEK 113

RESULT 7
 US-08-521-196-2
 Sequence 2, Application US/08591196
 Patent No. 5315921
 GENERAL INFORMATION:
 APPLICANT: Chatterjee, Swati K.
 APPLICANT: Foon, Kenneth A.
 TITLE OF INVENTION: MONOCLONAL ANTIBODY LAY AND USE FOR THE

US-09-283-533-2
 US-09-283-533-2
 Patent No. 6509016
 GENERAL INFORMATION:
 APPLICANT: Chatterjee, Malaya
 INVENTOR: Chatterjee, Malaya
 ADDRESS: Chatterjee, Sunil K.
 TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FORESTER
 STREET: 755 PAGE MILL ROAD
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 CDROM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 16-JUN-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 0.253
 TELECOMMUNICATIONS INFORMATION:
 REFERENCE/DOCKET NUMBER: 3044-20002.20
 TELEX: 706541 4940792
 INFORMATION FOR SEQ ID NO: 2:
 SOURCE: CHAT CHARACTERISTICS:
 SEQUENCE LENGTH: 444
 YRSI: amino acid
 TOFOGOY: linear
 MOLECULE TYPE: protein
 US-08-591-156-2

Query Match 94.6%; Score 561; Db 2; Length 149;
 Basic Locality 93.8%; Pctd. No. 1,8e+17;
 Matches 1053 Conservative 3; Mismatches 5; Indels 0; Gaps 0

QY 2 VLTGSSGSLSPYSIGQASISSTSGSSGSITNSHNTNLTLEWLFPGCSPPLLTYVNNRS 61
 DB 21 VHTDITLTLFGLTSLGQGISKGGSCGIVSHSNNTNLTEWLFPGCSPPLLTYVNNRS 80
 QY 62 GVDPFGSSSGSTPLFLASLSRNADLVGYVFCGSAHPVFGGDTLEIR 113
 DB 81 GVDPFRGSSSGSTPLFLASLSRNADLVGYVFCGSAHPVFGGDTLEIR 132

RESULT 8
 US-09-283-533-2
 Patent No. 6509016
 GENERAL INFORMATION:
 APPLICANT: Chatterjee, Malaya
 INVENTOR: Chatterjee, Malaya
 ADDRESS: Chatterjee, Sunil K.
 TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FORESTER
 STREET: 755 PAGE MILL ROAD
 CITY: PALO ALTO
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 CDROM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 16-JUN-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 0.253
 TELECOMMUNICATIONS INFORMATION:
 REFERENCE/DOCKET NUMBER: 3044-20002.20
 TELEX: 706541 4940792
 INFORMATION FOR SEQ ID NO: 2:
 SOURCE: CHAT CHARACTERISTICS:
 SEQUENCE LENGTH: 444
 YRSI: amino acid
 TOFOGOY: linear
 MOLECULE TYPE: protein
 US-08-591-156-2

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
INVENTOR: JAMES L. WATSON
ATTORNEY/AGENT INFORMATION:
NAME: SCHIFF, J. MICHAEL
REGISTRATION NUMBER: 40,233
PRACTICE ADDRESS: 10014-20002, 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEX: (415) 494-0792
INFORMATION FOR SEQ ID NO.: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE OF COMPOUND: protein
MOLECULE TYPE: protein

Query Match 94.6% Score 561, DB 4 Length 149,
Best Local Similarity 93.4% Pval 1e-47
Matches 105 Conservative 4 Mismatches 3 Indels 0 Gaps

Dy 62 CHRRPGSGGSGGGTAKSRNRSRGGYCCGCGHPTGCTCATATTTT 113
Dy 81 GVDFPSGSQGTFTLKSIRVARDLVYYCDSHPFPGCFKLETR 132

RESULT 9
US-08-752-844-66
Sequence 66, Application US/08/52844
GENERAL INFORMATION:
APPLICANT: Characterjee, Malaysia
APPLICANT: Foon, Kenneth A.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDING ADDRESS: ROBERTS
STREET 755 PAGE WILL RND
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZITE: 94304-1018
COMPUTER READABLE FORM:
MEDIA TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/752,844
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: Michael 423
REFERENCE/DOCKET INFORMATION: 30414-20002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEX: 706141 194-0792
INFORMATION FOR SEQ ID NO.: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 6018
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-752-844-66

Query Match Similarity 94.1%; Score 556; DB 2; Length 263;
Matches 104; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 IVYTSPLSLPVSAGQASISGSSGSIHNSNNTLWMLQKQSGPFLITYNSRS 61
DB 153 VLVNTPSLSLPVSAGQASISGSSGSIHNSNNTLWMLQKQSGPFLITYNSRS 212
QY 62 GVPEPSSSGSDTFLKISRPAEDGVYTCQSHVPTFGGKLEIK 112
DB 213 GVPEPSSSGSDTFLKISRPAEDGVYTCQSHVPTFGGKLEIK 263

RESULT 10
US-08-752-844-66
Sequence 66, Application US/0929353
Patent No. 6509016

GENERAL INFORMATION:
APPLICANT: Poon, Kenneth A, Malaysia
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORISON & FORESTER
STREET: 755 PEARL HILL ROAD
CITY: PEARL HILL ROAD
COUNTRY: USA
ZIP: 94304-1016

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA: Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/293,533
FILING DATE: 08/09/92
PRIORITY DATE: 08/09/92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
FILING DATE: INFORMATION:
NAME: SCHIE, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELEPHONE: (415) 494-0792
TELEFAX: (415) 494-0792

INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid
MOLECULE TYPE: protein

Query Match Similarity 94.1%; Score 556; DB 4; Length 263;
Matches 104; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 IVYTSPLSLPVSAGQASISGSSGSIHNSNNTLWMLQKQSGPFLITYNSRS 61
DB 153 VLVNTPSLSLPVSAGQASISGSSGSIHNSNNTLWMLQKQSGPFLITYNSRS 212
QY 62 GVPEPSSSGSDTFLKISRPAEDGVYTCQSHVPTFGGKLEIK 112
DB 213 GVPEPSSSGSDTFLKISRPAEDGVYTCQSHVPTFGGKLEIK 263

RESULT 11
US-08-752-844-15
Sequence 15, Application US/0912844
Patent No. 6315821

GENERAL INFORMATION:
APPLICANT: Chatterjee, Malay
APPLICANT: Poon, Kenneth A, Malaysia
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORISON & FORESTER
STREET: 755 PEARL HILL ROAD
CITY: PEARL HILL ROAD
COUNTRY: USA
ZIP: 94304-1016

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PEARLIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA: Release #1.0, Version #1.30
FILING DATE: 08/09/92
CLASSIFICATION: 423
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELEPHONE: (415) 494-0792
TELEFAX: (415) 494-0792

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
MOLECULE TYPE: peptide

Query Match Similarity 93.4%; Score 555; DB 2; Length 112;
Matches 104; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 IVYTSPLSLPVSAGQASISGSSGSIHNSNNTLWMLQKQSGPFLITYNSRS 61
DB 62 GVPEPSSSGSDTFLKISRPAEDGVYTCQSHVPTFGGKLEIK 112
QY 62 GVPEPSSSGSDTFLKISRPAEDGVYTCQSHVPTFGGKLEIK 112

US-08-591-196-15
Sequence 15, Application US/0859196
Patent No. 597316
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malay
APPLICANT: Poon, Kenneth A, Malaysia
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORISON & FORESTER
STREET: 755 PEARL HILL ROAD

CITY: PALO ALTO
STATE: CA
COUNTRY: USA
SERIAL: 9304-1018
COMPILED BY: JAMES R. ROHM,
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
VERSION: 5.04
CURRENT APPLICATION RELEASE #1.0, version #1.30
APPLICATION NUMBER: US/08/591.196
FILING DATE: 16-JAN-1996
CLASSIFICATION: 424
AUTHOR: JAMES R. ROHM
NAME: Schief, J. Michael
REGISTRAR NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.20
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ. ID NO. 15:
STRAND LENGTH: 112 amino acids
TYPE: amino acid
STRAND DENSITY: single
MOLECULE TYPE: linear
peptide
US-08-591-196-15

Query Match 93.64; Score 555; DB 2; Length 112;
Best Local Similarity 93.74; Prod No. 5e-47; 2; Indels 0; Gaps 0;
Matches 104; Conservative 5; Mismatches 2;

QY 2 IVTQSGPLSPVSGDAISGSSGSIYNSNGNTLWYLOKQSGPLLYKYSNRS 61
DB 2 VMTQPLSPVSGDAISGSSGSIYNSNGNTLWYLOKQSGPLLYKYSNRS 61
QY 62 GVDFKSSGSDTDFLTKISVBAEDGVYFCGSHVPTFGQKTLKLR 112
DB 62 GVDFKSSGSDTDFLTKISVBAEDGVYFCGSHVPTFGQKTLKLR 112

RESULT 13
US-09-293-533-15
Sequence 15, Application US/09293533
Patent No. 6509016
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Poon, Kenneth A.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF CANCER
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & ROESTER
P.O. BOX 145
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
COMPILED BY: JAMES R. ROHM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patent In Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293.533
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/752.844
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Schief, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ. ID NO. 15:
STRAND LENGTH: 112 amino acids
TYPE: amino acid
STRAND DENSITY: single
MOLECULE TYPE: linear
peptide
US-09-293-533-15

Query Match 93.64; Score 555; DB 4; Length 112;
Best Local Similarity 93.74; Prod No. 1.2e-46; 2; Indels 0; Gaps 0;
Matches 104; Conservative 5; Mismatches 2;

QY 2 IVTQSGPLSPVSGDAISGSSGSIYNSNGNTLWYLOKQSGPLLYKYSNRS 61
DB 2 VMTQPLSPVSGDAISGSSGSIYNSNGNTLWYLOKQSGPLLYKYSNRS 61
QY 62 GVDFKSSGSDTDFLTKISVBAEDGVYFCGSHVPTFGQKTLKLR 112
DB 62 GVDFKSSGSDTDFLTKISVBAEDGVYFCGSHVPTFGQKTLKLR 112

RESULT 14
US-09-192-945-4
Sequence 4, Application US/09192545
Patent No. 618044
GENERAL INFORMATION:
APPLICANT: Taya, Choji
APPLICANT: Yokokawa, Hiromichi
TITLE OF INVENTION: Anticanceric animal allergy models and methods for their use
CURRENT FILING DATE: 1998-11-13
CURRENT APPLICATION NUMBER: US/09/192.545
NUMBER OF SEQ. ID NOS.: 12
SOFTWARE: Patent In Ver. 2.0
SEQ. ID NO. 4
TYPE: peptide
FEATURE: Description of Artificial Sequence: Designed heavy
US-09-192-945-4

Query Match 93.64; Score 555; DB 3; Length 238;
Best Local Similarity 92.94; Prod No. 1.2e-46; 2; Indels 0; Gaps 0;
Matches 104; Conservative 5; Mismatches 2;

QY 2 IVTQSGPLSPVSGDAISGSSGSIYNSNGNTLWYLOKQSGPLLYKYSNRS 61
DB 2 VMTQPLSPVSGDAISGSSGSIYNSNGNTLWYLOKQSGPLLYKYSNRS 61
QY 62 GVDFKSSGSDTDFLTKISVBAEDGVYFCGSHVPTFGQKTLKLR 113
DB 81 GVDFKSSGSDTDFLTKISVBAEDGVYFCGSHVPTFGQKTLKLR 132

RESULT 15
US-08-331-3984-48
Sequence 48, Application US/083313984
Patent No. 6560013
GENERAL INFORMATION:
APPLICANT: Pastan, Ira

GenCore version 5.1.6
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OK protein - protein search using sw model

Run on: November 7, 2003, 07:21:19 Search time is 7937 Seconds

742,581 Million Cell updates/sec

Perfect score: 1 EVOLOSGGGLVKGSGSLK.....FTWYFVWGKGLVTVSA 122

Sequence: 1 EVOLOSGGGLVKGSGSLK.....FTWYFVWGKGLVTVSA 122

Scoring table: BLAST2

Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 9616882 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: 1: P121.*

2: P123.*

3: P123.*

4: P124.*

5: P124.*

6: P124.*

7: P124.*

8: P124.*

9: P124.*

10: P124.*

11: P124.*

12: P124.*

13: P124.*

14: P124.*

15: P124.*

16: P124.*

17: P124.*

18: P124.*

19: P124.*

20: P124.*

21: P124.*

22: P124.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	539.5	83.8	1122	IG heavy chain V x
2	518	80.4	826327	IG heavy chain V x
3	517.5	80.4	1117	IG heavy chain V x
4	514.5	79.9	855536	IG heavy chain V x
5	514.5	79.9	120	IG heavy chain V x
6	514.5	79.9	120	IG heavy chain V x
7	514.5	79.9	120	IG heavy chain V x
8	514.5	79.9	120	IG heavy chain V x
9	510.5	79.9	117	IG heavy chain V x
10	509	79.0	119	IG heavy chain V x
11	508.5	78.0	120	IG heavy chain V x
12	508.5	78.0	120	IG heavy chain V x
13	508.5	78.0	120	IG heavy chain V x
14	500.5	77.7	119	IG heavy chain V x
15	500.5	77.7	124	IG heavy chain V x
16	498	77.6	119	IG heavy chain V x
17	498	77.6	119	IG heavy chain V x
18	498	77.6	119	IG heavy chain V x
19	497	77.2	118	IG heavy chain V x
20	496	77.0	254	IG heavy chain V x
21	493	76.6	124	IG heavy chain V x
22	493	76.6	124	IG heavy chain V x
23	493	76.6	139	IG heavy chain V x
24	492.5	76.5	124	IG heavy chain V x
25	492.5	76.5	124	IG heavy chain V x
26	487	75.8	124	IG heavy chain V x
27	486	75.5	123	IG heavy chain V x
28	485.5	75.4	152	IG heavy chain V x
29	484.5	75.2	119	IG heavy chain V x

ALIGNMENTS

30	484	75.2	121	IG heavy chain V x
31	483.5	75.1	111	IG heavy chain V x
32	483	75.0	122	IG heavy chain V x
33	483	75.0	122	IG heavy chain V x
34	482	74.8	121	IG heavy chain V x
35	480.5	74.6	108	IG heavy chain V x
36	480.5	74.6	124	IG heavy chain V x
37	479.5	74.5	124	IG heavy chain V x
38	479.5	74.5	124	IG heavy chain V x
39	477.5	74.1	142	IG heavy chain V x
40	477	74.1	108	IG heavy chain V x
41	477	74.1	112	IG heavy chain V x
42	477	74.1	112	IG heavy chain V x
43	473.5	73.4	106	IG heavy chain V x
44	472.5	73.4	111	IG heavy chain V x
45	472.5	73.4	119	IG heavy chain V x

RESULT 1
E27888
IG heavy chain V region (H35-06) - mouse
C/Spectrum: Mus musculus (house mouse)
C/Accession: E27888
C/Comment: This sequence was determined from a hybridoma protein that binds influenza A virus hemagglutinin (HA) protein.
BIRD V. 5, 1577-1587, 1986
Article: Structural and functional implications of a restricted antibody response to influenza A virus hemagglutinin (HA) protein.
A/Accession: E27888
A/Molecule type: DNA
A/Residues: 1-122 <CDT>
A/Length: 122
A/Score: 539.5; DB 2; Length 122;
Best Local Similarity: 83.8%; Pred. No. 6,56-41;
Matches: 105; Conservative: 10; Indels: 1; Gaps: 1;
Query Match: 83.8%; Pred. No. 539.5; DB 2; Length 122;
Best Local Similarity: 86.1%; Pred. No. 6,56-41;
Matches: 105; Conservative: 10; Indels: 1; Gaps: 1;
1 EVOLOSGGGLVKGSGSLKCAAGFTFSSTNSVWVOTPERKLAWNTSSGGSTTY 60
1 DVALVSGGGLVKGSGSLKCAAGFTFSSTNSVWVOTPERKLAWNTSSGGSTTY 60
61 PSVQVGRFTSDNANTVLYQSSLSASDITMCYCRGGGFTWVWV FVWKGGLVTV 119
62 PSVQVGRFTSDNANTVLYQSSLSASDITMCYCRGGGFTWVWV FVWKGGLVTV 119
63 PSVQVGRFTSDNANTVLYQSSLSASDITMCYCRGGGFTWVWV FVWKGGLVTV 120
120 VS 121
121 VS 122
RESULT 2
E26327
IG heavy chain V region - mouse (fragment)
C/Spectrum: Mus musculus (house mouse)
C/Accession: E26327
C/Comment: This sequence was determined from a hybridoma protein that binds influenza A virus hemagglutinin (HA) protein.
BIRD V. 5, 1577-1587, 1986
Article: Structural and functional implications of a restricted antibody response to influenza A virus hemagglutinin (HA) protein.
A/Accession: E26327
A/Molecule type: DNA
A/Residues: 1-122 <CDT>
A/Length: 122
A/Score: 539.5; DB 2; Length 122;
Best Local Similarity: 83.8%; Pred. No. 6,56-41;
Matches: 105; Conservative: 10; Indels: 1; Gaps: 1;
Query Match: 83.8%; Pred. No. 539.5; DB 2; Length 122;
Best Local Similarity: 86.1%; Pred. No. 6,56-41;
Matches: 105; Conservative: 10; Indels: 1; Gaps: 1;
1 EVOLOSGGGLVKGSGSLKCAAGFTFSSTNSVWVOTPERKLAWNTSSGGSTTY 60
1 DVALVSGGGLVKGSGSLKCAAGFTFSSTNSVWVOTPERKLAWNTSSGGSTTY 60
61 PSVQVGRFTSDNANTVLYQSSLSASDITMCYCRGGGFTWVWV FVWKGGLVTV 119
62 PSVQVGRFTSDNANTVLYQSSLSASDITMCYCRGGGFTWVWV FVWKGGLVTV 119
63 PSVQVGRFTSDNANTVLYQSSLSASDITMCYCRGGGFTWVWV FVWKGGLVTV 120
120 VS 121
121 VS 122

Query Match 79.9%; Score 514.5; DB 2; Length 120;
 Best Local Similarity 85.1%; Pred. No. 16-38; Indels 1; Gaps 1;
 Matches 103; Conservative 3; Mismatches 14; Indels 1; Gaps 1;
 QY 2 VOLDSGGGLVVGSGSKIKSCAGSFFSTSTNVRQTPKRLKLVNATISGGSSSTY 61
 1 VOLDSGGGLVVGSGSKIKSCAGSFFSTSTNVRQTPKRLKLVNATISGGSSSTY 60
 QY 62 DSVKGFPSRDNAKNTLYLQNSLSASDPTATYVCSRGSGFTWVPDWAAGTLVY 121
 1 DSVKGFPSRDNAKNTLYLQNSLSASDPTATYVCSRGSGFTWVPDWAAGTLVY 121
 Db 61 DSVKGFPSRDNAKNTLYLQNSLSASDPTATYVCSRGSGFTWVPDWAAGTLVY 119
 QY 122 A 122
 Db 120 S 120

RESULT 7

809258

Ig heavy chain V region precursor - mouse (Eregment)

C/D/Ref: 23-Jan-1993 #sequence_revision 39-Jan-1993 #ext_change 23-Jul-1999

C/Accession: 809258

R/Hamada, H.; Meszara, K.; Tsuru, T.

Nucleic Acids Res. 18, 1990

A/Reference number: 809258; MIMD:90245594; PMID:2110659

A/Accession: 809258

A/Molecule type: DNA

A/Residues: 1-122 <CNR>

A/Sequence references: DBM:K51719; NID:953207; FIDM:CM45012.1; PID:9537545

A/Genetics:

A/Introns: 16/1

A/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Superfamily: Anticretetamer; immunoglobulin

F/34-117/Region: immunoglobulin homology <IMV>

Query Match

79.9%; Score 514.5; DB 2; Length 138;

Best Local Similarity 83.4%; Pred. No. 1-26-38;

Matches 102; Conservative 4; Mismatches 13; Indels 3; Gaps 1;

QY 1 EVOLDSGGGLVVGSGSKIKSCAGSFFSTSTNVRQTPKRLKLVNATISGGSSSTY 60

Db 20 EVLDSGGGLVVGSGSKIKSCAGSFFSTSTNVRQTPKRLKLVNATISGGSSSTY 79

QY 61 PSYKGFPSRDNAKNTLYLQNSLSASDPTATYVCSRGSGFTWVPDWAAGTLVY 120

Db 60 PSYKGFPSRDNAKNTLYLQNSLSASDPTATYVCSRGSGFTWVPDWAAGTLVY 136

QY 121 SA 122

Db 137 SA 138

RESULT 8

D27889

Ig heavy chain V region (H37-45) - mouse

C/Superfamily: Mus musculis (house mouse)

C/D/Ref: 15-Dec-1988 #sequence_revision 15-Dec-1988 #ext_change 16-Aug-1996

C/Accession: D27889

R/Catton, A.J.; Brownlee, G.G.; Straub, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A/Title: Structural and functional implications of a restricted antibody response to a

A/Reference number: A10143; MIMD:86306589; PMID:2427335

A/Accession: D27889

A/Molecule type: DNA

A/Residues: 1-121 <CNR>

A/Experimental source: strain Balb/c

A/Comment: This chain was isolated from the germline gene

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/KeyWords: heterocretetamer; immunoglobulin

F/15-98/Region: immunoglobulin homology <IMV>

Query Match 79.9%; Score 514.5; DB 2; Length 121;
 Best Local Similarity 83.4%; Pred. No. 26-38;
 Matches 101; Conservative 3; Mismatches 17; Indels 0; Gaps 0;
 QY 2 VOLDSGGGLVVGSGSKIKSCAGSFFSTSTNVRQTPKRLKLVNATISGGSSSTY 60
 1 VOLDSGGGLVVGSGSKIKSCAGSFFSTSTNVRQTPKRLKLVNATISGGSSSTY 60
 QY 61 PSYKGFPSRDNAKNTLYLQNSLSASDPTATYVCSRGSGFTWVPDWAAGTLVY 120
 1 PSYKGFPSRDNAKNTLYLQNSLSASDPTATYVCSRGSGFTWVPDWAAGTLVY 120
 Db 61 PSYKGFPSRDNAKNTLYLQNSLSASDPTATYVCSRGSGFTWVPDWAAGTLVY 120
 QY 121 S 121
 Db 121 S 121

RESULT 9

809258

Ig heavy chain V region (anti-DNA, clones 2B5VH, 6B8VH, and 3G9VH) - mouse (frag

C/Superfamily: Mus musculis (house mouse)

C/D/Ref: 16-Sep-1992 #sequence_revision 16-Sep-1992 #ext_change 16-Aug-1996

C/Accession: F10251; F10251; M.; Shun, H.; Radic, M. Z.; Plateraky, D.; Warshawski

J. Exp. Med. 171, 265-297, 1990

A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and

A/Reference number: F10251; MIMD:90111618; PMID:2104919

A/Accession: F10251

A/Molecule type: mRNA

A/Residues: 1-117 <SHL>

A/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Superfamily: Anticretetamer; immunoglobulin

F/15-98/Region: immunoglobulin homology <IMV>

F/31-35/Region: complementarity-determining 1

F/36-49/Region: framework 2; fixy-determining 2

F/57-58/Region: framework 3

F/59-108/Region: complementarity-determining 3

F/109-117/Region: framework 4

Query Match

79.3%; Score 510.5; DB 2; Length 117;

Best Local Similarity 82.5%; Pred. No. 2-16-38;

Matches 99; Conservative 5; Mismatches 13; Indels 3; Gaps 1;

QY 1 EVOLDSGGGLVVGSGSKIKSCAGSFFSTSTNVRQTPKRLKLVNATISGGSSSTY 60

Db 1 EVLDSGGGLVVGSGSKIKSCAGSFFSTSTNVRQTPKRLKLVNATISGGSSSTY 60

QY 61 PSYKGFPSRDNAKNTLYLQNSLSASDPTATYVCSRGSGFTWVPDWAAGTLVY 120

Db 61 PSYKGFPSRDNAKNTLYLQNSLSASDPTATYVCSRGSGFTWVPDWAAGTLVY 117

RESULT 10

D27889

Ig heavy chain V region (H36-2) - mouse

C/Superfamily: Mus musculis (house mouse)

C/D/Ref: 15-Dec-1988 #sequence_revision 15-Dec-1988 #ext_change 16-Aug-1996

C/Accession: D27889

R/Catton, A.J.; Brownlee, G.G.; Straub, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A/Title: Structural and functional implications of a restricted antibody response

A/Reference number: A10143; MIMD:86306589; PMID:2427335

A/Accession: D27889

A/Molecule type: DNA

A/Residues: 1-119 <CNR>

A/Experimental source: strain Balb/c

A/Comment: This chain was isolated from a hybridoma protein that binds influenza

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keyword: heterocercer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <RMS>

Query Match 79.0%; Score 509; DB 2; Length 119;

Best Local Similarity 81.8%; Pred. No. 3.1e-38;

Matches 99; Conservative 7; Mismatches 15; Indels 2; Gaps 1;

```
QY      1 EVQLDSGGGVYGGGSLKSCAGSPTSSSYTMSVWQTPKRLKLVATISGGSSSTYY 60
      1 EVQLDSGGGVYGGGSLKSCAGSPTSSSYTMSVWQTPKRLKLVATISGGSSSTYY 60
QY      61 PSYVGERFTSRDANKATLYLQMSLSSEDTMYCTREGGGFTVWYGPVWAGQGLTVY 120
      61 PSYVGERFTSRDANKATLYLQMSLSSEDTMYCTREGGGFTVWYGPVWAGQGLTVY 120
Db      61 SPYVGERFTSRDANKATLYLQMSLSSEDTMYCTREGGGFTVWAGQGLTVY 118
      61 SPYVGERFTSRDANKATLYLQMSLSSEDTMYCTREGGGFTVWAGQGLTVY 118
QY      121 S 121
      119 S 119
Db
```

RESULT 11

IG heavy chain V region P024 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 Sequence revision 03-Nov-1995 %text_change 23-Jul-1999

A/Accession: S55539

R/Boatger: V.; Boatger: A.; Lane, E.B.; Spruce, B.A.

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keyword: heterocercer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <RMS>

Query Match 79.9%; Score 509; DB 2; Length 121;

Best Local Similarity 81.8%; Pred. No. 3.9e-38;

Matches 99; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

```
QY      1 EVQLDSGGGVYGGGSLKSCAGSPTSSSYTMSVWQTPKRLKLVATISGGSSSTYY 60
      1 EVQLDSGGGVYGGGSLKSCAGSPTSSSYTMSVWQTPKRLKLVATISGGSSSTYY 60
QY      61 PSYVGERFTSRDANKATLYLQMSLSSEDTMYCTREGGGFTVWYGPVWAGQGLTVY 120
      61 PSYVGERFTSRDANKATLYLQMSLSSEDTMYCTREGGGFTVWYGPVWAGQGLTVY 120
Db      61 SPYVGERFTSRDANKATLYLQMSLSSEDTMYCTREGGGFTVWAGQGLTVY 120
      61 SPYVGERFTSRDANKATLYLQMSLSSEDTMYCTREGGGFTVWAGQGLTVY 120
QY      121 S 121
      121 S 121
Db
```

RESULT 13

IG heavy chain V region P022 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 Sequence revision 03-Nov-1995 %text_change 23-Jul-1999

A/Accession: S55539

R/Boatger: V.; Boatger: A.; Lane, E.B.; Spruce, B.A.

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

A/Reference number: 555528; MIMD:95239763; PMID:7536850

A/Accession: S55538

C/Superfamily: immunoglobulin V region; immunoglobulin homology

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 8.79573 Seconds

US-09-661-992b-86_COPY_1_122
652,278 Million call updates/sec

Title: 1 EYUQJESGGALYKRGSLK.....FTWVWYPDWMAKATLYA 122

Perfect score: 644

Sequence: 1 EYUQJESGGALYKRGSLK.....FTWVWYPDWMAKATLYA 122

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Minimum Match 100%

Listing first 45 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SDRAMS

Result No.	Score	Match	Query Length	DB ID	Description
1	469	72.6	117	1 HV55_MOUSE	P18526 mus musculus
2	464	72.0	117	1 HV55_MOUSE	P18525 mus musculus
3	462	71.7	98	1 HV55_MOUSE	P18528 mus musculus
4	460.5	70.3	117	1 HV55_MOUSE	P18529 mus musculus
5	441	68.5	136	1 HV42_MOUSE	P01783 mus musculus
6	433	67.2	117	1 HV55_MOUSE	P18524 mus musculus
7	436	68.1	117	1 HV55_MOUSE	P18525 mus musculus
8	436	68.1	117	1 HV55_MOUSE	P18526 mus musculus
9	417	64.8	122	1 HV33_HUMAN	P01764 mus musculus
10	417	64.8	122	1 HV33_HUMAN	P01765 mus musculus
11	416	64.6	119	1 HV38_MOUSE	P01808 mus musculus
12	413	64.1	114	1 HV32_MOUSE	P01783 mus musculus
13	413	64.1	114	1 HV32_MOUSE	P01784 mus musculus
14	409.5	63.6	121	1 HV33_HUMAN	P01764 mus musculus
15	404.5	62.8	115	1 HV32_MOUSE	P01801 mus musculus
16	404	62.7	116	1 HV32_MOUSE	P01781 mus musculus
17	402.4	62.4	122	1 HV32_MOUSE	P01764 mus musculus
18	402	62.4	126	1 HV32_MOUSE	P01765 mus musculus
19	402	62.4	126	1 HV32_MOUSE	P01766 mus musculus
20	401.5	62.3	123	1 HV19_MOUSE	P01788 mus musculus
21	401.5	62.3	117	1 HV02_CANPA	P01788 mus musculus
22	401.5	62.3	117	1 HV02_CANPA	P01789 mus musculus
23	400.5	62.2	123	1 HV23_MOUSE	P01765 mus musculus
24	399.5	62.0	115	1 HV33_HUMAN	P01765 mus musculus
25	398.5	61.9	120	1 HV32_MOUSE	P01766 mus musculus
26	398.5	61.9	120	1 HV32_MOUSE	P01767 mus musculus
27	397.5	61.7	123	1 HV23_MOUSE	P01765 mus musculus
28	397.5	61.7	123	1 HV23_MOUSE	P01766 mus musculus
29	397.5	61.7	144	1 HV26_MOUSE	P01795 mus musculus
30	397.5	61.7	144	1 HV26_MOUSE	P01796 mus musculus
31	396.5	61.6	116	1 HV33_HUMAN	P01802 mus musculus
32	396.5	61.6	116	1 HV33_HUMAN	P01803 mus musculus
33	394.5	61.3	113	1 HV27_MOUSE	P01796 mus musculus

34	394.5	61.3	113	1 HV30_MOUSE	P01799 mus musculus
35	393	61.0	113	1 HV37_MOUSE	P01807 mus musculus
36	391.5	60.8	115	1 HV37_MOUSE	P01808 mus musculus
37	391.5	60.8	115	1 HV37_MOUSE	P01809 mus musculus
38	390.5	60.6	111	1 HV35_MOUSE	P01804 mus musculus
39	390	60.5	119	1 HV33_HUMAN	P01775 mus musculus
40	389.5	60.5	119	1 HV31_HUMAN	P01776 mus musculus
41	388.5	60.4	122	1 HV38_MOUSE	P01770 mus musculus
42	388.5	60.4	122	1 HV38_MOUSE	P01771 mus musculus
43	388	60.2	120	1 HV31_HUMAN	P01782 mus musculus
44	386	59.9	123	1 HV02_CANPA	P01784 mus musculus
45	385.5	59.9	123	1 HV21_MOUSE	P01794 mus musculus

ALIGNMENTS

RESULT 1	STANDARD:	PRT: 117 AA.
ID HV55_MOUSE		
RC P18526	12902 NM; 493808427ACAG39A CAC64;	
DT 01-NOV-1999 (Ref. 16, Created)		
DT 01-NOV-1999 (Ref. 16, Last sequence update)		
DT 15-JUL-1999 (Ref. 38, Last annotation update)		
DE 15 heavy chain V region 345 precursor.		
OC Burykova; Metcalf; Chordata; Chelonia; Vertebrata; Eucleostomi;		
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
NCBI_TextID:109090;		
EN SOURCE FROM N.A.		
RC STRAIN:Balb/cJ.		
MD MEDLINE=9279149; PubMed=249654;		
FA Levy N.S., Malipiero U.V., Deleque S.C., Georharc P.J.		
KT the primary immune response." in Immunoglobulin Vh genes during		
RL J. Exp. Med. 169:2007-2013(1989).		
CC -1- MISC:LANEUS: THIS SEQUENCE BELONGS TO THE VH1783 SUBFAMILY.		
DR HV55_MOUSE		
DR HV55_MOUSE		
DR InterPro: IP0007110; IG-1Lk.		
DR InterPro: IP0003066; IG-MC.		
DR InterPro: IP0003596; IG-V.		
DR SMART: SM00406; IgV_1.		
DR PROSITE: PS00845; IG_Like_1.		
KW Immunoglobulin V region, Signal.		
FT CHAIN 20 117		
FT DOMAIN 20 49		
FT DOMAIN 50 54		
FT DOMAIN 55 68		
FT DOMAIN 86 117		
FT DISULFID 41 115		
FT NON_TER 117		
SQ SEQUENCE 117 AA; 12902 NM; 493808427ACAG39A CAC64;		
Query Match 72.8%; Score 469; DB 1; Length 117;		
Beet Local Similarity 91.8%; Pred. No. 1.1e+00;		
Matches 90; Conservative 2; Mismatches 6; Indels 0; Gaps 0.		
1 EYUQJESGGALYKRGSLKCAAGFTSTSTSMVQTPRKLELVNATISGGSSSTLY 60		
20 EYUQJESGGALYKRGSLKCAAGFTSTSTSMVQTPRKLELVNATISGGSSSTLY 79		
60 PQTVAKSTTSDNNTATLYKQSSLSFSTQVTCYR 98		
60 PQTVAKSTTSDNNTATLYKQSSLSFSTQVTCYR 117		
RESULT 2		
HV54_MOUSE		

[illegible]

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RESULT 5
HVS3 MOUSE
ID HVS3 MOUSE STANDARD; PRT: 117 AA.
AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
DR 01-NOV-1990 (Rel. 16, Last sequence update)
DB Ig heavy chain V region 5-76 precursor
OS Mus musculus (Mouse)
CC Bzikoyets; Melazoni; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID:10090;
CC [1]
CC SEQUENCE FROM N.A.
RC STRAIN=BAH/CJ19; PubMed:249654;
RA Levy N.S., Malpasro U.V., Lepecque S.G., Gearhart P.J.;
RA "Early onset of somatic mutation in immunoglobulin Vn genes during
the primary immune response (1989)."
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH/183 SUPERFAMILY.
DR PIR: J05056; HYMS57.
DR HBSF; P01810; REF.
DR Interpro; IPR00306; 1G.MC.
DR Interpro; IPR003596; 1G.V.
DR Pfam; PF00047; 1g.1.
DR PROSITE; PS50835; 1G.LIKE; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 45 117
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12991 MW, 934047827888820 CMO64;
Query Match
Beat Local Similarity 70.3%; Score 453; DB 1; Length 117;
Matches 87; Conservative 1; Mismatches 10; Indels 0; Gaps 0;
Db 1 EHYOJSSGGLVFGGSLKACAGCTGTSYMWVQYPERKRLVMTTSSGGSTYY 60
Oy 20 EYHVLHSGGLVFGGSLKACAGCTGTSYMWVQYPERKRLVMTTSSGGSTYY 79
Db 61 PSYKQRTTSSDQNTLYLQMSLASEDTNATYCA 98
Oy 80 PSYKQRTTSSDQNTLYLQMSLASEDTNATYCA 117

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RESULT 6
HVS3 MOUSE
ID HVS3 MOUSE STANDARD; PRT: 136 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DR 01-NOV-1990 (Rel. 16, Last sequence update)
DB Ig heavy chain V region MOPC 21 precursor (fragment).
OS Mus musculus (Mouse)
CC Bzikoyets; Melazoni; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID:10090;
CC [1]
CC SEQUENCE FROM N.A.
RC STRAIN=BAH/CJ19; PubMed:6789376;
RA Botchwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;

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```

RESULT 7
HVS3 MOUSE
ID HVS3 MOUSE STANDARD; PRT: 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DR 01-NOV-1990 (Rel. 16, Last sequence update)
DB Ig heavy chain V region MOPC 21 precursor.
OS Mus musculus (Mouse)
CC Bzikoyets; Melazoni; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID:10090;
CC [1]
CC SEQUENCE FROM N.A.
RC STRAIN=BAH/CJ19; PubMed:6789376;
RA Botchwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;

```

```

RESULT 8
HVS3 MOUSE
ID HVS3 MOUSE STANDARD; PRT: 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DR 01-NOV-1990 (Rel. 16, Last sequence update)
DB Ig heavy chain V region MOPC 21 precursor.
OS Mus musculus (Mouse)
CC Bzikoyets; Melazoni; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID:10090;
CC [1]
CC SEQUENCE FROM N.A.
RC STRAIN=BAH/CJ19; PubMed:6789376;
RA Botchwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;

```

EX MEDLINE:89273139; PubMed:249654;
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin V α genes during
 RT the primary immune response." 1991.
 CC 1- MISCELLANEOUS THIS SEQUENCE BELONGS TO THE VH118 SUPERFAMILY.
 DR PIR: J05053; HMMER.
 DR HSPF: P01810; SPSS.
 DR Interpro: IPR001065; 1g-118e.
 DR Interpro: IPR003596; 1g-118e.
 DR Interpro: IPR003596; 1g-118e.
 DR Pfam: PF00047; 1g1.1.
 DR SMART: SM0046; 1gV.1.
 KM Immunoglobulin V region; hybridoma; signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117
 FT NON TER 117 117
 SEQUENCE 117 AA; 12866 MW; 2CE3295F390F7258 CRC64;
 Query Match 67.2%; Score 433; DB 1; Length 117;
 Beat Local Similarity 85.7%; Pred. No. 5e-37;
 Matches 84; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 Oy 1 EVYGLSSGGVGLVGGSLKSGASGFTSSYTWVQTPFKGLGVAVATISGSGSTTY 60
 Db 20 DYVGLSSGGVGLVGGSLKSGASGFTSSYTWVQTPFKGLGVAVATISGSGSTTY 79
 DB 60 PTVKGRFTISNDANNTLYQMSLSSEDTALTYCA 117
 RESULT 9
 HVS5 MOUSE STANDARD; PRT: 117 AA.
 AC P18530; 1990 (Rel. 15; Created)
 DT 01-NOV-1990 (Rel. 15; Last sequence update)
 DT 15-JUL-1999 (Rel. 38; Last annotation update)
 DE Ig heavy chain V region 7-39 precursor.
 OS Mus musculus (Mouse)
 CC Mammalia; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_Taxid:10090;
 SN 111
 SN SOURCE FROM N.A.
 SN REF: 18530; 1990;
 RX MEDLINE:89279149; PubMed:249654;
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin V α genes during
 RT the primary immune response." 1991.
 CC 1- MISCELLANEOUS THIS SEQUENCE BELONGS TO THE VH118 SUPERFAMILY.
 DR PIR: J05053; HMMER.
 DR Interpro: IPR001065; 1g-118e.
 DR Interpro: IPR003596; 1g-118e.
 DR Interpro: IPR003596; 1g-118e.
 DR Pfam: PF00047; 1g1.1.
 DR SMART: SM0046; 1gV.1.
 KM Immunoglobulin V region; signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 Matches 79; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DISUFED 117 117 BY SIMILARITY.
 SEQUENCE 117 AA; 12992 MW; DSCA415D0F7774F CRC64;
 Query Match 66.1%; Score 426; DB 1; Length 117;
 Beat Local Similarity 85.7%; Pred. No. 1e-31;
 Matches 82; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 Oy 1 EVYGLSSGGVGLVGGSLKSGASGFTSSYTWVQTPFKGLGVAVATISGSGSTTY 60
 Db 20 DYVGLSSGGVGLVGGSLKSGASGFTSSYTWVQTPFKGLGVAVATISGSGSTTY 79
 DB 60 PTVKGRFTISNDANNTLYQMSLSSEDTALTYCA 117
 RESULT 9
 HVS5 HUMAN STANDARD; PRT: 117 AA.
 AC P01764;
 DT 21-JUL-1986 (Rel. 01; Created)
 DT 21-JUL-1986 (Rel. 01; Last sequence update)
 DT 15-JUL-1999 (Rel. 38; Last annotation update)
 DE Ig heavy chain V-II region 7-39 precursor.
 OS Homo sapiens (Human)
 CC Mammalia; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteleostomi; Primates; Catarrhini; Hominoidea; Homo.
 CC NCBI_Taxid:9606;
 SN 111
 SN SOURCE FROM N.A.
 RX MEDLINE:8110090; PubMed:6450418;
 RA Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Structure and multiplicity of genes for the human immunoglobulin
 RT heavy chain variable region." 1980.
 CC Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@ebi.ac.uk).
 DR EMBL: 000265; AAAS5516.1; -
 DR EMBL: M35415; AAAS8735.1; -
 DR PIR: A02047; HHR28.
 DR RefSeq: NM_000576; IGHW.
 DR Genbank: J05053; 1990;
 DR GO: GO:000576; C:cytocalculation; NAS.
 DR GO: GO:000823; P:antigen binding activity; NAS.
 DR UniProt: P01810; 1990; Immune response; NAS.
 DR Interpro: IPR003596; 1g-118e.
 DR Interpro: IPR003596; 1g-118e.
 DR Pfam: PF00047; 1g1.1.
 DR PROSITE: PS00835; 1g-118e.
 KM Immunoglobulin V region; signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH2.
 FT DOMAIN 20 117
 FT NON TER 117 117
 SEQUENCE 117 AA; E2826731FAC30F1 CRC64;
 Query Match 65.1%; Score 419; DB 1; Length 117;
 Beat Local Similarity 60.6%; Pred. No. 1.3e-35;
 Matches 79; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 40.323 seconds

782,516 Million cell updates/sec

US-09-661-992b-86_COPY_1_122

Sequence: 1 EVQVSGSGGLVPSGSLK.....FTVWVWDVWAGLVTVSIA 122

Scoring table: BLOSUM62

Gap: 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: sp.acetab.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.mammalia.*
6: sp.mammal.*
7: sp.mbc.*
8: sp.organelle.*
9: sp.plant.*
10: sp.porcine.*
11: sp.virus.*
12: sp.virus.*
13: sp.virus.*
14: sp.unclassified.*
15: sp.virus.*
16: sp.bacteriap.*
17: sp.archae.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	521	80.9	497	11	Q99KX4
2	515	80.0	119	11	Q92087
3	495	75.6	471	11	Q92087
4	487	75.6	471	11	Q92087
5	482.5	74.9	480	11	Q91XK1
6	466.5	72.4	486	11	Q91207
7	455.5	70.7	477	11	Q96B95
8	455.5	70.7	477	11	Q96B95
9	450	69.9	427	11	Q98J44
10	443.5	68.9	431	11	Q98J44
11	442	68.6	431	11	Q98J44
12	442	68.6	431	11	Q98J44
13	439.5	68.2	436	11	Q98J44
14	438	68.0	573	4	Q98J44
15	437.5	67.9	499	4	Q98J44
16	436	67.7	494	4	Q98J44

17	434.5	67.5	113	4	Q98J44
18	432	67.1	147	4	Q98J44
19	430	66.8	112	4	Q98J44
20	417	64.1	112	4	Q98J44
21	417	64.1	112	4	Q98J44
22	410.5	63.7	493	4	Q98J44
23	405	62.9	95	4	Q98J44
24	390.5	60.6	111	4	Q98J44
25	390.5	60.6	111	4	Q98J44
26	381	59.2	298	11	Q98J44
27	380.5	59.1	521	4	Q98J44
28	369	57.3	484	11	Q98J44
29	369	57.3	484	11	Q98J44
30	355.5	54.9	168	11	Q98J44
31	350	54.3	145	11	Q98J44
32	344.5	53.5	473	11	Q98J44
33	344.5	53.5	473	11	Q98J44
34	343.5	53.3	144	11	Q98J44
35	341.5	53.0	104	4	Q98J44
36	339	52.6	124	6	Q98J44
37	337	52.3	124	6	Q98J44
38	337	52.3	124	6	Q98J44
39	336	52.2	278	11	Q98J44
40	335.5	52.1	112	4	Q98J44
41	334	51.9	119	4	Q98J44
42	332	51.5	143	11	Q98J44
43	327	50.8	117	11	Q98J44
44	326.5	50.7	147	11	Q98J44
45	326.5	50.7	147	11	Q98J44

ALIGNMENTS

1	Q99KX4	PRELIMINARY	PTI; 487 AA.
2	Q99KX4	PRELIMINARY	PTI; 487 AA.
3	Q99KX4	PRELIMINARY	PTI; 487 AA.
4	Q99KX4	PRELIMINARY	PTI; 487 AA.
5	Q99KX4	PRELIMINARY	PTI; 487 AA.
6	Q99KX4	PRELIMINARY	PTI; 487 AA.
7	Q99KX4	PRELIMINARY	PTI; 487 AA.
8	Q99KX4	PRELIMINARY	PTI; 487 AA.
9	Q99KX4	PRELIMINARY	PTI; 487 AA.
10	Q99KX4	PRELIMINARY	PTI; 487 AA.
11	Q99KX4	PRELIMINARY	PTI; 487 AA.
12	Q99KX4	PRELIMINARY	PTI; 487 AA.
13	Q99KX4	PRELIMINARY	PTI; 487 AA.
14	Q99KX4	PRELIMINARY	PTI; 487 AA.
15	Q99KX4	PRELIMINARY	PTI; 487 AA.
16	Q99KX4	PRELIMINARY	PTI; 487 AA.
17	Q99KX4	PRELIMINARY	PTI; 487 AA.
18	Q99KX4	PRELIMINARY	PTI; 487 AA.
19	Q99KX4	PRELIMINARY	PTI; 487 AA.
20	Q99KX4	PRELIMINARY	PTI; 487 AA.
21	Q99KX4	PRELIMINARY	PTI; 487 AA.
22	Q99KX4	PRELIMINARY	PTI; 487 AA.
23	Q99KX4	PRELIMINARY	PTI; 487 AA.
24	Q99KX4	PRELIMINARY	PTI; 487 AA.
25	Q99KX4	PRELIMINARY	PTI; 487 AA.
26	Q99KX4	PRELIMINARY	PTI; 487 AA.
27	Q99KX4	PRELIMINARY	PTI; 487 AA.
28	Q99KX4	PRELIMINARY	PTI; 487 AA.
29	Q99KX4	PRELIMINARY	PTI; 487 AA.
30	Q99KX4	PRELIMINARY	PTI; 487 AA.
31	Q99KX4	PRELIMINARY	PTI; 487 AA.
32	Q99KX4	PRELIMINARY	PTI; 487 AA.
33	Q99KX4	PRELIMINARY	PTI; 487 AA.
34	Q99KX4	PRELIMINARY	PTI; 487 AA.
35	Q99KX4	PRELIMINARY	PTI; 487 AA.
36	Q99KX4	PRELIMINARY	PTI; 487 AA.
37	Q99KX4	PRELIMINARY	PTI; 487 AA.
38	Q99KX4	PRELIMINARY	PTI; 487 AA.
39	Q99KX4	PRELIMINARY	PTI; 487 AA.
40	Q99KX4	PRELIMINARY	PTI; 487 AA.
41	Q99KX4	PRELIMINARY	PTI; 487 AA.
42	Q99KX4	PRELIMINARY	PTI; 487 AA.
43	Q99KX4	PRELIMINARY	PTI; 487 AA.
44	Q99KX4	PRELIMINARY	PTI; 487 AA.
45	Q99KX4	PRELIMINARY	PTI; 487 AA.


```

AC 091261;
DT 01-DEC-2001 (TRENBERG, 19, Created)
DB 01-DEC-2001 (TRENBERG, 19, Last sequence update)
DR 01-DEC-2001 (TRENBERG, 19, Last sequence update)
DS Unknown (protein for IMAGE:4224494) (fragment, date)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxId:10090;
RN 1;
RP SEQUENCE FROM N.A.
RC SEQUENCE:
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; Acc107938; AB010798.1; -.
DR InterPro; IPR007110; 19-like.
DR InterPro; IPR003596; 19_v.
DR Pfam; PF00047; 19; 4; 19_v.
DR SMART; SM00406; 19v; 1; 19v; 4.
DR PROSITE; PS00290; 19-MHC; 2.
FT NON TER
SQ
SEQUENCE 480 AA; 51936 MW; 2089234EER2B41ED CIRC64;

Query Match
Best Local Similarity 74.9%; Score 482.5; DB 11; Length 480;
Beat Local Similarity 76.2%; Pred. No. 5.3e-41;
Matches 93; Conservative 14; Mismatches 10; Indels 5; Gaps 2;

CY 1 EVOLESGGGLVPGGSLKCSGASGFTFSYTWGNTQTRERLEMAVATISGGSGSTTY 60
DB 19 DVKLVSGGGLVPGGSLKCSGASGFTFSYTWGNTQTRERLEMAVATISGGSGSTTY 78
CY 61 PSYKGFRTSRNNKNTLYLONSLSBEDTNYCTCTRGSGFTWNTYDVGACTLVY 120
DB 79 PSWKGFRTSRNNKNTLYLONSLSBEDTNYCTCTRGSGFTWNTYDVGACTLVY 133
CY 121 SA 122
DB 134 SS 135

RESULT 6
Query Match
Best Local Similarity 70.7%; Score 455.5; DB 4; Length 597;
Beat Local Similarity 68.0%; Pred. No. 4e-38;
Matches 66; Conservative 16; Mismatches 18; Indels 3; Gaps 1;

ID 091207; PRELIMINARY; PRT; 486 AA.
AC 091207; 2001 (TRENBERG, 19, Created)
DT 01-DEC-2001 (TRENBERG, 19, Last sequence update)
DR 01-DEC-2001 (TRENBERG, 19, Last sequence update)
DS Hypothetical 52.7 kDa protein.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxId:10090;
RN 1;
RP SEQUENCE FROM N.A.
RC SEQUENCE:
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; Acc10324; AB010324.1; -.
DR InterPro; IPR003103; 19-like.
DR InterPro; IPR003596; 19_v.
DR Pfam; PF00047; 19; 4; 19_v.
DR SMART; SM00406; 19v; 1; 19v; 4.
DR PROSITE; PS00290; 19-MHC; 2.
FT Hypothetical protein.
SQ
SEQUENCE 486 AA; 4FFB93125DA870B CIRC64;

Query Match
Best Local Similarity 71.3%; Pred. No. 2.3e-39;
Matches 92; Conservative 10; Mismatches 14; Indels 13; Gaps 3;

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```

CY 1 EVOLESGGGLVPGGSLKCSGASGFTFSYTWGNTQTRERLEMAVATISGGSGSTTY 60
DB 20 EVOLESGGGLVPGGSLKCSGASGFTFSYTWGNTQTRERLEMAVATISGGSGSTTY 78
CY 61 PSYKGFRTSRNNKNTLYLONSLSBEDTNYCTCTRGSGFTWNTYDVGACTLVY 120
DB 79 PSWKGFRTSRNNKNTLYLONSLSBEDTNYCTCTRGSGFTWNTYDVGACTLVY 133
CY 121 SA 122
DB 134 QGRTTSS 142

RESULT 7
Query Match
Best Local Similarity 70.7%; Score 455.5; DB 4; Length 597;
Beat Local Similarity 68.0%; Pred. No. 4e-38;
Matches 66; Conservative 16; Mismatches 18; Indels 3; Gaps 1;

ID 091205; PRELIMINARY; PRT; 597 AA.
AC 091205; 2001 (TRENBERG, 19, Created)
DT 01-DEC-2001 (TRENBERG, 19, Last sequence update)
DR 01-DEC-2001 (TRENBERG, 19, Last sequence update)
DS Hypothetical protein.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxId:10090;
RN 1;
RP SEQUENCE FROM N.A.
RC SEQUENCE:
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; Acc107938; AB010798.1; -.
DR InterPro; IPR007110; 19-like.
DR InterPro; IPR003596; 19_v.
DR Pfam; PF00047; 19; 4; 19_v.
DR SMART; SM00406; 19v; 1; 19v; 4.
DR PROSITE; PS00290; 19-MHC; 3.
FT Hypothetical protein.
SQ
SEQUENCE 597 AA; 4FC3ABDECE235D9 CIRC64;

Query Match
Best Local Similarity 70.7%; Score 455.5; DB 4; Length 597;
Beat Local Similarity 68.0%; Pred. No. 4e-38;
Matches 66; Conservative 16; Mismatches 18; Indels 3; Gaps 1;

ID 091205; PRELIMINARY; PRT; 473 AA.
AC 091205; 2001 (TRENBERG, 19, Created)
DT 01-DEC-2001 (TRENBERG, 19, Last sequence update)
DR 01-DEC-2001 (TRENBERG, 19, Last sequence update)
DS Hypothetical protein.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxId:10090;
RN 1;
RP SEQUENCE FROM N.A.
RC SEQUENCE:
RA Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; Acc107938; AB010798.1; -.
DR InterPro; IPR007110; 19-like.
DR InterPro; IPR003596; 19_v.
DR Pfam; PF00047; 19; 4; 19_v.
DR SMART; SM00406; 19v; 1; 19v; 4.
DR PROSITE; PS00290; 19-MHC; 3.
FT Hypothetical protein.
SQ
SEQUENCE 597 AA; 4FC3ABDECE235D9 CIRC64;

```


NCBI_TaxId=9606;
 (1)
 SOURCE FROM N.A.
 MIM:138272.13; PubMed=614934;
 Wu X., Liu B., Van der Werpe P.L., Kalle N.N., Berny S.M.,
 Young D.C.;
 "Myosin-reactive autoantibodies in rheumatic carditis and normal
 clinical immunopathol. 67:184-192(1998).
 DR EMBL: AF035023; A05655.1; -
 DR HSP: F01772; 2P84.
 DR Interpro: IP007110; 19_11ke.
 DR Interpro: IP003596; 19_11ke.
 DR Pfam: PF00047; 19_11ke.
 DR SMART: SM00406; 19_11ke.
 DR PROSITE: PS0035; 19_11ke.
 FT NON_TER
 SO SEQUENCE 118 AA; 12843 MW; D063349P2AC14D CRC64;
 Query Match 68.6%; Score 442; DB 4; Length 116;
 Best Local Similarity 71.9%; Pred.No. 1.3e-37;
 Matches 87; Conservative 12; Mismatches 18; Indels 4; Gaps 1;
 QY 1 EVOLGSGGVVPGSGSLKASGASPTFTSTWVRCOTPERKRLMVAATISGSGSYTY 60
 DB 1 EVOLGSGGVVPGSGSLKASGASPTFTSTWVRCOTPERKRLMVAATISGSGSYTY 60
 QY 61 PSYVGEFTTSNDANNTLYLONSLESDTATYTCBEGGFVWYDVGACATLYVGS 120
 DB 61 ASYVGEFTTSNDANNTLYLONSLESDTATYTCBEGGFVWYDVGACATLYVGS 116
 QY 121 S 121
 DB 117 S 117
 RESULT 12
 ID 08WU1 PRELIMINARY; PRT; 613 AA.
 AC 08WU1 2003 (TReMBLrel. 20, Created)
 DT 01-MAR-2003 (TReMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NX NCBI_TaxId=9606;
 RX SOURCE FROM N.A.
 RC STRAUSPE-THOMAS;
 RA Strauspe-THOMAS;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 DR Interpro: IP007110; 19_11ke.
 DR Interpro: IP003596; 19_11ke.
 DR Pfam: PF00047; 19_11ke.
 DR SMART: SM00406; 19_11ke.
 DR PROSITE: PS0035; 19_11ke.
 FT NON_TER
 SO SEQUENCE 613 AA; 67286 MW; 60C7F550671B315 CRC64;
 Query Match 68.5%; Score 441; DB 4; Length 613;
 Best Local Similarity 67.7%; Pred.No. 1.3e-36;
 Matches 86; Conservative 14; Mismatches 15; Indels 12; Gaps 2;
 QY 1 EVOLGSGGVVPGSGSLKASGASPTFTSTWVRCOTPERKRLMVAATISGSGSYTY 60
 DB 20 QVAVESGGGVVPGSGSLKASGASPTFTSTWVRCOTPERKRLMVAATISGSGSYTY 79

QY 61 PSYVGEFTTSNDANNTLYLONSLESDTATYTCBEGGFVWYDVGACATLYVGS 116
 DB 60 ASYVGEFTTSNDANNTLYLONSLESDTATYTCBEGGFVWYDVGACATLYVGS 132
 QY 116 TLTVYSA 122
 DB 133 TLTVYSA 139
 RESULT 13
 ID 08WU3 PRELIMINARY; PRT; 116 AA.
 AC 08WU3 2003 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 (Fragment).
 OS Homo sapiens (human).
 OC Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NX NCBI_TaxId=9606;
 RX SOURCE FROM N.A.
 RC STRAUSPE-THOMAS;
 RA Young D.C.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
 DR EMBL: AF035023; A05655.1; -
 DR HSP: F01772; 2P84.
 DR Interpro: IP007110; 19_11ke.
 DR Interpro: IP003596; 19_11ke.
 DR Pfam: PF00047; 19_11ke.
 DR SMART: SM00406; 19_11ke.
 DR PROSITE: PS0035; 19_11ke.
 FT NON_TER
 SO SEQUENCE 116 AA; 12343 MW; D0A034815D0661 CRC64;
 Query Match 68.4%; Score 439.5; DB 4; Length 116;
 Best Local Similarity 72.7%; Pred.No. 1.3e-37;
 Matches 88; Conservative 10; Mismatches 18; Indels 5; Gaps 2;
 QY 2 VVGLGSGGVVPGSGSLKASGASPTFTSTWVRCOTPERKRLMVAATISGSGSYTY 61
 DB 1 VVGLGSGGVVPGSGSLKASGASPTFTSTWVRCOTPERKRLMVAATISGSGSYTY 60
 QY 62 PSYVGEFTTSNDANNTLYLONSLESDTATYTCBEGGFVWYDVGACATLYVGS 121
 DB 61 ASYVGEFTTSNDANNTLYLONSLESDTATYTCBEGGFVWYDVGACATLYVGS 115
 QY 122 A 122
 DB 116 A 116
 RESULT 14
 ID 08WU8 PRELIMINARY; PRT; 571 AA.
 AC 08WU8 2003 (TReMBLrel. 20, Created)
 DT 01-MAR-2003 (TReMBLrel. 20, Last sequence update)
 DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (human).
 OC Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NX NCBI_TaxId=9606;
 RX SOURCE FROM N.A.
 RC STRAUSPE-THOMAS;
 RA Strauspe-THOMAS;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 DR Interpro: IP007110; 19_11ke.
 DR Interpro: IP003596; 19_11ke.
 DR Pfam: PF00047; 19_11ke.
 DR SMART: SM00406; 19_11ke.
 DR PROSITE: PS0035; 19_11ke.
 FT NON_TER
 SO SEQUENCE 571 AA; 60728 MW; 60C7F550671B315 CRC64;
 Query Match 68.5%; Score 441; DB 4; Length 571;
 Best Local Similarity 67.7%; Pred.No. 1.3e-36;
 Matches 86; Conservative 14; Mismatches 15; Indels 12; Gaps 2;
 QY 1 EVOLGSGGVVPGSGSLKASGASPTFTSTWVRCOTPERKRLMVAATISGSGSYTY 60
 DB 20 QVAVESGGGVVPGSGSLKASGASPTFTSTWVRCOTPERKRLMVAATISGSGSYTY 79

RC SEQUENCE FROM N.A.
 RA STRAUBERG R.; 2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC021276; AAI21276.1; Iq-like.
 DR Interpro: IPR003100; Iq-like.
 DR Interpro: IPR003596; Iq.V.
 DR SMART: SM00406; IqV.1.
 DR PROSITE: PS00835; Iq_LIKE; 2.
 DR PROSITE: PS00290; Iq_MHC; 1.
 DR PROSITE: PS00290; Iq_MHC; 2.
 SO SEQUENCE 573 AA; 62967 MW; F0D7234403AC530 CRC64;

Query Match 68.0%; Score 436; DB 4; Length 573;
 Best Local Similarity 66.5%; Pred. No. 2,4e-36;
 Matches 95; Conservative 12; Mismatches 25; Indels 2; Gaps 1;
 Oy 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSSTYSWVRQPKRLRWVATISGGSSFTY 60
 Db 20 EVQLVDSGGGLVQPGGSLKLSCAASGFTFSSTYSWVRQPKRLRWVATISGGSSFTY 79
 Oy 61 PDGVKRRFTISRDNAKNTLYIQMSSLSLSEDTAMVYTCREQGFYNNYF--DYWGAGTLV 116
 Db 80 AGSVKRRFTISRDNAKNTLYIQMSSLSLSEDTAMVYTCREQGSSTYIGITFGMDVQCOITV 139
 Oy 119 TVSA 122
 Db 140 TVSS 143

RESULT 15

Q8NSK4 PRELIMINARY; PRT; 499 AA.
 AC Q8NSK1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 FN [1] "Cardiac-906".
 RP SEQUENCE FROM N.A.
 RC STRAUBERG R.; 2002)
 RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC032249; AAI2249.1; -.
 DR Interpro: IPR003599; Iq-1-like.
 DR SMART: SM00406; IqV.1.
 DR Interpro: IPR003597; Iq.CL.
 DR Interpro: IPR003006; Iq_MHC.
 DR Interpro: IPR003596; Iq.V.
 DR SMART: SM00406; IqV.1.
 DR SMART: SM00406; IqV.1.
 DR SMART: SM00406; IqV.1.
 DR PROSITE: PS00835; Iq_LIKE; 4.
 DR PROSITE: PS00835; Iq_MHC; 1.
 FM Hypothetical protein.

Query Match 67.9%; Score 437.5; DB 4; Length 499;
 Best Local Similarity 66.9%; Pred. No. 2,2e-36;
 Matches 85; Conservative 13; Mismatches 24; Indels 5; Gaps 1;
 Oy 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSSTYSWVRQPKRLRWVATISGGSSFTY 60
 Db 20 EVQLVDSGGGLVQPGGSLKLSCAASGFTFSSTYSWVRQPKRLRWVATISGGSSFTY 79
 Oy 61 PDGVKRRFTISRDNAKNTLYIQMSSLSLSEDTAMVYTCREQGFYNNYF--DYWGAGTLV 116
 Db 80 AGSVKRRFTISRDNAKNTLYIQMSSLSLSEDTAMVYTCREQGSSTYIGITFGMDVQCOITV 139

Db 80 AGSVKRRFTISRDNAKNTLYIQMSSLSLSEDTAMVYTCREQGSSTYIGITFGMDVQCOITV 139
 Oy 116 TVTVSA 122
 Db 140 TVTVSS 146
 Search completed November 7, 2003, 07:34:35
 Job time : 40.3323 secs

XX 13-SEP-2000; 2000MO-EP08936.
 XX 14-SEP-1999; 99AT-0001576.
 XX (BAXT) BAXTER AG.
 XX
 XX Schellinger F, Kerschbaurer R, Falkner F, Dornier F,
 XX WPI, 2001-290358/30.
 XX N-Peptide; AAF30732.
 XX
 XX New factor IX/factor IXa antibodies and their derivatives useful for
 XX haemorrhagic diathesis such as haemophilia A and haemorrhagic diathesis -
 XX Claim 12; Fig 16; 13ep; English.
 XX
 XX The present sequence is that of a single chain Fv (scFv) derivative
 XX of antibody 198/A82, comprising the heavy (VH) and light (VL) chain
 XX variable regions of 198/A82 joined by an artificial, flexible linker
 XX region. The heavy chain variable region of 198/A82 is joined to the
 XX light chain variable region of 198/A82 via a linker region of 198/A82
 XX an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
 XX antibodies of the invention. Anti-FIX/FIXa and their derivatives,
 XX activity or FIXa activating activity. Administration leads to an
 XX increase in the procoagulant activity of FIXa, even in the presence
 XX of FVIIa inhibitors. This allows for rapid blood coagulation even
 XX in haemorrhagic diathesis. The antibodies and their derivatives in a
 XX claimed pharmaceutical composition for treating patients with blood
 XX coagulation disorders, especially haemophilia A and haemorrhagic
 XX diathesis.
 XX
 XX Sequence 249 AA;
 XX
 XX Query Match 100.0%; Score 644; DB 22; Length 249;
 XX Local Similarity 96.78; Pred No. 1,55-52;
 XX Matches 122; Conservative 0; Mismatches 14-53; Indels 0; Gaps 0;
 XX
 XX 1 EVQLQSSGGGLVYFGGSLLKLSASGFTFSSTYSMSWVQTPERKLEWVAITISGGSSSTYY 60
 XX Db 1 EVQLQSSGGGLVYFGGSLLKLSASGFTFSSTYSMSWVQTPERKLEWVAITISGGSSSTYY 60
 XX 61 PSVYKSGPTLSPNDAAVNTYLVMSLSSEDTNMYCTCRSGGFTVNVYEDVWQAGATLYTV 120
 XX Db 61 PSVYKSGPTLSPNDAAVNTYLVMSLSSEDTNMYCTCRSGGFTVNVYEDVWQAGATLYTV 120
 XX 121 SA 122
 XX Db 121 SA 122
 XX
 XX RESULT 2
 XX HAZ20442 standard; Protein; 294 AA.
 XX
 XX HAZ20442;
 XX 21-0UN-2001 (first entry)
 XX
 XX Anti-FIX/FIXa antibody 198/B1-myc-tag fusion.
 XX
 XX Factor IX, FIX, Factor IXa, FIX, scFv, antibody, procoagulant;
 XX Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 XX haemorrhagic diathesis; haemostatic; antidysic; therapy; mouse;
 XX myc-tag.
 XX
 XX Chimeric - Mus musculus.
 XX Chimeric - Synthetic.
 XX Chimeric - Escherichia coli.

XX Key Location/Qualifiers
 XX Peptide 1..22
 XX Peptide /label= Signal_peptide
 XX Protein 23..294
 XX Protein /label= Mature_protein
 XX Region 23..271
 XX Region /label= scFv
 XX Region 23..144
 XX Misc-difference /note= encoded by GGN+
 XX Peptide 145..159
 XX Peptide /label= Linker
 XX Region /label= VL
 XX Peptide 272..274
 XX Peptide /label= Spacer
 XX Protein 275..289 myc_tag
 XX Peptide 287..289
 XX Peptide /label= Spacer
 XX Peptide 289..294 myc_tag
 XX /label= Hg_tag
 XX
 XX MO200101992-N2.
 XX
 XX 22-MAR-2001.
 XX
 XX 13-SEP-2000; 2000MO-EP08936.
 XX 14-SEP-1999; 99AT-0001576.
 XX (BAXT) BAXTER AG.
 XX
 XX Schellinger F, Kerschbaurer R, Falkner F, Dornier F,
 XX WPI, 2001-290358/30.
 XX N-Peptide; AAF30732.
 XX
 XX New factor IX/factor IXa antibodies and their derivatives useful for
 XX increasing antidysic activity of Factor IXa, and for treating blood
 XX coagulation disorders such as haemophilia A and haemorrhagic diathesis -
 XX Example 10; Fig 34; 13ep; English.
 XX
 XX The present sequence is that of a fusion protein comprising: a FcB
 XX leader, a single chain Fv (scFv) derivative of antibody 198/B1
 XX comprising the heavy (VH) and light (VL) chain variable regions of
 XX 198/B1 joined by an artificial, flexible linker region. The heavy
 XX chain variable region of 198/B1 is joined to the light chain variable
 XX region of 198/B1 via a linker region of 198/B1. This is an example of
 XX anti-human Factor IX (FIX)/activated Factor IX (FIXa) antibodies of
 XX the invention. Anti-FIX/FIXa antibodies and their derivatives,
 XX activity or FIXa activating activity. Administration leads to an
 XX increase in the procoagulant activity of FIXa, even in the presence
 XX of FVIIa inhibitors. This allows for rapid blood coagulation even
 XX in haemorrhagic diathesis. The antibodies and their derivatives in a
 XX claimed pharmaceutical composition for treating patients with blood
 XX coagulation disorders, especially haemophilia A and haemorrhagic
 XX diathesis. The scFv-myc-tag fusion was expressed in E. coli. It
 XX exhibited FVIIa-like activity.
 XX
 XX Sequence 294 AA;
 XX
 XX Query Match 96.98; Score 624; DB 22; Length 294;
 XX Local Similarity 96.78; Pred No. 1,55-52;
 XX Matches 118; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 1 EVQLQSSGGGLVYFGGSLLKLSASGFTFSSTYSMSWVQTPERKLEWVAITISGGSSSTYY 60
 XX Db 23 EVQLQSSGGGLVYFGGSLLKLSASGFTFSSTYSMSWVQTPERKLEWVAITISGGSSSTYY 82

61 PSYVGRFTISRDNNANTLYLQNSLSLSEDTANVYCRGGGPTVMVYEDVWGACTLVY 120
 Db 83 PSYVGRFTISRDNNANTLYLQNSLSLSEDTANVYCRGGGPTVMVYEDVWGACTLVY 142
 121 SA 122
 143 SS 144
 Db 143 SS 144
 RESEQU 3
 AA020438
 AA020438 standard; Protein; 325 AA.
 AA020438;
 21-JUN-2001 (first entry)
 Anti-FIX/FIXa antibody 198/B1 bivalent miniantibody.
 Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant; A;
 haemorrhagic diathesis; haemostatic; amolytic; therapy; mouse;
 bivalent antibody; plasmid p219-198A2B102.
 Chimeric - Mus musculus.
 Chimeric - Escherichia coli.
 Key location/Qualifiers
 Peptide 1..223
 /label= signal_peptide
 /note= "Pa1b leader"
 Protein 23..325 Mature_protein
 /label= scfv
 Protein 23..271
 /label= scfv
 Region 23..144
 Misc-difference 76 /label= VH
 Peptide 145..159
 /label= linker
 Region 145..159
 /label= VL
 Misc-difference 166
 /note= "encoded by GGN"
 Misc-difference /note= "encoded by TCM"
 Peptide 272..274
 /label= Spacer
 Protein 272..325
 /label= Hinge
 Protein 288..319
 /label= Helix
 Peptide 320..325
 /label= His_tag
 WC02001.1992-A2.
 22-MAR-2001.
 11-SEP-2000; 2000MO-EP06936.
 14-SEP-1999; 99AT-0001576.
 (BANT) BAXTER AG.
 Schefflinger F, Kerschbaum R, Falkner F, Dornier F,
 WPI, 2001-290358/30.
 N-PDB: AAF30728.
 New factor IX/factor IXa antibodies and their derivatives useful for

increasing amidolytic activity of factor IXa, and for treating blood
 coagulation disorders such as haemophilia A and haemorrhagic diathesis
 Example 16; Fig 28; 138pg; English.
 The present sequence is that of a bivalent miniantibody comprising
 a Pa1b leader peptide, the single chain Fv (scfv) fragment of
 antibody 198/B1 (Emclone AB2), an amphipathic helical structure
 and a C-terminal linker region (see AAF30728).
 Escherichia coli from plasmid p219p2A2B102 (see AAF30728).
 Antibody 198/B1 is an example of anti-human factor IX.
 FIX/activated factor IX (FIXa) antibodies of the invention, factor
 activity or FIXa activating activity. Administration leads to an
 increase in the procoagulant activity of FIXa, even in the presence
 of FIXa inhibitors. This allows for rapid blood coagulation even
 in the absence of FVIII or FVIIIa, and in the case of FVIIIa
 inhibitors. The antibodies of the invention are useful in a
 claimed pharmaceutical composition for treating patients with blood
 coagulation disorders, especially haemophilia A and haemorrhagic
 diathesis. The bivalent miniantibody exhibited FVIII-like
 activity.
 Sequence 325 AA;
 Query Match 96.8%; Score 624; DB 23; length 325;
 Best Local similarity 96.7%; Pval No. 1.6e-52;
 Matches 118; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 1 EVKLVSGCGVYRGGGSLGKASGGFSTSNVYCRGGGPTVMVYEDVWGACTLVY 60
 Db 23 EVKLVSGCGVYRGGGSLGKASGGFSTSNVYCRGGGPTVMVYEDVWGACTLVY 82
 61 PSYVGRFTISRDNNANTLYLQNSLSLSEDTANVYCRGGGPTVMVYEDVWGACTLVY 120
 Db 83 PSYVGRFTISRDNNANTLYLQNSLSLSEDTANVYCRGGGPTVMVYEDVWGACTLVY 142
 121 SA 122
 143 SS 144
 Db 143 SS 144
 RESEQU 4
 AA020437
 AA020437 standard; Protein; 732 AA.
 21-JUN-2001 (first entry)
 Anti-FIX/FIXa antibody 198/B1-alkaline phosphatase fusion.
 Factor IX; FIX; Factor IXa; FIXa; scfv; antibody; procoagulant;
 Factor VIII cofactor; blood coagulation disorders; haemophilia A;
 haemorrhagic diathesis; haemostatic; amolytic; therapy; mouse;
 alkaline phosphatase.
 Chimeric - Mus musculus.
 Chimeric - Escherichia coli.
 Chimeric - Escherichia coli.
 Key location/Qualifiers
 Peptide 1..22
 /label= signal_peptide
 Protein 23..312 Mature_protein
 /label= scfv
 Protein 23..271
 /label= scfv
 Region 23..144
 Misc-difference 76 /label= VH
 Peptide 145..159
 /note= "encoded by GGN"

0Y 1 EVQLQSSGQGLVYFGGGSLKSLCAAGSTFSSYNMHWOTPEKLEHWMTTSSGGSSSTYY 60
 0Y 1 EVQLQSSGQGLVYFGGGSLKSLCAAGSTFSSYNMHWOTPEKLEHWMTTSSGGSSSTYY 60
 0Y 61 PSYKGRFTISRDNAKNTLYLQWSSLSIEDTNMYTCRSGGFYMWYEDWAGTLYTV 120
 0Y 61 PSYKGRFTISRDNAKNTLYLQWSSLSIEDTNMYTCRSGGFYMWYEDWAGTLYTV 120
 0Y 121 SA 122
 0Y 121 SS 122
 DB 121 SS 122
 RESEQU 6
 ID ABE0555 standard; protein; 134 AA.
 AC ABE0555;
 DT 21-MAR-2003 (first entry)
 DE Murine antibody 14f3 heavy chain variable region.
 XX Mouse, monoclonal antibody; 14f3; osteopathic; antiinflammatory;
 XX antiarthritic; antiinflammatory; cyclostatic; antiprostaglandin;
 XX antiinflammatory; cyclostatic; antiprostaglandin; antidiabetic;
 XX bone cancer; osteolytic; osteoarthritis; immune disease; psoriasis;
 XX insulin-dependent diabetes; inflammatory bowel disease;
 XX multiple sclerosis; heavy chain variable region;
 XX complementary determining region; CDR.
 XX Key
 XX Location/Qualifiers
 XX Region 3
 XX Label= CDR1
 XX Region 50..66
 XX Label= CDR2
 XX Region 9
 XX Label= CDR3
 XX /Label= CDR3
 XX WO200295012-A1.
 XX 28-NOV-2002.
 XX 03-MAY-2002; 2002MO-US14246.
 XX 16-MAY-2001; 2001US-292031P.
 XX (SMK) SMITHKLINE BEECHAM CORP.
 XX (SMK) SMITHKLINE BEECHAM PLC.
 XX Sweet RM, Torrence NA, Wattam TJ
 XX WPI: 2003-156758/15.
 XX N-PSDB; ABE93987.
 XX New monoclonal antibody having the characteristics of a monoclonal
 XX antibody 14f3, useful for treating or preventing osteopathic diseases,
 XX e.g., rheumatoid arthritis, or osteoporosis, and immune diseases e.g.,
 XX psoriasis, or disease -
 XX Disclosure: Page 8; 51pp; English.
 XX The invention relates to a novel monoclonal antibody having the
 XX identifying characteristics of, or that is a monoclonal antibody 14f3.
 XX An antibody of the invention has osteopathic, antiinflammatory,
 XX antiarthritic, antiinflammatory, cyclostatic, antiprostaglandin,
 XX antidiabetic, antiinflammatory, cyclostatic, antiprostaglandin,
 XX of the invention may have a use in the treatment of osteopathic
 XX polypeptides are useful for treating or preventing osteopathic diseases,
 XX such as rheumatoid arthritis, osteoporosis, metastatic and primary bone
 XX cancer, wear debris induced osteolysis or osteoarthritis, and immune

CC diseases such as psoriasis, insulin-dependent diabetes, inflammatory
 CC bowel diseases or multiple sclerosis. The present sequence represents the
 CC heavy chain variable region of the murine monoclonal antibody 14f3 of the
 CC CDR 9.
 CC The sequence contains three complementary determining regions
 CC (CDR 9).
 XX Sequence 134 AA:
 XX Query Match 83.6%; Score 538.5; DB 24; Length 134;
 XX Best Local Similarity 85.2%; Pred. No. 1.2e-44;
 XX Matches 104; Conservative 4; Mismatches 13; Indels 1; Gaps 1;
 0Y 1 EVQLQSSGQGLVYFGGGSLKSLCAAGSTFSSYNMHWOTPEKLEHWMTTSSGGSSSTYY 60
 0Y 1 EVQLQSSGQGLVYFGGGSLKSLCAAGSTFSSYNMHWOTPEKLEHWMTTSSGGSSSTYY 60
 0Y 61 PSYKGRFTISRDNAKNTLYLQWSSLSIEDTNMYTCRSGGFYMWYEDWAGTLYTV 120
 0Y 61 PSYKGRFTISRDNAKNTLYLQWSSLSIEDTNMYTCRSGGFYMWYEDWAGTLYTV 119
 0Y 121 SA 122
 0Y 120 SS 121
 DB 120 SS 121
 RESEQU 7
 ID AAB20434 standard; protein; 249 AA.
 AC AAB20434;
 DT 21-JUN-2001 (first entry)
 DE Anti-FIX/FIXa antibody 193/K2 scFv.
 XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
 XX Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 XX haemorrhagic diathesis; haemostatic; antidalytic; therapy; mouse.
 XX Chimeric - Mus musculus.
 XX Chimeric - Synthetic.
 XX Key
 XX Location/Qualifiers
 XX Region 1
 XX Label= VH
 XX Region 98..110
 XX Label= CDR3
 XX Peptide 122..135 linker
 XX Protein 136..249
 XX /Label= VL
 XX Region 230..238
 XX /Label= CDR3
 XX WO200113992-A2.
 XX 22-MAR-2001.
 XX 13-SEP-2000; 2000MO-EP08936.
 XX 14-SEP-1999; 99AT-0001576.
 XX (BAXT) BAXTER AG.
 XX Schefflinger F, Kerechbauer R, Falkner F, Dornier F;
 XX WPI: 2001-290518/10.
 XX N-PSDB; AAB30724.
 XX New Factor IX/scFv IXa antibodies and their derivatives useful for
 XX increasing antithrombotic activity in the treatment of
 XX coagulation disorders such as haemophilia A and haemorrhagic diathesis -

PS Claim 10; Fig 15; 138pp; English.

CC The present sequence is that of a single chain Fv (scFv) derivative
CC of heavy and light chain variable regions of 193/K2 joined by a chain
CC variable regions of 193/K2 joined by a chain
CC peptide. The scFv was obtained by PCR amplification of cDNAs for
CC 193/K2 VH and VL regions and cloning in vector pDA2. 193/K2 is
CC an example of anti-human factor IX (FIX)/activated factor IX (aFIX)
CC including scFv and CDR3 fragments, have factor VIIa (FVIIa) cofactor
CC activity or FIXa activating activity. Administration leads to an
CC increase in the procoagulant activity of FIXa, even in the presence
CC of heparin. The scFv is useful for the treatment of patients with
CC in the absence of FVII or FVIIa, and in the case of FVIII, even
CC inhibitor patients. The antibodies and derivatives are used in a
CC claimed pharmaceutical composition for treating patients with blood
CC coagulation disorders, especially haemophilia A and haemorrhagic
CC diseases.

SO Sequence 249 AA;

Query Match 82.5%; Score 517.5; DB 22; Length 249;

Best Local Similarity 85.4%; Pred. No. 36-44; Matches 105; Conservative 8; Mismatches 7; Indels 3; Gaps 2;

CC 1 EVQVDSGGVGVFVPSGSLKLSAASGFTFSYTMWROTPRRLRWVATISGSSSTYY 60

CC 1 EVQVDSGGVGVFVPSGSLKLSAASGFTFSYTMWROTPRRLRWVATISGSSSTYY 60

CC 61 PSYSGEFTISRDNAKNTLYLQNSLSSEPTWYCTRESCGQFTWYFDWAGAGTLYV 119

CC 61 PSYSGEFTISRDNAKNTLYLQNSLSSEPTWYCTRESCGQFTWYFDWAGAGTLYV 118

CC 120 VSA 122

CC 119 VSS 121

DB 119 VSS 121

DB 119 VSS 121

DB 119 VSS 121

DB 119 VSS 121

DB 119 VSS 121

DB 119 VSS 121

DB 119 VSS 121

DB 119 VSS 121

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DB 119 VSS 121

PS Claim 10; Fig 15; 138pp; English.

CC The present sequence is that of a single chain Fv (scFv) derivative
CC of heavy and light chain variable regions of 193/K2 joined by a chain
CC variable regions of 193/K2 joined by a chain
CC peptide. The scFv was obtained by PCR amplification of cDNAs for
CC 193/K2 VH and VL regions and cloning in vector pDA2. 193/K2 is
CC an example of anti-human factor IX (FIX)/activated factor IX (aFIX)
CC including scFv and CDR3 fragments, have factor VIIa (FVIIa) cofactor
CC activity or FIXa activating activity. Administration leads to an
CC increase in the procoagulant activity of FIXa, even in the presence
CC of heparin. The scFv is useful for the treatment of patients with
CC in the absence of FVII or FVIIa, and in the case of FVIII, even
CC inhibitor patients. The antibodies and derivatives are used in a
CC claimed pharmaceutical composition for treating patients with blood
CC coagulation disorders, especially haemophilia A and haemorrhagic
CC diseases.

SO Sequence 121 AA;

Query Match 82.7%; Score 532.5; DB 23; Length 121;

Best Local Similarity 84.4%; Pred. No. 46-44; Matches 109; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

CC 1 EVQVDSGGVGVFVPSGSLKLSAASGFTFSYTMWROTPRRLRWVATISGSSSTYY 60

CC 1 EVQVDSGGVGVFVPSGSLKLSAASGFTFSYTMWROTPRRLRWVATISGSSSTYY 60

CC 61 PSYSGEFTISRDNAKNTLYLQNSLSSEPTWYCTRESCGQFTWYFDWAGAGTLYV 120

CC 61 PSYSGEFTISRDNAKNTLYLQNSLSSEPTWYCTRESCGQFTWYFDWAGAGTLYV 119

CC 121 SA 122

CC 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

DB 120 SS 121

XX glomerular nephritis; cancer; antibody; chromosome p921-22; T8a-8.
 OS Mus musculus.
 XX M0200183560-A1.
 XX
 XX
 PD 08-NOV-2001.
 XX
 XX 02-MAY-2001; 2001MC-USJ4151.
 XX
 PR 02-MAY-2000; 2000US-201344P.
 XX
 XX (OABR-) OAB RES FOUND.
 XX
 PI Zhou T, Ichikawa K, Kimberly RP, Koopman MJ;
 DR WPI, 2002-049338/06.
 DR N-9820; A4837062.
 PT Novel antibody specific for tumor necrosis factor-related
 PT apoptosis-inducing ligand, useful for inhibiting cell proliferation in
 PT cancer -
 PR
 PS Claim 26; Page 198-199; 2390P; English.
 XX
 XX The invention describes a novel antibody which recognizes a tumor
 XX necrosis factor-related apoptosis-inducing ligand (TRAIL) receptor
 XX DR5 (located on chromosome p921-22). The antibody has apoptosis-inducing
 XX activity to a cell expressing DR5 in vivo. It is also useful for
 XX preparing a therapeutic for selective apoptosis of abnormal or cell.
 XX The antibody is useful for inhibiting tumor growth in vivo, and
 XX preferably human breast, colon, colorectal, hepatocellular carcinoma,
 XX lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
 XX also be administered e.g., paclitaxel, taxol or cyclohexamide. The
 XX antibody is used to treat an autoimmune disease, systemic lupus
 XX erythematosus, rheumatoid arthritis, multiple sclerosis, Crohn's
 XX disease, graft-versus-host disease, Sjogren's syndrome, pernicious
 XX anemia, pernicious anaemia, Addison disease, scleroderma, Goodpasture's syndrome,
 XX autoimmune haemolytic anemia, sterility, myasthenia gravis, multiple
 XX sclerosis, myeloma, myeloid leukemia, myeloid leukaemia, myeloid
 XX allergy, atopic disease, atherosclerosis, myocarditis, cardiomyopathy,
 XX glomerular nephritis, hypoplastic anaemia, rejection after organ
 XX transplantation, and numerous malignancies of lung, prostate, liver,
 XX colorectal, gastric, pancreatic, breast, bladder, and lymphoma.
 XX 1001, 1147 heavy and 1198 chain CDRs of the mouse TRAIL (M0200183560 and
 XX A0072802), T8a-8 are shown in M027299 and A0072800.
 XX
 XX Sequence 464 AA;
 XX
 XX Query Match
 XX Beat Local Similarity 80.7%; Score 519.5; DB 23; Length 464;
 XX Matches 102; Conservative 2; Mismatches 15; Indels 3; Gaps 1;
 XX
 XX 1 EVQLQSSGQGLVKGSGSLKASCAAGFTFSYVSWVQPERKLEWAVITSSGGSTTY 60
 XX Db 20 EVQLVSSGGLVKGSGSLKASCAAGFTFSYVSWVQPERKLEWAVITSSGGSTTY 79
 XX QY 61 PSYKGFRTISDAKNTLYLQWSSLASSEDTNYTCREAGSFYNNWYDMMAGATLYV 120
 XX Db 80 PSYKGFRTISDAKNTLYLQWSSLASSEDTNYTCREAGSFYNNWYDMMAGATLYV 136
 XX QY 121 SA 122
 XX Db 137 SS 138
 XX
 XX RESULT 12
 XX AA089627
 XX ID AA089627 standard; protein, 118 AA.
 XX AC AA089627;
 XX DT 03-SEP-1998 (first entry)

XX
 XX Chimeric H chain SEQ ID NO:46 for an antibody against hTRP.
 DE
 XX Chimeric; antibody; human parathormone related peptide; hPRP; mouse;
 XX human parathormone related peptide; hPRP; mouse;
 XX human parathormone related peptide; hPRP; mouse;
 XX hypophosphemia; antigen; Vitamin D resistance; region;
 XX humanized.
 XX
 XX Synthetic.
 XX OS Chimeric; Mus sp.
 XX Chimeric - Homo sapiens.
 XX
 XX M0981388-A1.
 XX
 PD 02-APR-1998.
 XX
 XX 24-SEP-1997; 97NC-J03382.
 XX
 XX 24-JUL-1997; 97JP-0214168.
 XX
 XX 26-SEP-1996; 96JP-0255196.
 XX
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX
 PI Sato K, Wakabayashi Y, Yabuta N;
 DR WPI, 1996-130640/20.
 DR New chimeric antibodies against human parathormone related
 DR peptide (hPRP) - useful for e.g. treatment of hypercalcaemia and other
 DR disorders caused by malignant neoplasms (s)
 PT
 PT Claim 5; Page 111-112; 1839P; Japanese.
 XX
 XX New antibodies have been developed which are specific for human
 XX parathormone related peptide (hPRP). The antibodies comprise chimeric
 XX H chain regions of human and mouse antibodies, specifically a region of
 XX origin. The present sequence represents a specifically claimed region of
 XX an antibody of the invention. Host cells, transformed with vectors
 XX containing DNA encoding antibodies of the invention, can be used to
 XX produce the antibodies. The antibodies may be used to treat
 XX hypercalcaemia, hypercalcaemia, hypercalcaemia, hypercalcaemia,
 XX pancreas, lung, throat, larynx, tongue, gum, oesophagus, stomach, liver,
 XX breast, kidney, bladder, womb or prostate or malignant lymphoma. They
 XX may also be used for treatment of hypophosphemia such as that due to
 XX phlogism or to vitamin D resistance.
 XX
 XX Sequence 118 AA;
 XX
 XX Query Match
 XX Beat Local Similarity 80.6%; Score 519; DB 19; Length 118;
 XX Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;
 XX
 XX 1 EVQLVSSGQGLVKGSGSLKASCAAGFTFSYVSWVQPERKLEWAVITSSGGSTTY 60
 XX Db 1 EVQLVSSGQGLVKGSGSLKASCAAGFTFSYVSWVQPERKLEWAVITSSGGSTTY 60
 XX QY 61 PSYKGFRTISDAKNTLYLQWSSLASSEDTNYTCREAGSFYNNWYDMMAGATLYV 120
 XX Db 61 PSYKGFRTISDAKNTLYLQWSSLASSEDTNYTCREAGSFYNNWYDMMAGATLYV 116
 XX QY 121 SA 122
 XX Db 117 SA 118
 XX
 XX RESULT 13
 XX AA089627
 XX ID AA089627 standard; protein, 118 AA.
 XX AC AA089627;
 XX DT 14-APR-1999 (first entry)

DB Mouse humanised antibody #23-57-137-1 heavy chain mature protein.
 XX Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;
 KM inhibitor; humanised.
 XX Mus sp.
 OS Synthetic.
 XX MO9681329-AL.
 PD 19-NOV-1998.
 PD 13-NOV-1998; 98MO-JP02116.
 PR 18-JUL-1997; 97DP-0194445.
 PR 15-MAY-1997; 97DP-0125055.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Iishi K, Sato K, Tsumenari T;
 WP1; 1999-070101/06.
 XX Inhibitors of binding of parathyroid hormone related peptide to its
 PT receptor - useful for, e.g. treatment of cachexia arising from
 PS cancer or other diseases.
 XX Example 2; Page 72-73; 125pp; Japanese.
 XX The present invention describes compositions for the treatment of
 CC cachexia containing a substance which inhibits the binding of a
 CC parathyroid hormone related peptide (PTHrP) to its receptor, as an
 CC active component. This substance may be an antagonist to the receptor,
 CC or an antibody (preferably monoclonal) or antibody fragment,
 CC which is capable of binding to the receptor or the active component.
 CC The present invention also describes a humanised antibody prepared
 CC by hybridoma 23-57-137-1 (FEM BP-5631). The composition is used for
 CC the treatment of cachexia arising in connection with diseases such as
 CC present sequence represents mouse humanised antibody heavy chain from
 CC #23-57-137-1 from the present invention.
 XX Sequence 118 AA;
 SQ
 Query Match 80.6%; Score 519; DB 20; Length 118;
 Best Local Similarity 83.6%; Pred. No. 7.9e-43;
 Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;
 QY 1 EVQLDSGGGVYFGSGSLKSCASGFTFSYTWGQFTRERKLEWVAITISGSGSYTY 60
 DB 1 EVQLVDSGDVLYFGSGSLKSCASGFTFSYTWGQFTRERKLEWVAITISGSGSYTY 60
 QY 61 PSYVKGFTISRNNKNTLVQNSLRSDPTNYCTTRGGSGFTVMYFVWAGGLVTV 120
 DB 61 PSYVKGFTISRNNKNTLVQNSLRSDPTNYCTTRGGSGFTVMYFVWAGGLVTV 120
 QY 121 SA 122
 DB 117 SA 118

RESULT 14
 AA77502
 ID AA77502 standard; Protein; 118 AA.
 AC AA77502;
 XX AA77502;
 PD 26-APR-2000 (first entry)
 PR Peptide seq ID No: 46.
 XX Hypocalcaemic crisis; parathyroid hormone related peptide; PTHrP; tumour.

OS Mus muscula.
 XX W0200000219-AL.
 PD 06-JUN-2000.
 XX 25-JUN-1999; 99MO-JP03433.
 XX 26-JUN-1998; 98DP-010143.
 PA (CHUS) CHUGAI SEIYAKU KK.
 PI Sato K, Tsumenari T;
 WP1; 2000-117115/10.
 XX Treatment of hypocalcaemic crisis with a substance inhibiting binding
 PT of parathyroid hormone related peptide to its receptor
 PS Example 2; Page 87-88; 120pp; Japanese.
 XX The invention relates to a method of treatment of hypocalcaemic crisis.
 CC A composition for the treatment of hypocalcaemic crisis contains as
 CC active component a substance which inhibits the binding of parathyroid
 CC hormone related peptide (PTHrP) to its receptor. The inhibitor is used
 CC for the treatment of hypocalcaemic crisis, such as that associated with
 CC a malignant tumour.
 XX Sequence 118 AA;
 SQ
 Query Match 80.6%; Score 519; DB 21; Length 118;
 Best Local Similarity 83.6%; Pred. No. 7.9e-43;
 Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;
 QY 1 EVQLDSGGGVYFGSGSLKSCASGFTFSYTWGQFTRERKLEWVAITISGSGSYTY 60
 DB 1 EVQLVDSGDVLYFGSGSLKSCASGFTFSYTWGQFTRERKLEWVAITISGSGSYTY 60
 QY 61 PSYVKGFTISRNNKNTLVQNSLRSDPTNYCTTRGGSGFTVMYFVWAGGLVTV 120
 DB 61 PSYVKGFTISRNNKNTLVQNSLRSDPTNYCTTRGGSGFTVMYFVWAGGLVTV 120
 QY 121 SA 122
 DB 117 SA 118

RESULT 15
 AA663382
 ID AA663382 standard; Protein; 118 AA.
 AC AA663382;
 XX AA663382;
 PD 15-OCT-2001 (first entry)
 PR Amino acid sequence of a murine polypeptide.
 XX Parathyroid hormone-associated peptide; PTHrP; dental disease.
 XX Mus muscula.
 XX W0200154725-AL.
 PD 02-APR-2001.
 XX 14-DEC-2000; 2000MO-JP08975.
 XX 25-JUN-2000; 2000DP-0093034.
 XX (CHUS) CHUGAI SEIYAKU KK.
 PI Kato A, Shukri M, Shujimoto T;

```

DR  WPI, 2001-663459/50.
XX  Parathyroid hormone-associated peptide binding inhibitors useful for
PT  treating dental disease.
PT  Disclosures: Page 102-103; 140pp; Japanese.
XX  The specification describes a treatment for dental diseases. The
CC  treatment comprises a substance that inhibits binding between
CC  parathyroid hormone-associated peptide and a protein, which is
CC  present sequence represents a murine protein, which is used in the
CC  course of the invention.
XX  Sequence 118 AA:
SQ  Sequence 118 AA:
Query Match 80.6%; Score 519; DB 22; Length 118;
Best Local Similarity 89.6%; Pred.No. 7.9e-43;
Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;
DB 1 EVOLVSGGGLVKKRGSALSCAAGPTTSYTSWVQTPKKLELVAVITSSGGSSSTYY 60
DB 1 EVOLVSGGGLVKKRGSALSCAAGPTTSYTSWVQTPKKLELVAVITSSGGSSSTYY 60
DB 61 PDSVKGRFTISDNNASTLYLQSSLSASEDTMMVYCTRSQGGFTVMVYPDVWQAGTLVTV 120
DB 61 PDSVKGRFTISDNNASTLYLQSSLSASEDTMMVYCTRSQGGFTVMVYPDVWQAGTLVTV 116
DB 121 SA 122
DB 117 SA 118

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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:30:19, Search time 107.015 Seconds

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155,799 Million cell updates/sec

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Listing first 45 summaries

Database:

Published Applications NA*

1 /cgn1.6/prodata/2/pubpa/US07_PUBCOMB.pep.*

2 /cgn1.6/prodata/2/pubpa/ECT_NEW_PUB.pep.*

3 /cgn1.6/prodata/2/pubpa/US06_NEW_PUB.pep.*

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9 /cgn1.6/prodata/2/pubpa/US06_PUBCOMB.pep.*

10 /cgn1.6/prodata/2/pubpa/US06_PUBCOMB.pep.*

11 /cgn1.6/prodata/2/pubpa/US06_PUBCOMB.pep.*

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13 /cgn1.6/prodata/2/pubpa/US06_PUBCOMB.pep.*

14 /cgn1.6/prodata/2/pubpa/US06_PUBCOMB.pep.*

15 /cgn1.6/prodata/2/pubpa/US06_PUBCOMB.pep.*

16 /cgn1.6/prodata/2/pubpa/US06_PUBCOMB.pep.*

17 /cgn1.6/prodata/2/pubpa/US06_PUBCOMB.pep.*

18 /cgn1.6/prodata/2/pubpa/US06_PUBCOMB.pep.*

SUMMARIES

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Query Match	Length	DB ID	Description
1	529.5	82.2	123	10	US-09-144-886-60
2	529.5	81.9	140	14	US-10-006-773-4
3	519.5	80.7	115	12	US-10-275-180A-61
4	519.5	80.7	115	12	US-10-275-180A-61
5	519.5	80.7	115	12	US-10-275-180A-61
6	519.5	80.7	115	12	US-10-275-180A-61
7	519.5	80.7	115	12	US-10-275-180A-61
8	519.5	80.7	115	12	US-10-275-180A-61
9	519.5	80.7	115	12	US-10-275-180A-61
10	519.5	80.7	115	12	US-10-275-180A-61
11	519.5	80.7	115	12	US-10-275-180A-61
12	519.5	80.7	115	12	US-10-275-180A-61
13	519.5	80.7	115	12	US-10-275-180A-61
14	519.5	80.7	115	12	US-10-275-180A-61
15	519.5	80.7	115	12	US-10-275-180A-61

16	517.5	80.4	155	12	US-10-077-824-7
17	517.5	80.4	155	12	US-10-077-824-7
18	517.5	80.4	155	12	US-10-077-824-7
19	517.5	80.4	155	12	US-10-077-824-7
20	517.5	80.4	155	12	US-10-077-824-7
21	517.5	80.4	155	12	US-10-077-824-7
22	517.5	80.4	155	12	US-10-077-824-7
23	517.5	80.4	155	12	US-10-077-824-7
24	517.5	80.4	155	12	US-10-077-824-7
25	517.5	80.4	155	12	US-10-077-824-7
26	517.5	80.4	155	12	US-10-077-824-7
27	517.5	80.4	155	12	US-10-077-824-7
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29	517.5	80.4	155	12	US-10-077-824-7
30	517.5	80.4	155	12	US-10-077-824-7
31	517.5	80.4	155	12	US-10-077-824-7
32	517.5	80.4	155	12	US-10-077-824-7
33	517.5	80.4	155	12	US-10-077-824-7
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35	517.5	80.4	155	12	US-10-077-824-7
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37	517.5	80.4	155	12	US-10-077-824-7
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40	517.5	80.4	155	12	US-10-077-824-7
41	517.5	80.4	155	12	US-10-077-824-7
42	517.5	80.4	155	12	US-10-077-824-7
43	517.5	80.4	155	12	US-10-077-824-7
44	517.5	80.4	155	12	US-10-077-824-7
45	517.5	80.4	155	12	US-10-077-824-7

ALIGNMENTS

RESULT 1
US-09-144-886-60
Sequence 60, Application US/09144886
GENERAL INFORMATION:
APPLICANT: Martex, James D
TITLE OF INVENTION: Reclaiming Neurotoxic
FILE REFERENCE: 2500.11780
CURRENT APPLICATION NUMBER: US/09/144, 886
CURRENT FILING DATE: 1998-08-31
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 60
LENGTH: 123
ORIGIN: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-60

Query Match: 82.2%; Score 529.5; DB 10; Length 123;
Best Local Similarity: 80.5%; Pred. No. 4,642;
Matches 59; Conservative 13; Indels 1; Gaps 1;
DB 1 EVQQLDSGGSLVWPGSSAKL.....FTNNVTDVWAGLVWYSA 122
DB 61 PSYKGRITSSDNKATLYQVSSALREEDPYMTYRSGQVWVFPVWAGLVWYSA 119
DB 61 PSYKGRITSSDNKATLYQVSSALREEDPYMTYRSGQVWVFPVWAGLVWYSA 120
DB 120 VSA 122
DB 121 VSA 123

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RESULT 2
US-10-066-773-4
Sequence 4, Application US/10066773
Publication No. US2003013932A1
GENERAL INFORMATION:
APPLICANT: Jungman, Richard P.
TITLE OF INVENTION: Anticodons as Chimeric Effector Cell Receptors Against Tumor Ant
FILE REFERENCE: PCT NUMBER: US/10/006,773
CURRENT FILING DATE: 2001-12-10
PRIOR FILING DATE: 2000-11-30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 140
PERCENT: 100.00
OTHER INFORMATION: Description of Artificial Sequence./No. US2003013932A1 = Sync
US-10-066-773-4
Query Match 81.9%; Score 537.5; DB 14; Length 140;
Similarity 82.4%; P-Value 1.6e-42;
Matches 103; Conservative 5; Mismatches 10; Indels 7; Gaps 2;
DB 1 EVOLVEDGGGVYFPGGKATLKQASGFTFSTWNGVTFERKELRWVATISGGGSGTYY 60
QY 1 PSYKGFRTSRNNANTLYLQNSLSRSDPMATCTRGSGFTWVFWGAGTLYV 117
DB 20 EYVYSGGCVLPDQSLKQASGFTFSTWNGVTFERKELRWVATISGGGSGTYY 79
QY 61 PSYKGFRTSRNNANTLYLQNSLSRSDPMATCTRGSGFTWVFWGAGTLYV 135
DB 80 PSYKGFRTSRNNANTLYLQNSLSRSDPMATCTRGSGFTWVFWGAGTLYV 135
QY 118 VTYSA 122
DB 136 VTYSB 140
RESULT 3
US-10-286-132A-61
Sequence 61, Application US/10286132A
Publication No. US2003013932A1
GENERAL INFORMATION:
APPLICANT: Zhou, Tong
APPLICANT: Kimbrey, Robert P.
APPLICANT: Kimbrey, William J.
APPLICANT: Ouyang, Jun
APPLICANT: Lobuglio, Albert S.
APPLICANT: Bubbsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIGENIC SELECTIVE FOR A TUMOR NEOPLASIA
FILE REFERENCE: 21085, 0029305
CURRENT APPLICATION NUMBER: US/10/281,479A
PRIOR APPLICATION NUMBER: 60/293,478
PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/346,402
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: PCT/US01/4151
PRIOR APPLICATION NUMBER: 60/201,344
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.0
SEQ ID NO 61
LENGTH: 119
PERCENT: 100.00
OTHER INFORMATION: Description of Artificial Sequence
FEATURE:
ORGANISM: artificial sequence

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OTHER INFORMATION: Description of Artificial Sequence./No. US2003013932A1 = Sync
US-10-281-479A-61
Query Match 80.7%; Score 519.5; DB 12; Length 119;
Similarity 83.6%; P-Value 1.8e-41;
Matches 102; Conservative 15; Indels 3; Gaps 1;
DB 1 EVOLVEDGGGVYFPGGKATLKQASGFTFSTWNGVTFERKELRWVATISGGGSGTYY 60
QY 1 BMDVSGGCVLPDQSLKQASGFTFSTWNGVTFERKELRWVATISGGGSGTYY 60
DB 61 PSYKGFRTSRNNANTLYLQNSLSRSDPMATCTRGSGFTWVFWGAGTLYV 120
QY 61 PSYKGFRTSRNNANTLYLQNSLSRSDPMATCTRGSGFTWVFWGAGTLYV 117
DB 121 SA 122
QY 118 SS 119
RESULT 4
US-10-275-180A-61
Sequence 61, Application US/10275180A
Publication No. US20030139687A1
GENERAL INFORMATION:
APPLICANT: The Dana Research Foundation
APPLICANT: Kimbrey, Robert P.
APPLICANT: Kimbrey, William J.
APPLICANT: Ouyang, Jun
APPLICANT: Lobuglio, Albert S.
APPLICANT: Bubbsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTING FOR A TUMOR NEOPLASIA FACTOR-RELATED APOT
FILE REFERENCE: 21085, 0029305
CURRENT APPLICATION NUMBER: US/10/275,180A
PRIOR APPLICATION NUMBER: 60/293,478
PRIOR FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.0
SEQ ID NO 61
LENGTH: 119
PERCENT: 100.00
OTHER INFORMATION: Description of Artificial Sequence
FEATURE:
ORGANISM: Artificial Sequence
OTHER INFORMATION: Description of Artificial Sequence./No. US20030139687A1 =
US-10-275-180A-61
Query Match 80.7%; Score 519.5; DB 12; Length 119;
Similarity 83.6%; P-Value 1.8e-41;
Matches 102; Conservative 15; Indels 3; Gaps 1;
DB 1 EVOLVEDGGGVYFPGGKATLKQASGFTFSTWNGVTFERKELRWVATISGGGSGTYY 60
QY 1 EYVYSGGCVLPDQSLKQASGFTFSTWNGVTFERKELRWVATISGGGSGTYY 60
DB 61 PSYKGFRTSRNNANTLYLQNSLSRSDPMATCTRGSGFTWVFWGAGTLYV 120
QY 61 PSYKGFRTSRNNANTLYLQNSLSRSDPMATCTRGSGFTWVFWGAGTLYV 117
DB 121 SA 122
QY 118 SS 119
RESULT 5
US-10-286-132A-61
Sequence 61, Application US/10286132A
Publication No. US2003013932A1
GENERAL INFORMATION:
APPLICANT: Zhou, Tong
APPLICANT: Kimbrey, Robert P.
APPLICANT: Kimbrey, William J.
APPLICANT: Ouyang, Jun
APPLICANT: Lobuglio, Albert S.
APPLICANT: Bubbsbaum, Donald J.

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Qy      1 EVOLVSGGGLVVEGSLKSCASGPFSSYTMWROTPEERLEMAVATISSGGSSTYY 60
Db      1 EVOLVSGGGLVVEGSLKSCASGPFSSYTMWROTPEERLEMAVATISSGGSSTYY 60
Qy      61 PSYVGKFTIRNNANNTVTLQMSLSASBPFTSYGMSMTROTPEERLEMAVATISSGGSSTYY 120
Db      61 PSYVGKFTIRNNANNTVTLQMSLSASBPFTSYGMSMTROTPEERLEMAVATISSGGSSTYY 116
Qy      121 SA 122
Db      117 SA 118

RESULT 12
US-10-169-003-46
/ Sequence 76, Application US/0169003
/ Publication No US200301044182A1
/ GENERAL INFORMATION:
/ APPLICANT: CHUGAI SEIYAKU KASEIHIKI YAKUSHI
/ TITLE OF INVENTION: S. Infection Antibody Composition and Pharmaceutical Preparation fo
/ FILE REFERENCE: PH-1093-PCT
/ CURRENT APPLICATION NUMBER: US/10/169-003
/ PRIOR FILING DATE: 1999-05-15/0296/02116
/ PRIOR FILING DATE: 1999-12-28
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: Patentin Ver. 2.0
/ LENGTH: 118
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-10-169-003-46
Query Match      80.6%; Score 519; DB 15; Length 118;
Best Local Similarity 83.6%; Pred. No. 4,1e-41;
Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;
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Db      1 EVOLVSGGGLVVEGSLKSCASGPFSSYTMWROTPEERLEMAVATISSGGSSTYY 60
Qy      61 PSYVGKFTIRNNANNTVTLQMSLSASBPFTSYGMSMTROTPEERLEMAVATISSGGSSTYY 120
Db      61 PSYVGKFTIRNNANNTVTLQMSLSASBPFTSYGMSMTROTPEERLEMAVATISSGGSSTYY 116
Qy      121 SA 122
Db      117 SA 118

RESULT 13
US-09-423-800-76
/ Sequence 76, Application US/09423800
/ Publication No US20020153563A1
/ GENERAL INFORMATION:
/ APPLICANT: SANO, KOH
/ TITLE OF INVENTION: KACHEION KACHEION REMEDY
/ FILE REFERENCE: 04853-0036
/ CURRENT APPLICATION NUMBER: US/09/423-800
/ PRIOR FILING DATE: 1999-11-12
/ PRIOR FILING DATE: 1999-05-15/0296/02116
/ PRIOR FILING DATE: 1997-05-15/194445/1997
/ PRIOR FILING DATE: 1997-07-18
/ NUMBER OF SEQ ID NOS: 87
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 76

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/ LENGTH: 137
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-423-800-76
Query Match      80.6%; Score 519; DB 10; Length 137;
Best Local Similarity 83.6%; Pred. No. 4,9e-41;
Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;
Qy      1 EVOLVSGGGLVVEGSLKSCASGPFSSYTMWROTPEERLEMAVATISSGGSSTYY 60
Db      20 EVOLVSGGGLVVEGSLKSCASGPFSSYTMWROTPEERLEMAVATISSGGSSTYY 79
Qy      61 PSYVGKFTIRNNANNTVTLQMSLSASBPFTSYGMSMTROTPEERLEMAVATISSGGSSTYY 120
Db      80 PSYVGKFTIRNNANNTVTLQMSLSASBPFTSYGMSMTROTPEERLEMAVATISSGGSSTYY 135
Qy      121 SA 122
Db      136 SA 137

RESULT 14
US-10-337-981-76
/ Sequence 76, Application US/10337981
/ Publication No US2003010482A1
/ GENERAL INFORMATION:
/ APPLICANT: SANO, KOH
/ TITLE OF INVENTION: KACHEION KACHEION REMEDY
/ FILE REFERENCE: 04853-0036
/ CURRENT APPLICATION NUMBER: US/10/337-981
/ PRIOR FILING DATE: 2003-01-08
/ PRIOR FILING DATE: 1998-05-15/0296/02116
/ PRIOR FILING DATE: 1997-05-15
/ PRIOR FILING DATE: 1997-07-18
/ NUMBER OF SEQ ID NOS: 87
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 76
/ LENGTH: 137
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-337-981-76
Query Match      80.6%; Score 519; DB 12; Length 137;
Best Local Similarity 83.6%; Pred. No. 4,9e-41;
Matches 102; Conservative 5; Mismatches 11; Indels 4; Gaps 1;
Qy      1 EVOLVSGGGLVVEGSLKSCASGPFSSYTMWROTPEERLEMAVATISSGGSSTYY 60
Db      20 EVOLVSGGGLVVEGSLKSCASGPFSSYTMWROTPEERLEMAVATISSGGSSTYY 79
Qy      61 PSYVGKFTIRNNANNTVTLQMSLSASBPFTSYGMSMTROTPEERLEMAVATISSGGSSTYY 120
Db      80 PSYVGKFTIRNNANNTVTLQMSLSASBPFTSYGMSMTROTPEERLEMAVATISSGGSSTYY 135
Qy      121 SA 122
Db      136 SA 137

RESULT 15
US-09-881-823-12
/ Sequence 12, Application US/09881823
/ Patent No. US2002006066A1
/ GENERAL INFORMATION:
/ APPLICANT: ANDERSON, MAXWELL
/ APPLICANT: ANDERSON, SHIRIE

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; APPLICANT: TRINH, RYAN
; APPLICANT: WINS, LETITIA
; APPLICANT: WINS, LETITIA
; FILE REFERENCE: 22851-032
; CURRENT FILING DATE: 2001-06-15
; CURRENT APPLICATION NUMBER: US-09/681,823
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US-07/398,577
; PRIOR FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 12
; SEQ ID NO: 13
; SEQ ID NO: 14
; TYPE: PRT
; ORGANISM: Murine
US-09-681-823-12

Query March 80.4% Score 517.5; DB 9; Length 144;
Beat Local Similarity 80.5%; Pred.No.7.1e-41;
Matches 99; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

Cy 1 EVKQVSGGGLVWKGSGILSCAGPTTSYTWGQTPRRLFWYWTGSGGSSYY 60
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Db 20 DVKLVSGGGLVWKGSGILSCAGPTTSYTWGQTPRRLFWYWTGSGGSSYY 60
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Cy 61 POSVKGRTTSRDKAKPTLYLQNSLRSEPTMYCTRECGGPTMYN-EDWAGAGT 119
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Db 80 POSVKGRTTSRDKAKPTLYLQNTLSKSDYMYCSDSDSGYGSYYVMDVMDQGT 139
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Cy 120 USA 122
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 Job time : 107.015 secs

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OW protein - protein search, using ew model

Run on: November 7, 2003, 07:21:18 / Search time 17.9172 Seconds

(without alignments)
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Title: US-09-661-992b-86_COPY_1_122

Perfect score: 644
Sequence: 1 EYOLQSGGIVAGPCDSKLK.....FTNNVTDVGMQIVYVSA 122

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Searched: 328717 seqs, 42310856 residues

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Maximum Match 1008
Listing first 45 summaries

Database :

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3: /cgn2_6/procdet1/1aa/5B_CONB.pep.*
4: /cgn2_6/procdet1/1aa/6A_CONB.pep.*
5: /cgn2_6/procdet1/1aa/6B_CONB.pep.*
6: /cgn2_6/procdet1/1aa/backfil1ea1.pep.*

Recd No. is the number of results prefixed by chance to have a score greater than or equal to the score of the entry being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	511.5	78.5	119	US-08-976-678A-1	Sequence 1, App1
2	505.5	78.5	119	US-08-976-678A-1	Sequence 1, App1
3	502.7	78.5	135	US-08-976-788A-16	Sequence 16, App1
4	501.5	77.9	119	US-08-976-678A-3	Sequence 3, App1
5	500.5	77.7	119	US-08-483-199-16	Sequence 16, App1
6	500.5	77.7	119	US-08-483-199-16	Sequence 16, App1
7	500.5	77.7	119	US-08-483-199-16	Sequence 16, App1
8	494.7	76.7	118	US-08-326-362-2	Sequence 2, App1
9	490.7	76.1	115	US-08-976-788A-20	Sequence 20, App1
10	489.5	76.0	239	US-08-553-978A-18	Sequence 18, App1
11	489.5	76.0	239	US-08-553-978A-18	Sequence 18, App1
12	488.7	75.8	123	US-08-956-212-3	Sequence 3, App1
13	486.7	75.5	120	US-07-934-373C-4	Sequence 4, App1
14	486.7	75.5	120	US-08-976-162C-4	Sequence 4, App1
15	485.5	75.4	121	US-08-146-266C-4	Sequence 4, App1
16	485.5	75.4	121	US-08-146-266C-4	Sequence 4, App1
17	485.5	75.4	123	US-08-944-587-13	Sequence 13, App1
18	483.5	75.3	136	US-08-976-183A-32	Sequence 32, App1
19	483.5	75.3	136	US-08-976-183A-32	Sequence 32, App1
20	483.5	75.1	136	US-08-976-183A-32	Sequence 32, App1
21	483.5	75.1	136	US-08-976-183A-32	Sequence 32, App1
22	483.5	75.1	136	US-08-976-183A-32	Sequence 32, App1
23	483.5	75.0	136	US-08-976-183A-32	Sequence 32, App1
24	483.5	74.9	125	US-08-868-366-10	Sequence 10, App1
25	482.5	74.9	125	US-08-331-398A-55	Sequence 55, App1
26	482.5	74.9	125	US-08-331-398A-55	Sequence 55, App1
27	482.5	74.9	125	US-08-331-398A-55	Sequence 55, App1
28	482.5	74.9	125	US-08-331-398A-55	Sequence 55, App1
29	482.5	74.9	125	US-08-331-398A-55	Sequence 55, App1
30	482.5	74.9	125	US-08-331-398A-55	Sequence 55, App1
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33	482.5	74.9	125	US-08-331-398A-55	Sequence 55, App1
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35	482.5	74.9	125	US-08-331-398A-55	Sequence 55, App1
36	482.5	74.9	125	US-08-331-398A-55	Sequence 55, App1
37	482.5	74.9	125	US-08-331-398A-55	Sequence 55, App1
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42	482.5	74.9	125	US-08-331-398A-55	Sequence 55, App1
43	482.5	74.9	125	US-08-331-398A-55	Sequence 55, App1
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29	481.5	74.7	122	US-07-934-373C-21	Sequence 21, App1
30	481.5	74.7	122	US-08-437-642B-21	Sequence 21, App1
31	481.5	74.7	122	US-08-437-642B-21	Sequence 21, App1
32	481.5	74.7	122	US-08-437-642B-21	Sequence 21, App1
33	479.5	74.5	117	US-07-339-922A-16	Sequence 16, App1
34	479.5	74.5	237	US-08-224-591-16	Sequence 16, App1
35	479.5	74.5	237	US-08-224-591-16	Sequence 16, App1
36	479.5	74.5	237	US-08-224-591-16	Sequence 16, App1
37	479.5	74.5	241	US-08-926-789-18	Sequence 18, App1
38	479.5	74.5	245	US-08-926-789-18	Sequence 18, App1
39	479.5	74.5	245	US-08-926-789-18	Sequence 18, App1
40	479.5	74.5	245	US-08-926-789-18	Sequence 18, App1
41	479.5	74.3	239	US-08-452-164A-57	Sequence 57, App1
42	478.5	74.3	239	US-08-452-164A-57	Sequence 57, App1
43	478.5	74.3	239	US-08-452-164A-57	Sequence 57, App1
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45	478.5	74.3	239	US-08-452-164A-57	Sequence 57, App1
46	476.5	74.1	140	US-08-882-607-32	Sequence 32, App1
47	476.5	74.1	140	US-08-882-607-32	Sequence 32, App1
48	476.5	74.1	140	US-08-882-607-32	Sequence 32, App1
49	476.5	74.1	140	US-08-882-607-32	Sequence 32, App1
50	476.5	74.1	140	US-08-882-607-32	Sequence 32, App1

ALIGNMENTS

RESULT 1
PCT-US94-07659-2
GENERAL INFORMATION PCT/US94/07659
INVENTOR: Young, Peter
APPLICANT: Young, Peter
INVENTOR: Gross, Mitchell
APPLICANT: Gross, Mitchell
INVENTOR: Harte, Mark
APPLICANT: Harte, Mark
INVENTOR: Jackson, Jeffrey R.
APPLICANT: Jackson, Jeffrey R.
TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESSES: 21
ADDRESS: Smithline Beecham Corporation - Corp.
ADDRESS: Smithline Beecham Corporation - Corp.
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-2799
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC compatible DOS
SOFTWARE: Patent release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CLASSIFICATION:
PCT-US94/07659
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/050,534
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
TELEPHONE: (610) 270-5024
TELEFAX: (610) 270-5024
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE LENGTH: 247 amino acids
TYPE: amino acids
TOPOLOGY: linear
PCT-US94-07659-2
Query Match 79.4%; Score 511.5; DB 5; Length 247;

Best Local Similarity 82.0%; Pred. No. 86-47;
Matches 100; Conservative 5; Mismatches 14; Indels 3; Gaps 1;
QY EVQLVDSGGGLVWGSGSLKSLASQSPFSSTVMNVRQTPERLELVAVATISSGSSSTYY 60
DB 20 EVHVSQGLVWGSGSLKSLASQSPFSSTVMNVRQTPERLELVAVATISSGSSSTYY 79
QY 61 PSYKQPTFSRQNKNTLYLQNSLRASDPTMYCYRSGGGLTMMVYDWGAGDLYY 120
DB 80 PSYKQPTFSRQNKNTLYLQNSLRASDPTMYCYRSGGGLTMMVYDWGAGDLYY 136
QY 121 SA 122
DB 137 SS 138

RESULT 3
US-08-475-674A-1
Sequence 1, Application US/08875674A
Patent No. 6572857
GENERAL INFORMATION:
INVENTOR: CASIMIRO, J. E.
APPLICANT: LOPEZABENO VALLANARES, J.
APPLICANT: P REZ RODR GUEZ, R.
APPLICANT: SIERRA BL GUEZ, P.
TITLE OF INVENTION: Anti-C66 monoclonal antibodies and their uses
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 4
ADDRESSER: Jackman, Siegel Marullo Atomsen & Greenspan, P.C.
CITY: San Francisco
STATE: New York
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk 3.5" (1.4 MB).
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Word Perfect 5.0 for Windows 95.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875, 674A
CLASSIFICATION: 7-310-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCJ/CU96/00004
FILING DATE: 18-NOV-1996
PRIORITY DATE: 18-NOV-1996
NAME: HENRY A. MARZULLO, JR.
REGISTRATION NUMBER: 20,910
TELEPHONE: (914) 723-4300
TELEFAX: (914) 723-4301
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acid residues.
TYPE: Amino acid.
STRANDEDNESS: Unknown.
TOPOLOGY: Unknown.
MOLECULAR TYPE: Protein.
HYPOCHROMIC: No.
FRAGMENT TYPE: N Terminal fragment.
ORGANISM: Mice Balb/C
INDIVIDUAL ISOLATE: lot CIA
TISSUE TYPE: Murine hybridoma
CLONE: Sub-clone for CIA
FEATURES:
IDENTIFICATION METHOD: Experimental.
OTHER INFORMATION: Sequence corresponding to the variable region

Patent No. 6572857
OTHER INFORMATION: of the heavy chain of the monoclonal antibody recognizing h
OTHER INFORMATION: designated as sub-clone for CIA.
US-08-875-674A-1
Query Match 78.5%; Score 505.5; DB 4; Length 119;
Best Local Similarity 82.0%; Pred. No. 146-46;
Matches 100; Conservative 17; Indels 3; Gaps 1;
QY EVQLVDSGGGLVWGSGSLKSLASQSPFSSTVMNVRQTPERLELVAVATISSGSSSTYY 60
DB 1 EVQLVDSGGGLVWGSGSLKSLASQSPFSSTVMNVRQTPERLELVAVATISSGSSSTYY 117
QY 61 PSYKQPTFSRQNKNTLYLQNSLRASDPTMYCYRSGGGLTMMVYDWGAGDLYY 120
DB 81 PSYKQPTFSRQNKNTLYLQNSLRASDPTMYCYRSGGGLTMMVYDWGAGDLYY 117
QY 121 SA 122
DB 118 SS 119

RESULT 3
US-08-579-378A-16
Sequence 16, Application US/08579378A
Patent No. 6210671
INVENTOR: CO. Man Sung
APPLICANT: CO. Man Sung
TITLE OF INVENTION: Humanized Antibodies Reactive with
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS: 20
ADDRESSER: Townsend and Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Present Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/579, 378A
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/160, 074
FILING DATE: 30-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963, 946
FILING DATE: 17-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9511895-8
FILING DATE: 17-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9511696-8
FILING DATE: 19-SEP-1995
ATTORNEY/AGENT INFORMATION:
ADDRESSER: LEBESCHNEZ, JOE O.
REGISTRATION NUMBER: 11623-002220
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
FAX: 415-326-2400
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: Amino acid
TOPOLOGY: Linear
MOLECULAR TYPE: protein
US-08-579-378A-16

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Query Match 78.04; Score 502; DB 3; Length 135;
Similarity 78.04; Pred. No. 47e-46;
Matches 98; Conservative 9; Mismatches 9; Indels 6; Gaps 2;

DB 1 EVYQSSGGVLYPFGSGLKLSGASGSPFSTYSWNRQTPERRLEMAVATISGSGSSTYY 60
20 EVYQSSGGVLYPFGSGLKLSGASGSPFSTYSWNRQTPERRLEMAVATISGSGSSTYY 78
QY 61 PSYKGFRTISDNKANTLYLQMSLRSEEDPMYCTCRGGGFTVMYFVDWAGTLVTV 120
DB 79 PSYKGFRTISDNKANTLYLQMSLRSEEDPMYCTCRGGGFTVMYFVDWAGTLVTV 133
QY 121 SA 122
DB 134 SS 135

RESULT 4
US-08-875-674A-3
Patent No. 6572857
GENERAL INFORMATION:
APPLICANT: MONTANO, CASIMIRO, J. E.
INVENTOR: MONTANO, CASIMIRO, J. E.
APPLICANT: P. REZ RODRIGUEZ, R.
APPLICANT: SIERRA, ELIZABETH, P.
APPLICANT: TORO, BRAVO, E. R.
TITLE OF INVENTION: Anti-CD6 monoclonal antibodies and their uses
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lackebeck Siegel Marzullo Aronson & Greenspan, P.C.
STREET: One Chase Road
CITY: Secaucus, NJ 07094
STATE: N.J.
COUNTRY: U.S.A.
ZIP: 10583
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk 3.5" (1.4 MB)
OPERATING SYSTEM: Windows 95
SOFTWARE: Word Perfect 5.0 for Windows 95.
CURRENT APPLICATION DATA:
PILING DATE: 17-JULY-1997
CLASSIFICATION: D510
PILING DATE: 18-JULY-1996
ATTORNEY/AGENT INFORMATION:
NAME: ABRAMS, RICHARD, JR.
REFERENCE/DOCKET NUMBER: P-12
TELEPHONE: (914) 723-4300
TELEFAX: (914) 723-4300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acid residues.
STRANDS: 1
TOPOLOGY: Unknown.
MOLBIOL TYPE: Unknown.
MOLBIOL TYPE: Protein
MOLBIOL TYPE: NO
ORIGINAL SOURCE:
SOURCE: P. REZ RODRIGUEZ, R.
CELL LINE: 98 2/3 CHO
IMMEDIATE SOURCE:
CLONE: sub-clone for t1a
FEATURES:
IDENTIFICATION METHOD: By similarity with known sequence.

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OTHER INFORMATION: Sequence corresponding to the humanized
Patent No. 6572857
GENERAL INFORMATION: variant of sub-clone for t1a recognizing human CD6, particle
OTHER INFORMATION: to the variable region of the heavy chain.
US-08-875-674A-3

Query Match 77.94; Score 501.5; DB 4; Length 119;
Similarity 72.04; Pred. No. 3.7e-46;
Matches 100; Conservative 18; Mismatches 18; Indels 3; Gaps 1;

DB 1 EVYQSSGGVLYPFGSGLKLSGASGSPFSTYSWNRQTPERRLEMAVATISGSGSSTYY 60
20 EVYQSSGGVLYPFGSGLKLSGASGSPFSTYSWNRQTPERRLEMAVATISGSGSSTYY 78
QY 61 PSYKGFRTISDNKANTLYLQMSLRSEEDPMYCTCRGGGFTVMYFVDWAGTLVTV 120
DB 61 PSYKGFRTISDNKANTLYLQMSLRSEEDPMYCTCRGGGFTVMYFVDWAGTLVTV 117
QY 121 SA 122
DB 118 SS 119

RESULT 5
US-08-475-000-16
Patent No. 661467
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
INVENTOR: RING, DAVID B.
TITLE OF INVENTION: ANTIBODY-BINDING SITES OF ANTIBODY
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: 4500 Central Expressway
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94602-8097
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 07-JUN-1995
CLASSIFICATION: D510
PILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: SWEETLAND, PAUL
REFERENCE/DOCKET NUMBER: 0880.007
TELEPHONE: (510) 601-2688
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLBIOL TYPE: Unknown.
MOLBIOL TYPE: protein
US-08-475-000-16

Query Match 77.74; Score 500.5; DB 2; Length 119;
Similarity 74.54; Pred. No. 4.7e-46;
Matches 97; Conservative 10; Mismatches 12; Indels 3; Gaps 1;

DB 1 EVYQSSGGVLYPFGSGLKLSGASGSPFSTYSWNRQTPERRLEMAVATISGSGSSTYY 60
20 EVYQSSGGVLYPFGSGLKLSGASGSPFSTYSWNRQTPERRLEMAVATISGSGSSTYY 78
QY 61 PSYKGFRTISDNKANTLYLQMSLRSEEDPMYCTCRGGGFTVMYFVDWAGTLVTV 120
DB 61 PSYKGFRTISDNKANTLYLQMSLRSEEDPMYCTCRGGGFTVMYFVDWAGTLVTV 110
QY 121 SA 122
DB 118 SS 119

```

Db 61 PDYSKRFVSRDINASSLYLQNSLSRSEDTALTYCARYGAG--DAMFRAYGGGLTVV 117
QY 121 SA 122
||
Db 118 SA 119

US-08-483-199-16

```

1 GENERAL INFORMATION:
2 APPLICANT: RING, DAVID B.
3 TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
4 TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
5 NUMBER OF SEQUENCES: 18
6
7 Correspondence Address:

```

```

? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/483,199
? FILING DATE: 07-JUN-1995

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MOLECULE TYPE: protein

Query Match	77.7%	Score 500.5;	DB 2;	Length 119;
Best Local Similarity	79.5%	Pred. No. 4.7e-46;		
Matches	97;	Conservative	10;	Mismatches 12;
				Indels 3

[illegible]

RESOLUT. 7
US80-464-508-16
Serial No. 16, Application US/06464508
Patent No. 5948647
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
NUMBER OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SOURCES: 18

CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, P.O. BOX 8097
CITY: Emeryville

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,508

MOLECULE TYPE: protein
US-08-484-508-16

Query Match 77.7%; Score 500.5; DB:2; Length 119;
Best Local Similarity 79.5%; Pred. No. 4.7e-46;
Matches 97; Conservative 10; Mismatches 12; Indels 3; Gaps 1;

```

Qy      61 PSVVGKFTTSDNAKATLYLQMSLRSEDTMYCTREGGSPYNAVYDVWAGATLVY 12
        |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      61 PSVVGKFTVSNDNASSLYLGSSLRSEDTLYLCRTGG--DAWFAYMQGLTVY 11
        |||||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Qy      121 SA 122
        |||
Db      118 SA 119

```

US-08-326-362-2
Sequence 2, 5/3/99/1
PATENT NO. 5/3/99/1
CLASSIFICATION:
APPLICANT: Roseler, Klaus
APPLICANT: Seeman, Gerhard
APPLICANT: Diebold, Wolfgang
TITLE OF INVENTION: Monoclonal Anti-Ganglioside Antibody,
NUMBER OF SHEETS: 4
TITLE OF SECOND INVENTION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pineacon, Henderson, Parabow, Garrett &
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: Washington
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
FILED IN: 10/1/99
OPERATING SYSTEM: PC-9505/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/06/326,362
 FILING DATE: 19-MAR-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA: US 06/032,863
 APPLICATION NUMBER: US 06/032,863
 FILING DATE: 19-MAR-1992
 APPLICATION NUMBER: DE P 42 08 795.3
 FILING DATE: 19-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 REFERENCE/DOCKET NUMBER: 32,220
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4400
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acids
 LENGTH: 118
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-06-326-362-2
 Query Match 76.7% Score 494, DB 1, Length 118;
 Best Local Similarity 79.5% Pred. No. 2,3e-45;
 Matches 97, Conservative 7, Mismatches 14, Indels 4, Gaps 1;
 QY 1 EVQLDSGGVAVKPGKSLTSCASGPTSTYMWVQRPPEKLEWVAISGGSSITY 60
 DB 1 QVQLDSGGVAVKPGKSLTSCASGPTSTYMWVQRPPEKLEWVAISGGSSITY 60
 QY 61 PSVKGFTFSRNMANTLYLQNSLSASPTDPAWYCTRECGGFTWVPMVQAGTLVY 120
 DB 61 PSVKGFTFSRNMANTLYLQNSLSASPTDPAWYCTRECGGFTWVPMVQAGTLVY 120
 QY 121 SA 122
 DB 117 SS 118
 RESULT 9
 US-06-579-378A-20
 Sequence: 20, Application US/06579378A
 GENERAL INFORMATION:
 APPLICANT: CO. Man Sung
 TITLE OF INVENTION: Mutated Antibodies Reactive with
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jomenee and Howard and Trey
 ONE NEW BLISS, Suite 2000
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/06/579,378A
 FILING DATE: 27-DEC-95
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/060,074
 FILING DATE: 19-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/883,946
 FILING DATE: 01-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 9512895, 8

FILING DATE: 17-AUG-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 9514696.8
 FILING DATE: 19-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 REFERENCE/DOCKET NUMBER: 11823-002220
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-326-2422
 TELEFAX: 415-326-2422
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acids
 LENGTH: 135
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-06-579-378A-20
 Query Match 76.1% Score 490, DB 3, Length 135;
 Best Local Similarity 78.1% Pred. No. 7,2e-45;
 Matches 96, Conservative 10, Mismatches 10, Indels 6, Gaps 2;
 QY 1 EVQLDSGGVAVKPGKSLTSCASGPTSTYMWVQRPPEKLEWVAISGGSSITY 60
 DB 2 EVQLDSGGVAVKPGKSLTSCASGPTSTYMWVQRPPEKLEWVAISGGSSITY 60
 QY 61 PSVKGFTFSRNMANTLYLQNSLSASPTDPAWYCTRECGGFTWVPMVQAGTLVY 120
 DB 79 PSVKGFTFSRNMANTLYLQNSLSASPTDPAWYCTRECGGFTWVPMVQAGTLVY 133
 QY 121 SA 122
 DB 134 SS 135
 RESULT 10
 PCT-US96-13152-4
 Sequence: 13, Application PCT/US9613152
 GENERAL INFORMATION:
 APPLICANT: Martin, Ulrich, et al.
 TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fa
 NUMBER OF SEQUENCES: 4
 ADDRESSES: Felle & Lynch
 ADDRESSEE: Acta; Norman D. Hanson
 STREET: 408 Third Avenue
 STATE: New York
 COUNTRY: U.S.A.
 CITY: 10012
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Computer Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/13152
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/576,953
 FILING DATE: 27-DEC-95
 FILING DATE: 27-DEC-95
 APPLICATION NUMBER: EP 95 112 895.8
 APPLICATION NUMBER: EP 95 114 969.9
 FILING DATE: 19-SEP-95
 ATTORNEY/AGENT INFORMATION:
 REFERENCE/DOCKET NUMBER: 30,946
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 686-2500

TELEFAX: (212) 818-3884
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 Length: 443
 Type: amino acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 PCT:0936-1152.4

Query Match 76.11; Score 490; DB 5; Length 443;
 Best Local Similarity 78.71; Pred. No. 3.3e-44;
 Matches 96; Mismatches 10; Indels 6; Gaps 2;

QY 1 EVOLSSQGLVKEKCSLSCASGFPSSTYMTNATGTEPRLEWVATISGSGSTYY 60
 DB 1 EVOLSSQGLVKEKCSLSCASGFPSSTYMTNATGTEPRLEWVATISGSGSTYY 59
 QY 61 PSYKGFPTSPNANATYLTIONSSLRSDPTMYCTREGGFTWYVDMGAGTLYV 120
 DB 60 PSYKGFPTSPNANATYLTIONSSLRSDPTMYCTREGGFTWYVDMGAGTLYV 114
 QY 121 SA 122
 DB 115 SS 116

RESULT 11
 US-08-553-497a-18
 US-08-553-497a-18 Application US/08553497a
 Patent No. 5844093

GENERAL INFORMATION:
 APPLICANT: KETTERBROUGH, C. A.
 ATTORNEY/AGENT INFORMATION:
 NAME: ANSELL, KEITH H.
 APPLICANT: GUSKOW, DETLEF
 APPLICANT: ADAM, JAMES
 APPLICANT: ROBERTS, TIANHONG
 APPLICANT: ROBERTS, ELIZABET
 APPLICANT: BLASCO, FRANCESC
 APPLICANT: PIULANT, JAMES
 TITLE OF INVENTION: ANTI-BGP SINGLE-CHAIN PVS AND ANTI-BGP
 TITLE OF INVENTION: ANTIBODIES
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MILLER, WHITE, ZELAND & BRANNIGAN, P.C.
 STREET: 1200 LAMARCON BLVD. SUITE 1400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: US

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 CLASSIFICATION: 16-NOV-1995
 APPLICATION NUMBER: US/08/553-497a
 FILING DATE: 17-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/EP95/00978
 FILING DATE: 16-MAR-1995
 PRIOR APPLICATION NUMBER: EP 94104160.0
 FILING DATE: 17-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 94118970.6
 FILING DATE: 17-MAR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: HAWLEY-KING, DIANA
 REGISTRATION NUMBER: 33,302
 REFERENCE/DOCKET NUMBER: MEXICO 1726

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-243-6333
 TELEFAX: 703-243-6410
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 Length: 239
 Type: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: protein
 US-08-553-497a-18

Query Match 76.04; Score 489.5; DB 2; Length 239;
 Best Local Similarity 80.54; Pred. No. 1.7e-44;
 Matches 99; Mismatches 12; Indels 5; Gaps 2;

QY 1 EVOLSSQGLVKEKCSLSCASGFPSSTYMTNATGTEPRLEWVATISGSGSTYY 60
 DB 1 EVOLSSQGLVKEKCSLSCASGFPSSTYMTNATGTEPRLEWVATISGSGSTYY 60
 QY 61 PSYKGFPTSPNANATYLTIONSSLRSDPTMYCTREGGFTWYVDMGAGTLYV 119
 DB 61 PSYKGFPTSPNANATYLTIONSSLRSDPTMYCTREGGFTWYVDMGAGTLYV 116
 QY 120 VSA 122
 DB 117 VAS 119

RESULT 12
 US-08-356-272-3
 US-08-356-272-3 Application US/08056272
 Patent No. 5766946

GENERAL INFORMATION:
 APPLICANT: Clarifigila Dr., Maurizio
 ATTORNEY/AGENT INFORMATION:
 NAME: SANCHEZ, MONOLICAL
 NUMBER OF SEQUENCES: Monoclonal Antibodies to glycoprotein P
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Patent and Trademark Department, Sandoz
 STREET: 1900 East Avenue
 CITY: East Hanover
 STATE: N. J.
 COUNTRY: U. S. A.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 CLASSIFICATION: 15-DEC-1994
 APPLICATION NUMBER: US/08/356-272
 FILING DATE: 15-DEC-1994
 PRIOR APPLICATION DATA:
 CLASSIFICATION: G01N33/574
 CLASSIFICATION: G01N33/577
 CLASSIFICATION: G01N33/575
 PRIOR APPLICATION DATA: 61/439/395
 APPLICATION NUMBER: IT RM92000457
 FILING DATE: 17-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO RCT/EP93/0133
 FILING DATE: 16-JUN-1993
 PRIOR APPLICATION NUMBER: NO
 ATTORNEY/AGENT INFORMATION:
 NAME: MARLE, CARL W.
 REGISTRATION NUMBER: 40,721
 REFERENCE/DOCKET NUMBER: 118-8040
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (201) 503-6177
 TELEFAX: (201) 503-6807
 TELEFAX: 240867
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:

LENGTH: 123 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-356-272-3

Query Match 75.8%; Score 486; DB 1; Length 123;
 Best Local Similarity 79.2%; Pred. No. 16-44;

Matches 99; Conservative 9; Mismatches 11; Indels 6; Gaps 3;

QY 1 EVOLSSGGGLVX-FGGSKLTKGQASGPTSSSYNGWQTPKELKEMWATISSGSSY 59
 DB 1 QVQLSSGGGLVX-FGGSKLTKGQASGPTSSSYNGWQTPKELKEMWATISSGSSY 60
 QY 60 YPPSVKGFPTSDNANNTLYLQNSLRSDNMYCTIR-EGGGFTWMTDPWAGATL 117
 DB 61 PDSVKGFTSDNANNTLYLQNSLRSDNMYCTIR-EGGGFTWMTDPWAGATL 117
 QY 118 YTVSA 122
 DB 118 YTVSA 122
 DB 118 YTVSA 122

RESULT 13
 US-07-934-373C-4
 Sequence 4; Application US/07934373C
 Patent No. 6054237

GENERAL INFORMATION:
 APPLICANT: Paul J. Carter
 ATTORNEY/AGENT INFORMATION:
 FILING DATE: 15-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/07/934,373C
 FILING DATE: 15-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05126
 FILING DATE: 15-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/15272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P070922
 TELEPHONE: 650/952-9881
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 123 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Minitel (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/934,373C
 FILING DATE: 15-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05126
 FILING DATE: 15-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/15272
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 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P070922
 TELEPHONE: 650/952-9881
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 123 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

Query Match 75.5%; Score 486; DB 2; Length 120;
 Best Local Similarity 77.0%; Pred. No. 1,76-44;
 Matches 94; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVOLSSGGGLVX-FGGSKLTKGQASGPTSSSYNGWQTPKELKEMWATISSGSSY 60
 DB 1 QVQLSSGGGLVX-FGGSKLTKGQASGPTSSSYNGWQTPKELKEMWATISSGSSY 60

DB 1 EVOLSSGGGLVX-FGGSKLTKGQASGPTSSSYNGWQTPKELKEMWATISSGSSY 60
 QY 61 PDSVKGFTSDNANNTLYLQNSLRSDNMYCTIR-EGGGFTWMTDPWAGATL 120
 DB 61 ADVSKGFPTSDNANNTLYLQNSLRSDNMYCTIR-EGGGFTWMTDPWAGATL 118
 QY 121 SA 122
 DB 121 SA 122
 DB 119 SA 120

RESULT 14
 US-08-437-642B-4
 Sequence 4; Application US/08437642B
 Patent No. 6054237

GENERAL INFORMATION:
 APPLICANT: Paul J. Carter
 ATTORNEY/AGENT INFORMATION:
 FILING DATE: 15-JUN-1992
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05126
 FILING DATE: 15-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/15272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P070922C1
 TELEPHONE: 650/952-9881
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Minitel (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05126
 FILING DATE: 15-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/15272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P070922C1
 TELEPHONE: 650/952-9881
 TELEFAX: 650/952-9881
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

Query Match 75.5%; Score 486; DB 3; Length 120;
 Best Local Similarity 77.0%; Pred. No. 1,76-44;
 Matches 94; Conservative 9; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVOLSSGGGLVX-FGGSKLTKGQASGPTSSSYNGWQTPKELKEMWATISSGSSY 60
 DB 1 QVQLSSGGGLVX-FGGSKLTKGQASGPTSSSYNGWQTPKELKEMWATISSGSSY 60
 QY 61 PDSVKGFTSDNANNTLYLQNSLRSDNMYCTIR-EGGGFTWMTDPWAGATL 120
 DB 61 ADVSKGFPTSDNANNTLYLQNSLRSDNMYCTIR-EGGGFTWMTDPWAGATL 118
 QY 121 SA 122
 DB 121 SA 122
 DB 119 SA 120

Db 61 ADSVKQFTISRDSDSKNTLYLQWNSLRAPETVAVYQADNRGAVS--YFDWNGGTLVTV 118

QY 121 SA 122

Db 119 SS 120

RESUME 15
US-08-146-206C-4
Sequence 4, Application US/08146206C
Patent No. 6407211
GENERAL INFORMATION:
Inventor: Paul J.
Applicant: Presis, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
COMPILED BY: Genentech, Inc.
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIA TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPILED BY: Genentech, Inc.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Malign (Genentech)
CURRENT APPLICATION DATA: 08/08/146-206C
FILING DATE: 17-Nov-01
CLASSIFICATION: 530
PRIORITY DATA:
PUBLICATION NUMBER: 07/715272
PRIORITY: 04-Nov-99
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
TELEPHONE: 650/225-1994
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/952-9881
INFORMATION: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
US-08-146-206C-4

Query Match 75.5%; Score 486; DB 4; Length 120;
Best Local Similarity 77.0%; Fred. No. 1.7e-44;
Matches 57; Conserved 5; Mismatches 17; Indels 2; Gaps 1;

QY 1 HVQDQSGGVLPFGSLKSLCAAGTFPSSTMSWVQTPPEELMVAATISQGSSTYY 60
Db 1 EVQVDSGGGVLPFGSLKSLCAAGTFPSSTMSWVQTPPEELMVAATISQGSSTYY 60
QY 61 PSYVKGFTISRDNAKNTLYLQWNSLRAPETVAVYQADNRGAVS--YFDWNGGTLVTV 120
Db 61 ADSVKQFTISRDSDSKNTLYLQWNSLRAPETVAVYQADNRGAVS--YFDWNGGTLVTV 118

QY 121 SA 122
Db 119 SS 120

Search completed: November 7, 2003, 07:30:10
Job time : 17.9172 secs

GenScope version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 8.07477 seconds

(without alignments)
652,278 Million cell updates/sec

Title: us-09-661-992b-86_COPY_138_249

Sequence: 1 EVLUTSPASLAVSAGRAAT.....QQSNEDEPFRGTGRLERK 112

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Display first 45 summaries

Database : SwissProt_41.4

Prefix No. is the number of results predicted by chance to have a score as good as the best score observed, assuming the scores are distributed as derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	512	91.1	111	KVH_MOUSE	P01660 mus musculu
2	512	87.7	111	KVH_MOUSE	P01663 mus musculu
3	512	87.7	111	KVJ_MOUSE	P01661 mus musculu
4	511	87.5	131	KVJ_MOUSE	P01661 mus musculu
5	490	83.9	132	KVJ_MOUSE	P01659 mus musculu
6	468	80.1	111	KVH_MOUSE	P01665 mus musculu
7	468	80.1	111	KVH_MOUSE	P01665 mus musculu
8	467	80.0	111	KVH_MOUSE	P01667 mus musculu
9	465	79.6	111	KVH_MOUSE	P01671 mus musculu
10	458	78.1	111	KVH_MOUSE	P01664 mus musculu
11	458	78.3	111	KVJ_MOUSE	P01662 mus musculu
12	457	78.3	111	KVJ_MOUSE	P01662 mus musculu
13	456	78.1	111	KVH_MOUSE	P01673 mus musculu
14	456	78.1	111	KVH_MOUSE	P01673 mus musculu
15	440	75.4	110	KVJ_MOUSE	P01664 mus musculu
16	440	75.3	111	KVJ_MOUSE	P01664 mus musculu
17	439	75.2	111	KVJ_MOUSE	P01665 mus musculu
18	439	75.2	111	KVJ_MOUSE	P01665 mus musculu
19	431	73.6	111	KVJ_MOUSE	P01674 mus musculu
20	431	73.6	111	KVJ_MOUSE	P01674 mus musculu
21	422	72.3	108	1	P01657 mus musculu
22	412	70.5	111	KVH_MOUSE	P01655 mus musculu
23	412	70.5	111	KVH_MOUSE	P01655 mus musculu
24	375	64.1	114	KVJ_MOUSE	P01649 mus sapien
25	375	63.7	108	1	P01649 mus sapien
26	370.5	63.4	133	KVH_MOUSE	P00437 homo sapien
27	368.5	63.4	133	KVH_MOUSE	P00437 homo sapien
28	368.5	63.4	133	KVH_MOUSE	P01651 mus sapien
29	353	60.4	108	1	P01651 mus sapien
30	352.5	60.4	129	KVH_MOUSE	P01650 homo sapien
31	352	60.3	108	1	P01650 homo sapien
32	352	60.3	108	1	P01650 homo sapien
33	350.5	60.0	109	KVH_MOUSE	P01650 homo sapien

ALIGNMENTS

RESULT 1	KVH_MOUSE	STANDARD	PR1	111 AA
1	KVH_MOUSE			
2	P01660	(Rel. 01, Created)		
3	21-JUL-1986	(Rel. 01, Last sequence update)		
4	21-JUL-1986	(Rel. 01, Last annotation update)		
5	15-JUL-1999	(Rel. 38, Last annotation update)		
6	19 kappa chain V-III region	PC 3741/TEBC 111.		
7	19 kappa chain V-III region	PC 3741/TEBC 111.		
8	19 kappa chain V-III region	PC 3741/TEBC 111.		
9	19 kappa chain V-III region	PC 3741/TEBC 111.		
10	19 kappa chain V-III region	PC 3741/TEBC 111.		
11	19 kappa chain V-III region	PC 3741/TEBC 111.		
12	19 kappa chain V-III region	PC 3741/TEBC 111.		
13	19 kappa chain V-III region	PC 3741/TEBC 111.		
14	19 kappa chain V-III region	PC 3741/TEBC 111.		
15	19 kappa chain V-III region	PC 3741/TEBC 111.		
16	19 kappa chain V-III region	PC 3741/TEBC 111.		
17	19 kappa chain V-III region	PC 3741/TEBC 111.		
18	19 kappa chain V-III region	PC 3741/TEBC 111.		
19	19 kappa chain V-III region	PC 3741/TEBC 111.		
20	19 kappa chain V-III region	PC 3741/TEBC 111.		
21	19 kappa chain V-III region	PC 3741/TEBC 111.		
22	19 kappa chain V-III region	PC 3741/TEBC 111.		
23	19 kappa chain V-III region	PC 3741/TEBC 111.		
24	19 kappa chain V-III region	PC 3741/TEBC 111.		
25	19 kappa chain V-III region	PC 3741/TEBC 111.		
26	19 kappa chain V-III region	PC 3741/TEBC 111.		
27	19 kappa chain V-III region	PC 3741/TEBC 111.		
28	19 kappa chain V-III region	PC 3741/TEBC 111.		
29	19 kappa chain V-III region	PC 3741/TEBC 111.		
30	19 kappa chain V-III region	PC 3741/TEBC 111.		
31	19 kappa chain V-III region	PC 3741/TEBC 111.		
32	19 kappa chain V-III region	PC 3741/TEBC 111.		
33	19 kappa chain V-III region	PC 3741/TEBC 111.		

Db 63 PAFSGSGSRDPDTLTINPVPADVAATYCCQSNEDPTFGGATLEIK 111

RESULT 2

AC P01661 STANDARD; PRT; 111 AA.

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1] TaxId=10090;
RP SEQUENCE

RK MEDLINE=79073152; PubMed=103003;
RT "Reorganization of genetic information may produce immunoglobulin diversity.";
RL Nature 276:785-790 (1978).
RS P016792.F03
DR InterPro: IPR003006; 19-11k.
DR InterPro: IPR003596; 19-V.
DR SMART: SM00466; 19-V.
DR PROSITE: PS50835; 16 LITS.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 39 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 92 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 123 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12005 MW; 3909761913453CB CRC64;

Query Match 88.5% Score 517; DB 1; Length 111;
Best Local Similarity 89.9% Pred. No. 6.2e-46;
Matches 98; Conservative 5; Indels 0; Gaps 0;

Qy 3 VTGSPASLAVSAGQRTATCSAESVDVSYGNPHTYQIQPQPTLLTYSANLSGI 62
Db 3 VTGSPASLAVSAGQRTATCSAESVDVSYGNPHTYQIQPQPTLLTYSANLSGI 62
Qy 63 PAFSGSGSRDPDTLTINPVPADVAATYCCQSNEDPTFGGATLEIK 111
Db 63 PAFSGSGSRDPDTLTINPVPADVAATYCCQSNEDPTFGGATLEIK 111

RESULT 3

AC P01661 STANDARD; PRT; 111 AA.

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1] TaxId=10090;
RP SEQUENCE (AB03.22)
RP MEDLINE=79012520; PubMed=99744;
RT "Antibody diversity: multiple genes encode structurally related mouse kappa variable regions.";
RA McKean D.J., Bell M., Porter M.;
RM 131 AA

RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).

RK SEQUENCE (PC 9245).
RT "Reorganization of genetic information may produce immunoglobulin diversity.";
RL Nature 276:785-790 (1978).
RS P016792.F03
DR InterPro: IPR003006; 19-11k.
DR InterPro: IPR003596; 19-V.
DR SMART: SM00466; 19-V.
DR PROSITE: PS50835; 16 LITS.
KW Immunoglobulin V region.
FT DOMAIN 1 24 FRAMEWORK-1.
FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 39 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 92 92 FRAMEWORK-3.
FT DOMAIN 102 111 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; DTDP060930453CB CRC64;

Query Match 87.7% Score 512; DB 1; Length 111;
Best Local Similarity 89.9% Pred. No. 2.1e-47;
Matches 98; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 3 VTGSPASLAVSAGQRTATCSAESVDVSYGNPHTYQIQPQPTLLTYSANLSGI 62
Db 3 VTGSPASLAVSAGQRTATCSAESVDVSYGNPHTYQIQPQPTLLTYSANLSGI 62
Qy 63 PAFSGSGSRDPDTLTINPVPADVAATYCCQSNEDPTFGGATLEIK 111
Db 63 PAFSGSGSRDPDTLTINPVPADVAATYCCQSNEDPTFGGATLEIK 111

RESULT 4

AC P01661 STANDARD; PRT; 131 AA.

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1] TaxId=10090;
RP SEQUENCE OF 1-35.
RK MEDLINE=79235697; PubMed=98179;
RT "Primary structure of a terminal extra peptide segment linked to the variable and constant regions of immunoglobulin light chain precursors: implications for the organization and controlled expression of immunoglobulin genes.";
RL Biochemistry 17:1292-1300 (1978).
RN [2]
RP SEQUENCE OF 21-131.
RK MEDLINE=79140285; PubMed=4691517;
RT "Mouse immunoglobulin chain kappa pattern of sequence variation among kappa chains with inbred sequence differences.";
RL Biochemistry 13:760-771 (1973).
RN REVISIONS
RA McKean D.J., Bell M., Porter M.;
RM 131 AA

"Mechanisms of antibody diversity: multiple genes encode structurally related mouse kappa variable regions".
 DR Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
 DR R88: P01672; 1986.
 DR R88: P01672; 1986.
 DR Interpro: IPR007210; Ig L-like.
 DR Interpro: IPR003066; Ig MC.
 DR Interpro: IPR003595; Ig V.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 DR Immunoglobulin V region; Signal.
 DR CHAIN 1 21 131 IG KAPPA CHAIN V-II REGION MOPC 63.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 59 80 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 81 112 FRAMEWORK-3.
 FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 122 131 BY SIMILARITY.
 FT NON_TER 131 131 BY SIMILARITY.
 DR SEQUENCE 131 AA; 14291 MW; D2132630D808A CR6C4;
 Query Match 87.5%; Score 511; DB 1; Length 131;
 Best Local Similarity: 89.9%; Fwd. No. 3-26-47; Indels 0; Gaps 0;
 Matches 98; Conservative 5; Mismatches 6;
 3 VITGSPASVLSVSGATITSCASRSYSDYVYPMHWYQIQCPKPLLYVANSLSG1 62
 23 VITGSPASVLSVSGATITSCASRSYSDYVYPMHWYQIQCPKPLLYVANSLSG1 62
 63 PAFSGSGSGPTLTINPVAZDAVATYCCGSDNPDLTGVGTPLTLEIK 112
 DB 83 PAFSGSGSGPTLTINPVAZDAVATYCCGSDNPDLTGVGTPLTLEIK 131
 ID KAPPA MOUSE STANDARD; FRT; 132 AA.
 AC P01659;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region MOPC 321 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Artiodactyla; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID:10090;
 DR SEQUENCE OF 1-37.
 DR MEDLINE:78238897; PubMed:981179;
 DR Burtstein V., Schneider 1.;
 DR "The variable and constant regions of immunoglobulin light chain precursor: implications on the organization and controlled expression of immunoglobulin genes".
 DR J. Immunol. 151:4592-4600(1993).
 DR SEQUENCE OF 21-132.
 DR MEDLINE:7310244; PubMed:4130623;
 DR "Mouse immunoglobulin chain. Partial amino acid sequence of a kappa chain".
 DR Biochemistry 12:749-759(1973).
 DR -1- HENCE-ONES PROTEIN HAS ALSO DETERMINED IT DIFFERS FROM THAT REPORTED FOR MOUSE MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY RESIDUES.
 DR PIR: P01672; 1986.
 DR R88: P01672; 1986.
 DR Interpro: IPR007210; Ig L-like.

Interpro: IPR003066; IG MC.
 DR Interpro: IPR003596; Ig V.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 DR Immunoglobulin V region; Bence-Jones protein; Signal.
 DR CHAIN 1 20 IG KAPPA CHAIN V-II REGION MOPC 321.
 FT DOMAIN 21 132 FRAMEWORK-1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 59 73 FRAMEWORK-2.
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 122 131 FRAMEWORK-4.
 FT DISULFID 132 131 BY SIMILARITY.
 FT NON_TER 132 132 BY SIMILARITY.
 DR SEQUENCE 132 AA; 15233 MW; 973809DB773B59 CR6C4;
 Query Match 82.7%; Score 490; DB 1; Length 132;
 Best Local Similarity: 78.4%; Fwd. No. 5-58-45; Indels 0; Gaps 0;
 Matches 86; Conservative 20; Mismatches 4;
 3 VITGSPASVLSVSGATITSCASRSYSDYVYPMHWYQIQCPKPLLYVANSLSG1 62
 23 VITGSPASVLSVSGATITSCASRSYSDYVYPMHWYQIQCPKPLLYVANSLSG1 62
 63 PAFSGSGSGPTLTINPVAZDAVATYCCGSDNPDLTGVGTPLTLEIK 112
 DB 83 PAFSGSGSGPTLTINPVAZDAVATYCCGSDNPDLTGVGTPLTLEIK 132
 ID KAPPA MOUSE STANDARD; FRT; 112 AA.
 AC P01659;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-II region TERC 124.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Artiodactyla; Rodentia; Sciurognathi; Muridae; Mus.
 NCBI_TaxID:10090;
 DR SEQUENCE.
 DR MEDLINE:7311025; PubMed:4691517;
 DR McKean D.J.; Porter M.; Hood L.E.;
 DR "Mouse immunoglobulin chains. Pattern of sequence variation among kappa chain vHc limited sequence differences".
 DR J. Immunol. 151:4592-4600(1993).
 DR R88: P01672; 1986.
 DR Interpro: IPR007210; Ig L-like.
 DR Interpro: IPR003066; Ig MC.
 DR Interpro: IPR003595; Ig V.
 DR SMART: SM00406; IgV; 1.
 DR PROSITE: PS00835; IG_LIKE; 1.
 DR Immunoglobulin V region.
 DR CHAIN 1 24 FRAMEWORK-1.
 FT DOMAIN 24 38 FRAMEWORK-2.
 FT DOMAIN 39 53 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 61 73 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 113 121 FRAMEWORK-4.
 FT DISULFID 122 131 BY SIMILARITY.
 FT NON_TER 132 132 BY SIMILARITY.
 DR SEQUENCE 112 AA; 12333 MW; 7CDD32DB86E5D71 CR6C4;
 Query Match 82.7%; Score 490; DB 1; Length 112;
 Best Local Similarity: 78.4%; Fwd. No. 5-58-45; Indels 0; Gaps 0;
 Matches 86; Conservative 18; Mismatches 6;

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OY 3 VTGSPALVAGCATITSCASSTVSYGVGNHMTQOIQPQPKLLIYASNESGI 62
Db 3 VTGSPALVAGCATITSCASSTVSYGVGNHMTQOIQPQPKLLIYASNESGI 62
OY 63 PARSSGSRDPTLTINVPADVATYYCOSNEDPTFGGTGLTLEIK 112
Db 63 PARSSGSRDPTLTINVPADVATYYCOSNEDPTFGGTGLTLEIK 112

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RESULT 7

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KRN MOUSE STANDARD; PRT; 111 AA.
ID KRN MOUSE
AC P01665;
DR 21-JUL-1986 (Rel. 01, Created)
DR 15-JUL-1999 (Rel. 01, Last sequence update)
DR 15-JUL-1999 (Rel. 36, Last annotation update)
DE 1g kappa chain V-II region PC 7183.
OS Mus musculus (Mouse)
OC Mus musculus (Mouse)
NCBI_TaxID=10090.

```

```

RN SEQUENCE
RX MEDLINE=7907152; PubMed=103003;
RA Weigert M., Garmalan L., Loh E., Schilling J., Hood L.R.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
PIR: B01937; KXN83.
DR HSBP; P01679; XN83.
DR InterPro; IPR007110; 1g-like.
DR InterPro; IPR003596; 1g-V.
DR Pfam; PF00047; 1g; 1. 2L-.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00855; IG_LIKE; 1.
FT DOMAIN 1 24 38 FRAMEWORK-1.
FT DOMAIN 2 39 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 4 61 92 FRAMEWORK-2.
FT DOMAIN 5 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 6 102 111 FRAMEWORK-4.
FT NON TER 111 112 BY SIMILARITY.
SQ SEQUENCE 111 AA; 11952 MM; 20589BS/OC306031 CIRC64;

```

```

Query Match
Best Local Similarity 80.0%; Score 468 DB 1; Length 111;
Matches 90; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

```

```

OY 3 VTGSPALVAGCATITSCASSTVSYGVGNHMTQOIQPQPKLLIYASNESGI 62
Db 3 VTGSPALVAGCATITSCASSTVSYGVGNHMTQOIQPQPKLLIYASNESGI 62
OY 63 PARSSGSRDPTLTINVPADVATYYCOSNEDPTFGGTGLTLEIK 112
Db 63 PARSSGSRDPTLTINVPADVATYYCOSNEDPTFGGTGLTLEIK 112

```

RESULT 8

```

KRN MOUSE STANDARD; PRT; 111 AA.
ID KRN MOUSE
AC P01665;
DR 21-JUL-1986 (Rel. 01, Created)
DR 15-JUL-1999 (Rel. 01, Last sequence update)
DR 15-JUL-1999 (Rel. 36, Last annotation update)
DE 1g kappa chain V-II region PC 7043.
OS Mus musculus (Mouse)
OC Mus musculus (Mouse)
NCBI_TaxID=10090.

```

```

OX NCBI_TaxID=10090;

```

```

RN SEQUENCE
RX MEDLINE=7907152; PubMed=103003;
RA Weigert M., Garmalan L., Loh E., Schilling J., Hood L.R.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
PIR: B01937; KXN83.
DR HSBP; P01679; XN83.
DR InterPro; IPR007110; 1g-like.
DR InterPro; IPR003596; 1g-V.
DR Pfam; PF00047; 1g; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00855; IG_LIKE; 1.
FT DOMAIN 1 24 38 FRAMEWORK-1.
FT DOMAIN 2 39 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 4 61 92 FRAMEWORK-2.
FT DOMAIN 5 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 6 102 111 FRAMEWORK-4.
FT NON TER 111 112 BY SIMILARITY.
SQ SEQUENCE 111 AA; 12002 MM; 765FC56C6306D92 CIRC64;

```

```

Query Match
Best Local Similarity 80.0%; Score 467; DB 1; Length 111;
Matches 90; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

```

```

OY 3 VTGSPALVAGCATITSCASSTVSYGVGNHMTQOIQPQPKLLIYASNESGI 62
Db 3 VTGSPALVAGCATITSCASSTVSYGVGNHMTQOIQPQPKLLIYASNESGI 62
OY 63 PARSSGSRDPTLTINVPADVATYYCOSNEDPTFGGTGLTLEIK 112
Db 63 PARSSGSRDPTLTINVPADVATYYCOSNEDPTFGGTGLTLEIK 112

```

RESULT 9

```

KRN MOUSE STANDARD; PRT; 111 AA.
ID KRN MOUSE
AC P01667;
DR 21-JUL-1986 (Rel. 01, Created)
DR 15-JUL-1999 (Rel. 01, Last sequence update)
DR 15-JUL-1999 (Rel. 36, Last annotation update)
DE 1g kappa chain V-II region PC 6100.
OS Mus musculus (Mouse)
OC Mus musculus (Mouse)
NCBI_TaxID=10090.

```

```

RN SEQUENCE
RX MEDLINE=7907152; PubMed=103003;
RA Weigert M., Garmalan L., Loh E., Schilling J., Hood L.R.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity."
PIR: B01937; KXN83.
DR HSBP; P01679; XN83.
DR InterPro; IPR007110; 1g-like.
DR InterPro; IPR003596; 1g-V.
DR Pfam; PF00047; 1g; 1.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00855; IG_LIKE; 1.
FT DOMAIN 1 24 38 FRAMEWORK-1.
FT DOMAIN 2 39 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 54 60 COMPLEMENTARITY-DETERMINING-2.

```



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DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003006; IG-MHC.
DR InterPro: IPR003596; IG-V.
DR SMART: SMO0406; IG-V.
DR PROSITE: PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 29 FRAMEWORK-2.
FT DOMAIN 3 53 FRAMEWORK-3.
FT DOMAIN 4 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 61 FRAMEWORK-3.
FT DOMAIN 6 92 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 MA.
SQ SEQUENCE 111 AA; 1164 MW; E2IAD9A9655962 CRC64;

Query Match 78.1%; Score 457; DB 1; Length 111;
Best Local Similarity 80.7%; Pred. No. 1.4e-41;
Matches 89; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 3 VLTQSPALVAVSGGRATISCAESVDVSYGVNFMHWYQOIPOPPPELLLYRANLSGGI 62
DB 63 PARFSGSGSDPTLTINPVADAVYVYCOQNSMDPFLFTGTMTLEIK 111
63 PARFSGSGSDPTLTINPVADAVYVYCOQNSMDPFLFTGTMTLEIK 111

RESULT 13
KVYU MOUSE STANDARD; PRT; 111 AA.
ID K33970
DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 29 FRAMEWORK-2.
FT DOMAIN 3 53 FRAMEWORK-3.
FT DOMAIN 4 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 61 FRAMEWORK-3.
FT DOMAIN 6 92 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 MA.
SQ SEQUENCE 111 AA; 12039 MW; 184698841885826 CRC64;

Query Match 78.1%; Score 456; DB 1; Length 111;
Best Local Similarity 80.7%; Pred. No. 1.8e-41;
Matches 89; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

```

```

OY 3 VLTQSPALVAVSGGRATISCAESVDVSYGVNFMHWYQOIPOPPPELLLYRANLSGGI 62
DB 63 PARFSGSGSDPTLTINPVADAVYVYCOQNSMDPFLFTGTMTLEIK 111
63 PARFSGSGSDPTLTINPVADAVYVYCOQNSMDPFLFTGTMTLEIK 111

RESULT 14
KVYU MOUSE STANDARD; PRT; 111 AA.
ID K33970
DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 29 FRAMEWORK-2.
FT DOMAIN 3 53 FRAMEWORK-3.
FT DOMAIN 4 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 61 FRAMEWORK-3.
FT DOMAIN 6 92 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 MA.
SQ SEQUENCE 111 AA; 12038 MW; E838A231609452E CRC64;

Query Match 79.8%; Score 456; DB 1; Length 111;
Best Local Similarity 79.8%; Pred. No. 1.8e-41;
Matches 87; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

OY 3 VLTQSPALVAVSGGRATISCAESVDVSYGVNFMHWYQOIPOPPPELLLYRANLSGGI 62
DB 63 PARFSGSGSDPTLTINPVADAVYVYCOQNSMDPFLFTGTMTLEIK 111
63 PARFSGSGSDPTLTINPVADAVYVYCOQNSMDPFLFTGTMTLEIK 111

RESULT 15
KVYU MOUSE STANDARD; PRT; 111 AA.
ID K33970
DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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CY NCBI_textID=10090;
RP SEQUENCE.
RX MEDLINE:79073152; PubMed:103003;
RA Weisger M., Gershtalden L., Job E., Schilling J., Hood L.R.;
RT The sequence of the human immunoglobulin heavy chain
RT diversity."
RL Nature 276:785-790(1978) .
CC -1- MISCELLANEOUS: THE FC 4285 AND FC 4039 SEQUENCES ARE IDENTICAL.
DR HBBP 20157; KIMRS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR InterPro; IPR003597; Ig_C.
DR SMART; SM00406; Cys1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FM Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 2 33 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 3 53 FRAMEWORK-2.
FT DOMAIN 4 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 5 61 FRAMEWORK-3.
FT DOMAIN 6 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 7 102 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11986 MW; BP36CS9AA7858467 CRC64;

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Query_Match Similarity 77.14; Score 450; DB 1; Length 111;
Best Local Similarity 78.94; Pred.No. 7.6e-41;
Matches 86; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

```

```

CY 3 VLTGSPALAVLGLQKATISCRASESYDSYGVNFMNMQIQIPKLTIVPNSLSGT 62
DB 3 VLTGSPALAVLGLQKATISCRASESYDSYGVNFMNMQIQIPKLTIVPNSLSGT 62
CY 63 PARPSGSGSCTDFTLTINVEADVATYYCCQSNEDPTFGTGRATK 111
DB 63 PARPSGSGSCTDFTLTINVEADVATYYCCQSNEDPTFGTGRATK 111

```

Search completed: November 7, 2003, 07:28:08
Job time : 8.07477 secs


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QY 3 VITROSPASLAVS/GQARATICSAEVS-VNSGVNPNWYQIQQPQPLLITYASNSLS 61
DB 22 VITROSPASLAVS/GQARATICSAEVS-VNSGVNPNWYQIQQPQPLLITYASNSLS 61
QY 63 IANFSGSGSRPTLTITNPEVDVAVYTCQGSNDLPTFGVTLERIK 112
DB 82 VITROSPASLAVS/GQARATICSAEVS-VNSGVNPNWYQIQQPQPLLITYASNSLS 112

RESULT 12
ID 08K1P3 PRELIMINARY: PRT: 112 AA.
AC 08K1P3; 2003 (TEMBelrel: 22, Created)
DT 01-OCT-2002 (TEMBelrel: 22, Last sequence update)
DE 01-08-2002 (TEMBelrel: 22, Last annotation update)
DE Anti-Vipase light chain variable region (Fragment)
OC Mus musculus (Mouse).
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC NCI1_TaxID=10090.
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=BLM/c; TISSUE=Hypermunized spleen;
RC STRAIN=BLM/c; TISSUE=Hypermunized spleen; Nishiyama Y., Paul S.;
RT "Immunoprecipitation and identification of L-Vipase response to the p-
RT entanlome of Vip and identification of L-Vipase vt domains."
RT Submitted (May-2002) to the EMBL/Genbank/DBD databases.
DR InterPro: IPRO03599; 19.v.
DR InterPro: IPRO07110; 19-11ke.
DR InterPro: IPRO03006; 19-MEC.
DR InterPro: IPRO03596; 19.v.
DR Pfam: PF00047; 19.1.
DR SMART; SM00409; 19.1.
DR SMART; SM00406; 19.v.
DR PROSITE; PS50835; 19_LIKE; 1.
FT NON_TER 112
SQ SEQUENCE 112 AA; 12017 MW; 22D05B541CDB18 CRC64;

Query Match
Best Local Similarity: 59.28; Score 345.5; DB 11; Length 112;
Matches 68; Conservative 15; Mismatches 22; Indels 5; Gaps 1;

QY 3 VITROSPASLAVS/GQARATICSAEVS-VNSGVNPNWYQIQQPQPLLITYASNSLS 62
DB 3 VITROSPASLAVS/GQARATICSAEVS-VNSGVNPNWYQIQQPQPLLITYASNSLS 62
QY 63 IANFSGSGSRPTLTITNPEVDVAVYTCQGSNDLPTFGVTLERIK 112
DB 82 VITROSPASLAVS/GQARATICSAEVS-VNSGVNPNWYQIQQPQPLLITYASNSLS 112

RESULT 13
ID 09UL3 PRELIMINARY: PRT: 108 AA.
AC 09UL3; 2003 (TEMBelrel: 13, Created)
DT 01-MAY-2003 (TEMBelrel: 13, Last sequence update)
DT 01-MAY-2003 (TEMBelrel: 23, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment)
OC Mus musculus (Human)
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Cetartiodactyla; Homo.
OC NCI1_TaxID=9606.
RN [1]
RP MEDLINE=98271139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Betney S.M.,
RA Young D.C.;

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RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RC Clin. Immunol. Immunopathol. 87:184-192 (1998).
DB 63 IANFSGSGSRPTLTITNPEVDVAVYTCQGSNDLPTFGVTLERIK 112
DB 82 VITROSPASLAVS/GQARATICSAEVS-VNSGVNPNWYQIQQPQPLLITYASNSLS 112
QY 63 IANFSGSGSRPTLTITNPEVDVAVYTCQGSNDLPTFGVTLERIK 112
DB 82 VITROSPASLAVS/GQARATICSAEVS-VNSGVNPNWYQIQQPQPLLITYASNSLS 112

RESULT 14
ID 08K1P3 PRELIMINARY: PRT: 114 AA.
AC 08K1P3; 2003 (TEMBelrel: 22, Created)
DT 01-OCT-2002 (TEMBelrel: 22, Last sequence update)
DE 01-08-2002 (TEMBelrel: 22, Last annotation update)
DE Anti-Vipase light chain variable region (Fragment)
OC Mus musculus (Mouse).
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC NCI1_TaxID=10090.
RN [1]

SEQUENCE FROM N.A.
RC STRAIN=BLM/c; TISSUE=Hypermunized spleen;
RC STRAIN=BLM/c; TISSUE=Hypermunized spleen; Nishiyama Y., Paul S.;
RT "Immunoprecipitation and identification of L-Vipase response to the p-
RT entanlome of Vip and identification of L-Vipase vt domains."
RT Submitted (May-2002) to the EMBL/Genbank/DBD databases.
DR InterPro: IPRO03599; 19.v.
DR InterPro: IPRO07110; 19-11ke.
DR InterPro: IPRO03006; 19-MEC.
DR InterPro: IPRO03596; 19.v.
DR Pfam: PF00047; 19.1.
DR SMART; SM00409; 19.1.
DR SMART; SM00406; 19.v.
DR PROSITE; PS50835; 19_LIKE; 1.
FT NON_TER 114
SQ SEQUENCE 114 AA; 11162 MW; 8BD833D8E3E8F01 CRC64;

Query Match
Best Local Similarity: 59.08; Score 344.5; DB 11; Length 114;
Matches 67; Conservative 17; Mismatches 23; Indels 3; Gaps 1;

QY 3 VITROSPASLAVS/GQARATICSAEVS-VNSGVNPNWYQIQQPQPLLITYASNSLS 62
DB 3 VITROSPASLAVS/GQARATICSAEVS-VNSGVNPNWYQIQQPQPLLITYASNSLS 62
QY 63 IANFSGSGSRPTLTITNPEVDVAVYTCQGSNDLPTFGVTLERIK 112
DB 82 VITROSPASLAVS/GQARATICSAEVS-VNSGVNPNWYQIQQPQPLLITYASNSLS 112
QY 60 IANFSGSGSRPTLTITNPEVDVAVYTCQGSNDLPTFGVTLERIK 109
DB 60 IANFSGSGSRPTLTITNPEVDVAVYTCQGSNDLPTFGVTLERIK 109

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XX PF 13-SEP-2000; 2000MO-EP08936.
 XX MM 14-SEP-1999; 99AT-0001576.
 XX MM (BAXT) BAXTER AG.
 XX PA
 XX PI Schellinger F, Kerschbaum R, Falkner F, Dornier F,
 XX WPI, 2001-290358/30.
 XX N-PDB: AAF30732.
 XX PF New factor IX/factor IXa antibodies and their derivatives useful for
 XX increasing antioxytic activity of factor IXa and for treating blood
 XX coagulation disorders such as haemophilia A and haemorrhagic diathesis -
 XX Claim 12; Fig 16; 138pp; English.
 XX
 XX The present sequence is that of a single chain Fv (scfv) derivative
 XX of antibody 198/A82, comprising the heavy (VH) and light (VL) chain
 XX variable regions of 198/A82 joined by an artificial, flexible linker
 XX region. The heavy chain variable region of 198/A82 is joined to the
 XX 198/A82 VH and VL regions and cloning in vector pDAP2 of 198/A82 is
 XX an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
 XX antibodies of the invention. Anti-FIX/FIXa and their derivatives,
 XX including the heavy chain variable region of 198/A82, are useful as
 XX activity or FIXa activating activity. Administration leads to a collector
 XX increase in the procoagulant activity of FIXa, even in the presence
 XX of FVIIa inhibitors. This allows for rapid blood coagulation even
 XX in haemorrhagic patients. The antibodies and their derivatives in a
 XX claimed pharmaceutical composition for treating patients with blood
 XX coagulation disorders, especially haemophilia A and haemorrhagic
 XX diathesis.

XX Sequence 249 AA;
 XX
 XX Query Match 100.0%; Score 584; DB 22; Length 249;
 XX Best Local Similarity 100.0%; Pred. No. 2,3e-41;
 XX Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 1 EVYVQSGKALVSGDPAITSGKASSTSYGNNMHWQIQFQPPULLLYASNNESG 60
 DB 138 EVYVQSGKALVSGDPAITSGKASSTSYGNNMHWQIQFQPPULLLYASNNESG 197
 0Y 61 GPARSGSGSRDPTLTINVEDADVATVYCOOSSEDPYTFGCTGLAKLR 112
 DB 198 GPARSGSGSRDPTLTINVEDADVATVYCOOSSEDPYTFGCTGLAKLR 249

RESULT 2
 ID AAE50442; standard; Protein: 294 AA.
 XX AAE50442;
 DT 21-JUN-2001 (first entry)
 XX
 XX Anti-FIX/FIXa antibody 198/B1-myc-tag fusion.
 XX
 XX Factor IX; FIX; Factor IXa; FIXa; scfv; antibody; procoagulant;
 XX Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 XX haemorrhagic diathesis; haemostatic; antioxytic; therapy; mouse;
 XX myc-tag;
 XX
 XX Chimeric - Mus musculus.
 XX Chimeric - Synthetic.
 XX Chimeric - Escherichia coli.
 XX
 XX Key Location/Qualifiers
 XX Peptide 1..222
 XX /Label: Signal_peptide
 XX Protein 23..294

FT /label= Mature_protein
 FT Protein 23..271
 FT /label= scfv
 FT Region 23..144
 FT /label= VH
 FT Misc-difference 76
 FT /note= "Encoded by GGN"
 FT Peptide 145..159
 FT 146-162 Linker
 FT Region /label= VL
 FT Peptide 272..274
 FT /label= Spacer
 FT Protein /label= myc_tag
 FT Peptide 287..288
 FT /label= myc_tag
 FT Peptide /label= His_tag
 XX
 XX MO20011992-N2.
 XX
 XX 22-MAR-2001.
 XX
 XX 13-SEP-2000; 2000MO-EP08936.
 XX
 XX 14-SEP-1999; 99AT-0001576.
 XX (BAXT) BAXTER AG.
 XX
 XX Schellinger F, Kerschbaum R, Falkner F, Dornier F,
 XX WPI, 2001-290358/30.
 XX N-PDB: AAF30732.
 XX PF New factor IX/factor IXa antibodies and their derivatives useful for
 XX increasing antioxytic activity of factor IXa, and for treating blood
 XX coagulation disorders such as haemophilia A and haemorrhagic diathesis -
 XX Example 16; Fig 34; 138pp; English.
 XX
 XX The present sequence is that of a fusion protein comprising: a Palb
 XX leader; a single chain Fv (scfv) derivative of antibody 198/B1
 XX consisting of a heavy chain variable region of 198/B1 joined to the
 XX 198/B1 joined by an artificial, flexible linker peptide; a spacer;
 XX a myc-tag peptide; a spacer; and a C-terminal 6His affinity tail.
 XX 198/B1 is an example of anti-human Factor IX (FIX)/activated Factor
 XX IX (FIXa) antibodies of the invention. Anti-FIX/FIXa antibodies and
 XX their derivatives, including the heavy chain variable region of 198/B1,
 XX are useful as activity or FIXa activating activity. Administration leads to an
 XX increase in the procoagulant activity of FIXa, even in the presence
 XX of FVIIa inhibitors. This allows for rapid blood coagulation even
 XX in haemorrhagic patients. The antibodies and derivatives are used in a claimed
 XX pharmaceutical composition for treating patients with blood
 XX coagulation disorders, especially haemophilia A and haemorrhagic
 XX diathesis. The antibodies and their derivatives are expressed in E. coli. It
 XX exhibited FVIII-like activity.

XX Sequence 294 AA;
 XX
 XX Query Match 98.1%; Score 573; DB 22; Length 294;
 XX Best Local Similarity 100.0%; Pred. No. 2,3e-41;
 XX Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

0Y 3 VTGPGKALVSGDPAITSGKASSTSYGNNMHWQIQFQPPULLLYASNNESG 62
 DB 162 VTGPGKALVSGDPAITSGKASSTSYGNNMHWQIQFQPPULLLYASNNESG 221
 0Y 63 PARGSGSGSRDPTLTINVEDADVATVYCOOSSEDPYTFGCTGLAKLR 112
 DB 222 PARGSGSGSRDPTLTINVEDADVATVYCOOSSEDPYTFGCTGLAKLR 771

DT 09-JAN-2003 (updated)
 DT 01-OCT-1991 (first entry)
 DB Murine 184 light chain-2 variable region.
 XX Monoclonal antibody; complementarity determining region; CDR;
 XX Integrin; hypidroma 184; protein REI; day/Rel; 19.
 KM
 XX Mus sp.
 OS
 XX EP438312-A.
 XX EP438312-A.
 XX 24-JUN-1991.
 PD
 XX 17-JAN-1991; 91EP-0300367.
 XX
 XX 20-DEC-1990; 90US-0627421.
 PR
 XX 19-JAN-1990; 90US-0467532.
 PR
 XX (MERI) MERCK & CO INC.
 XX (LAWM)/ LAW M P.
 PA
 XX Law WP, Mark GE, Schmidt JM, Slinger II;
 DT
 XX NFI: 1991-216985/30.
 DR
 XX N-FSDB; AAO12684.
 XX
 XX New recombinant immunoglobulin (s) reactive with leukocyte CD18
 PT antigen - comprise human beta chain variable region of a murine
 PT complementarity regions useful in treatment of inflammation
 XX
 XX Disclosure; Fig 25; 77pp; English.
 XX
 XX A recombinant human Ig comprises a human heavy chain framework
 CC and murine CDRs (with the heavy chain framework mutated at sites
 CC near the CDRs), a human light chain framework and murine CDRs.
 CC The heavy chain framework is derived from a human monoclonal
 CC antibody from which the CDRs were derived. It is designated
 CC mutated gal/Rel. The human Ig is capable of binding to a human
 CC CD18 integrin.
 CC The heavy chain framework is derived from
 CC (HCC HS 10164) protein. The heavy chain framework is derived from
 CC human myeloma protein REI (EP-239400).
 CC See also AAO12683-84.
 CC Updated on 09-JAN-2003 to add missing OS field.)
 CC Updated on 25-MAR-2003 to correct PA field.)
 CC
 XX Sequence 112 AA;
 SQ
 XX
 XX Query Match
 XX Best Local Similarity 92.8%; Score 542; DB 13; Length 112;
 XX Matches 104; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY
 XX 3 VTGSPSLAVSICGARTICGASBSVDYGVFHHVYCOI RQPFPLLTYASNSISGI 62
 XX 3 VTGSPSLAVSICGARTICGASBSVDYGVFHHVYCOI RQPFPLLTYASNSISGI 62
 DB 63 PARFSGSGSRPTLTINPEVDVAIVYCOQSNEDLPFGQPTLAKIR 112
 QY 63 PARFSGSGSRPTLTINPEVDVAIVYCOQSNEDLPFGQPTLAKIR 112
 DB 63 PARFSGSGSRPTLTINPEVDVAIVYCOQSNEDLPFGQPTLAKIR 112
 RESULT 7
 ID ABB77332 standard; Protein; 112 AA.
 XX ABB77332;
 XX 17-JUN-2002 (first entry)
 DT
 XX Mouse 184 light chain variable region SEQ ID NO 37.

XX Mouse; human; immunoglobulin; antigenicity; immunogenicity.
 XX
 XX Mus sp.
 OS
 XX US2002034765-A1.
 XX
 XX 21-MAR-2002.
 PD
 XX 16-MAR-2001; 2001US-0810502.
 XX
 XX 19-AUG-1993; 93US-0109187.
 PR
 XX 01-MAR-1995; 96US-0609218.
 PR
 XX 17-NOV-1991; 91US-0702217.
 PR
 XX (MERI) MERCK & CO INC.
 PA
 XX Daugherty BL, Mark GE, Fedian BA;
 DT
 XX WFI: 2002-338924/37.
 DR
 XX
 XX Identifying and replacing immunoglobulin surface amino acid residues
 PT useful for converting the antigenicity of a first mammalian species to
 PT a second mammalian species
 XX
 XX Example 1; Fig 12; 36pp; English.
 XX
 XX The invention relates to identifying differences (1) in mammalian species
 CC specific surface amino acid residues on an immunoglobulin which converts
 CC the antigenicity of a first mammalian species to a second mammalian
 CC species and (2) in mammalian species amino acid residues which convert the
 CC immunoglobulin surface amino acid residues which convert the
 CC antigenicity of a first mammalian species to that of a second mammalian
 CC species.
 CC The method simultaneously reduces the immunogenicity and
 CC antigenicity of a first mammalian species and the replacement of exterior
 CC amino acid residues has no effect on protein size and structure.
 CC The method also provides a method for preparing a recombinant antibody
 CC primer used in the construction of the "wheeler" 184 heavy and light
 CC chain variable regions plus those necessary to fuse the human signal and
 CC intron 1 region.
 CC That of the mouse 184 light chain variable region.
 CC
 XX Sequence 112 AA;
 SQ
 XX
 XX Query Match
 XX Best Local Similarity 92.8%; Score 542; DB 23; Length 112;
 XX Matches 104; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY
 XX 3 VTGSPSLAVSICGARTICGASBSVDYGVFHHVYCOI RQPFPLLTYASNSISGI 62
 XX 3 VTGSPSLAVSICGARTICGASBSVDYGVFHHVYCOI RQPFPLLTYASNSISGI 62
 DB 63 PARFSGSGSRPTLTINPEVDVAIVYCOQSNEDLPFGQPTLAKIR 112
 QY 63 PARFSGSGSRPTLTINPEVDVAIVYCOQSNEDLPFGQPTLAKIR 112
 DB 63 PARFSGSGSRPTLTINPEVDVAIVYCOQSNEDLPFGQPTLAKIR 112
 RESULT 8
 ID AAB7494 standard; Protein; 111 AA.
 XX AAB7494;
 XX 25-MAR-2003 (updated)
 DT
 XX 06-JUN-1994 (first entry)
 DT
 XX Murine anti-CD18 Ab 60.3 light chain.
 XX
 XX Monoclonal antibody; MAb; heavy chain; light chain;
 XX polypeptide chain reaction; PCR; chain; 184;
 XX immunoglobulin; humanized antibody; leukocyte; integrin.

DT 24-OCT-2001 (first entry)
 XX Anticancer serum light chain variable region.
 XX Anticancer serum light chain variable region.
 XX Antibody; gene therapy; HIV; human immunodeficiency virus; tumour;
 XX metabolic disorder; immune disorder; auto-immune disorder; lysosome;
 XX antibody light chain variable region; serum.
 XX Synthetic.
 XX W0200149713-A2.
 XX 12-JUL-2001.
 XX 29-DEC-2000; 2000WO-IT00554.
 XX 30-DEC-1999; 99IT-RM00803.
 XX (CNEN) ENNA ENTE NUOVE TECNOLOGIE ENERGIA.
 XX (CONS) SOC CONSORTELE METEOROLOGICO AGROFIS SRL.
 XX Benvenuto E, Francioni R, Desiderio A, Tavolozzi P;
 XX NPI: 2001-502555/55.
 XX
 XX Disclousure; Fig 4, 10pp; English.
 XX The invention relates to peptides which are able to confer stability and
 XX solubility to an antibody comprising these peptides. The peptides
 XX are especially H-FR1, H-FR2, H-FR3, H-FR4, L-FR1, L-FR2, L-FR3 or L-FR4
 XX present within a variable region of an antibody which makes the antibody
 XX H-FR4 are present within the variable region of an antibody which makes the antibody
 XX antibody, covalently linked to the H-FR1, H-FR2, H-FR3 in the order
 XX (H-FR1)-(H-FR2)-(H-FR3)-(H-FR4) and
 XX (H-FR1)-(H-FR2)-(H-FR3)-(H-FR4) and
 XX linked to the L-FR1, L-FR2, L-FR3 in the order (L-FR1)-(L-FR2)-(L-FR3)-(L-FR4)
 XX the variable region of the light chain of the order (L-FR1)-(L-FR2)-(L-FR3)-(L-FR4)
 XX (L-FR2)-(L-FR3)-(L-FR4) and (L-FR3)-(L-FR4) and
 XX polynucleotides (e.g. by gene therapy) are useful for the manufacture
 XX or plant cell. The pathologies are infectious (e.g. viral infections such
 XX as HIV, human immunodeficiency virus, infectious), tumour, metabolic and
 XX represents the antibody serum light chain variable region, used as
 XX a basis for making mutant antibodies.
 XX Sequence 112 AA:
 XX
 XX Query Match 90.1%; Score 526; DB 22; Length 112;
 XX Match Local Similarity 93.6%; Pred. No. 9.1e-38;
 XX Matches 102; Mismatches 2; Indels 0; Gaps 0;
 XX
 XX 4 LUGSPALVAVLQGGATISGKASVSVDYVYPMHQQGQPPKILYRANMSTGIP 63
 XX 4 LUGSPALVAVLQGGATISGKASVSVDYVYPMHQQGQPPKILYRANMSTGIP 63
 XX 4 LUGSPALVAVLQGGATISGKASVSVDYVYPMHQQGQPPKILYRANMSTGIP 63
 XX 4 LUGSPALVAVLQGGATISGKASVSVDYVYPMHQQGQPPKILYRANMSTGIP 63
 XX 64 ARFSGSGSHDTPLTINPAPADAVVYCCSGNDPPTFGQGYKLETR 112
 XX 64 ARFSGSGSHDTPLTINPAPADAVVYCCSGNDPPTFGQGYKLETR 112
 XX
 XX RESULT 13
 XX 11 AN007497 standard; Protein, 252 AA.
 XX

AC AN007497;
 XX
 DT 24-OCT-2001 (first entry)
 XX Synthetic antibody scFv(F8).
 XX Anticancer serum light chain variable region.
 XX Antibody; gene therapy; HIV; light chain;
 XX immunodeficiency virus; tumour; metabolic disorder;
 XX human immunodeficiency virus; infectious (e.g. viral infections such
 XX as HIV, human immunodeficiency virus, infectious), tumour, metabolic and
 XX represents the synthetic antibody light chain variable region, used as
 XX a basis for making mutant antibodies incorporating the peptides of the
 XX invention.
 XX Sequence 252 AA:
 XX
 XX Query Match 90.1%; Score 526; DB 22; Length 252;
 XX
 XX Key Location/Qualifiers
 XX 1..125
 XX Protein
 XX /label=VA
 XX /note="heavy chain variable region"
 XX /note="40
 XX /label=light chain peptide
 XX /note="This peptide is specifically claimed in claim 17-
 XX 141..252
 XX /note="light chain variable region"
 XX
 XX W0200149713-A2.
 XX 12-JUL-2001.
 XX 29-DEC-2000; 2000WO-IT00554.
 XX 30-DEC-1999; 99IT-RM00803.
 XX (CNEN) ENNA ENTE NUOVE TECNOLOGIE ENERGIA.
 XX (CONS) SOC CONSORTELE METEOROLOGICO AGROFIS SRL.
 XX Benvenuto E, Francioni R, Desiderio A, Tavolozzi P;
 XX NPI: 2001-502555/55.
 XX N-FR1, N-FR2, N-FR3, N-FR4
 XX
 XX Peptides which are able to confer stability and solubility to an
 XX antibody comprising these peptides, useful for treating pathologies
 XX (e.g. tumour) associated with accumulation of a molecule inside or
 XX outside a tumour, or animal cell -
 XX
 XX Example 1; Page 81; 10pp; English.
 XX The invention relates to peptides which are able to confer stability and
 XX solubility to an antibody comprising these peptides. The peptides
 XX are especially H-FR1, H-FR2, H-FR3, H-FR4, L-FR1, L-FR2, L-FR3 or L-FR4
 XX present within a variable region of an antibody which makes the antibody
 XX H-FR4 are present within the variable region of an antibody which makes the antibody
 XX antibody, covalently linked to the H-FR1, H-FR2, H-FR3 in the order
 XX (H-FR1)-(H-FR2)-(H-FR3)-(H-FR4) and
 XX (H-FR1)-(H-FR2)-(H-FR3)-(H-FR4) and
 XX linked to the L-FR1, L-FR2, L-FR3 in the order (L-FR1)-(L-FR2)-(L-FR3)-(L-FR4)
 XX the variable region of the light chain of the order (L-FR1)-(L-FR2)-(L-FR3)-(L-FR4)
 XX (L-FR2)-(L-FR3)-(L-FR4) and (L-FR3)-(L-FR4) and
 XX polynucleotides (e.g. by gene therapy) are useful for the manufacture
 XX or plant cell. The pathologies are infectious (e.g. viral infections such
 XX as HIV, human immunodeficiency virus, infectious), tumour, metabolic and
 XX represents the synthetic antibody light chain variable region, used as
 XX a basis for making mutant antibodies incorporating the peptides of the
 XX invention.

Best Local Similarity 93.6%, Pred. No. 2e-37/
Matches 103; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

4 VITQSPNLAIVSGQRRATISCRASESVSYGNSPMHYKQKQPPGLLYVANSLESGI 63
Db 144 VITQSPNLAIVSGQRRATISCRASESVSYGNSPMHYKQKQPPGLLYVANSLESGI 203

64 PARFSGSGSRITDTLTINVPEDVAVTYCOOSNEDEPFGQCTLEIKR 112
Db 204 PARFSGSGSRITDTLTINVPEDVAVTYCOOSNEDEPFGQCTLEIKR 252

RESULT 14

AAK29008 standard; Protein: 131 AA.

AAK29008;

25-MAR-2003 (updated)

30-MAR-1993 (first entry)

p64-k4 protein product.

Human; antibody; interleukin-6; receptor; IL-6R; light chain; L; H;

heavy chain; variable region; mouse; monoclonal; hybridoma; NUK64-7;

plasma; p64 k4; p64-h3.

Synthetic.

Key

Location/Qualifiers

/note="Signal peptide"

21..131

/note="Mature peptide"

NO9219759-A1.

12-NOV-1992.

24-MAR-1992; 92MO-JP00544.

25-MAR-1991; 91JG-0095476.

15-FEB-1992; 92JF-0032064.

(CHUS) CHUGAI SEIYAKU KK.

Bending MM, Jones ST, Saldanha JM, Sato K, Tsuchiya M,

NPI, 1992-39882/48.

N-PDB; AAQ30757.

Reconstituted human antibody to human interleukin-6 receptor -

FT has low antigenicity and contains mouse V-region complementarity

determining regions

Disclosure: Page 124-125; 207pp; Japanese.

The sequences given in AAK29008-09 were encoded by plasmids which were

used in example 1 to illustrate the production of a human antibody which

recognises human interleukin-6 receptor (IL-6R). The antibody which

was used in example 1 was produced from a mouse monoclonal antibody produced from the

hybridoma NUK64-7 which contained the plasmids p64-k4 and p64-h3.

(Updated on 25-MAR-2003 to correct RN field.)

Sequence 131 AA;

Query Match 89.7%; Score 524; DB 13; Length 131;

Best Local Similarity 89.7%; Pred. No. 2e-37/
Matches 101; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

3 VITQSPNLAIVSGQRRATISCRASESVSYGNSPMHYKQKQPPGLLYVANSLESGI 62

Db 23 VITQSPNLAIVSGQRRATISCRASESVSYGNSPMHYKQKQPPGLLYVANSLESGI 82

63 PARFSGSGSRITDTLTINVPEDVAVTYCOOSNEDEPFGQCTLEIKR 111
Db 83 PARFSGSGSRITDTLTINVPEDVAVTYCOOSNEDEPFGQCTLEIKR 131

AAK29008 standard; Protein: 131 AA.

AAK29008;

07-JUL-1998 (first entry)

Light chain of NUK475.11.

Human; antibody; platelet; beta receptor; PDGF-beta; inhibitor;

internal hyperplasia; vasculature; restenosis; angioplasty; light chain.

Key

Location/Qualifiers

/note="Mature protein"

43..58

Complementarity determining region 1"

73..80

Complementarity determining region 2"

112..120

Complementarity determining region 3"

NO9737029-A1.

09-OCT-1997.

19-MAR-1997; 97MO-US04198.

22-MAR-1996; 96JG-0621751.

(BOER) BOEHRINGER MANNHEIM GMBH.

(PROCT) PROTEIN DESIGN LABS INC.

Chang CN, Landolfi NF, Martin U,

NPI, 1997-50314/46.

N-PDB; AAT90985.

Antibodies to platelet derived growth factor beta receptor - inhibit

PDGF-beta-induced proliferation of cells expressing the receptor, used

particularly for inhibiting intimal hyperplasia

Claim 11, Fig 7b; 87pp; English.

This is the amino acid sequence for the light chain of NUK475.11, a

novel antibody which specifically binds to the platelet derived

growth factor beta receptor (PDGF-beta), but not within the fifth

extracellular domain of the receptor. The antibody is a heavy chain

BB-induced proliferation of a cell expressing the PDGF-beta receptor.

The antibody can be used in a method of inhibiting intimal hyperplasia

in the vasculature of a mammal. The antibodies can be used for the

involvement of platelet-derived growth factor activity such as disorders

involving proliferation of cells, restenosis, and including

restenosis following angioplasty.

Sequence 131 AA;

Query Match 92.7%; Score 521; DB 18; Length 131;

Best Local Similarity 92.7%; Pred. No. 2.8e-37/
Matches 101; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

3 VITQSPNLAIVSGQRRATISCRASESVSYGNSPMHYKQKQPPGLLYVANSLESGI 62

Db	23	VITQSPPLAVSLQDQATISCDASSVDSYGSFPMKTCQKQOQPKLLTRASNDMSGI	82
Qy	63	PARFGSGSRTPDFTITINPVFADVDVATYYCCQSNEDPLTGTGTRELEIK	111
Db	83	PARFGSGSRTPDFTITINPVFADVDVATYYCCQSNEDPLTGTGTRELEIK	131

Search completed: November 7, 2003, 07:27:03
 Job time : 49.2991 secs

GenCore version 5.1.6
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OK protein - protein search, using sw model

Run on: November 7, 2003, 07:30:13 / Search time 88.243 seconds
(without alignment)
135.799 Million cell updates/sec

Title: US-09-661-992b-86_COPY_138_249

Perfect score: 584
Sequence: 1 EMBL/GENB/AF052608.1.....COSMEDP/REGULATR 112

Scoring table:
Gap 10.0, Gapext 0.5

Searched: 644079 seqs, 17174292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0
Maximum Match 1000
Limiting filter 45 numhits

Database: 1: Published Applications PA.*

- 2: /cgn2_6/pdata/2/pubpa/US07_PUBCOMB.pep.*
- 3: /cgn2_6/pdata/2/pubpa/ECT_NEW_PUB.pep.*
- 4: /cgn2_6/pdata/2/pubpa/US06_NEW_PUB.pep.*
- 5: /cgn2_6/pdata/2/pubpa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/pdata/2/pubpa/ECTUS_PUBCOMB.pep.*
- 7: /cgn2_6/pdata/2/pubpa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/pdata/2/pubpa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/pdata/2/pubpa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/pdata/2/pubpa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/pdata/2/pubpa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/pdata/2/pubpa/US09_PUBCOMB.pep.*
- 13: /cgn2_6/pdata/2/pubpa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/pdata/2/pubpa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/pdata/2/pubpa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/pdata/2/pubpa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/pdata/2/pubpa/US10_PUBCOMB.pep.*
- 18: /cgn2_6/pdata/2/pubpa/US06_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
similarity to the query of the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	542	92.8	112	9	US-09-810-502-37
2	542	92.8	112	9	US-09-810-502-37
3	526	90.1	112	12	US-10-169-351-43
4	526	90.1	112	12	US-10-169-351-43
5	525	89.9	112	10	US-09-144-886-80
6	525	89.9	112	10	US-09-144-886-80
7	514	88.0	112	12	US-10-169-351-43
8	514	88.0	112	12	US-10-169-351-43
9	513	87.8	112	10	US-09-144-886-80
10	513	87.8	112	10	US-09-144-886-80
11	505	86.2	114	9	US-09-810-502-36
12	499	85.4	112	10	US-09-144-886-80
13	494	84.6	112	9	US-09-810-502-36
14	493	84.6	112	9	US-09-810-502-36
15	475	82.5	158	12	US-10-169-351-48

16	475	81.5	111	12	US-10-169-351-47	Sequence 77, App1
17	475	81.5	108	12	US-10-169-351-44	Sequence 44, App1
18	474	81.2	108	12	US-10-169-351-46	Sequence 46, App1
19	474	81.2	108	12	US-10-169-351-48	Sequence 48, App1
20	472	80.8	108	12	US-10-169-351-45	Sequence 45, App1
21	471.5	80.7	112	12	US-10-169-351-43	Sequence 82, App1
22	471	80.7	108	12	US-10-169-351-36	Sequence 36, App1
23	471	80.7	108	12	US-10-169-351-40	Sequence 40, App1
24	467	80.0	108	12	US-10-169-351-41	Sequence 41, App1
25	467	80.0	108	12	US-10-169-351-42	Sequence 42, App1
26	466	79.8	132	10	US-09-810-502-37	Sequence 109, App1
27	464	79.5	128	10	US-09-810-502-38	Sequence 110, App1
28	464	79.5	128	10	US-09-810-502-39	Sequence 111, App1
29	459	78.2	112	12	US-10-169-351-40	Sequence 2, App1
30	459	78.2	112	12	US-10-169-351-41	Sequence 3, App1
31	445	76.2	129	9	US-09-810-502-37	Sequence 6, App1
32	445	76.2	129	9	US-09-810-502-38	Sequence 7, App1
33	445	76.2	128	12	US-10-169-351-43	Sequence 54, App1
34	444	76.0	112	15	US-10-169-351-44	Sequence 55, App1
35	444	76.0	112	15	US-10-169-351-45	Sequence 56, App1
36	444	76.0	131	9	US-09-810-502-37	Sequence 2, App1
37	443	75.9	269	14	US-10-027-770-2	Sequence 2, App1
38	442	75.7	106	9	US-09-810-502-38	Sequence 6, App1
39	442	75.7	106	11	US-09-810-502-39	Sequence 6, App1
40	442	75.7	269	14	US-10-027-770-2	Sequence 6, App1
41	441.5	75.4	151	12	US-10-222-056-33	Sequence 33, App1
42	441.5	75.4	151	12	US-10-222-056-34	Sequence 34, App1
43	437	74.8	271	12	US-10-053-550-18	Sequence 12, App1
44	437	74.8	271	12	US-10-053-550-19	Sequence 13, App1
45	434	74.3	112	10	US-09-144-886-95	Sequence 95, App1

ALIGNMENTS

RESULT 1
US-09-810-502-37
Sequence 37, Application US/09810502
Patient No.: US2002034755A1
GenBank Accession: U09810.5
Applicant: Pelian, Eduardo A.
Mark, George E, Bruce L.
Title of Invention: OF NANTBODY VARIANTS DOMAINS
Number of Sequences: 38
Correspondence Address:
Inventors: Mark, George E, Bruce L.
City: New York
State: New York
Country: USA
Filing Date: 09/05/2001
Priority Application Number: 09/055,280
Filing Date: 01-Aug-1997
Filing Date: 01-Mar-1996
Filing Date: 01-Mar-1996
Application Number: 08/109,187
Filing Date: 19-Jun-1993
Filing Date: 07/02, 217
Filing Date: 07/02, 217
Attorney/Agent Information:
Name: Hand, J. Mark

REGISTRATION NUMBER: 36,545
 REFERENCE/DOCKET NUMBER: 104100C
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 313-594-9505
 TELEFAX: 313-594-9720
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 STRANDNESS: single
 NOTES:
 TOPOLGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 37:
 US-09-910-502-37

Query Match 32.8%; Score 542; DB 3; Length 112;
 Best Local Similarity 34.8%; Pred. No. 1.9e-42;
 Matches 104; Conservative 3; Mismatches 0; Gaps 0;

0y 3 VTGSPALAVLQGNATISCSASVDYGVNPMWQIQIQPPKLLVYASMLESGI 62
 Db 3 VTGSPALAVLQGNATISCSASVDYGVNPMWQIQIQPPKLLVYASMLESGI 62

0y 63 PARFSGSGRTDFLTINPEVDADVATYCCQGNEDPTFGTGRLETR 112
 Db 63 PARFSGSGRTDFLTINPEVDADVATYCCQGNEDPTFGTGRLETR 112

RESULT 2
 US-09-144-886-81
 Sequence 81; Application US/09144886
 Patent No. US200201551141
 GENERAL INFORMATION:
 APPLICANT: Amersiofer, Peter
 TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralise
 CURRENT FILING DATE: 1998-08-31
 CURRENT APPLICATION NUMBER: 09/144,886
 NUMBER OF SEQ ID NOS: 98
 SEQ ID NO 81: 112
 LENGTH: 112
 TYPE: PRT
 STRANDNESS: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: BONT/7 clone
 US-09-144-886-81

Query Match 90.2%; Score 527; DB 10; Length 112;
 Best Local Similarity 93.6%; Pred. No. 1.9e-42;
 Matches 102; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

0y 4 LTGSPALAVLQGNATISCSASVDYGVNPMWQIQIQPPKLLVYASMLESGI 63
 Db 4 LTGSPALAVLQGNATISCSASVDYGVNPMWQIQIQPPKLLVYASMLESGI 63

0y 64 ARFSGSGRTDFLTINPEVDADVATYCCQGNEDPTFGTGRLETR 112
 Db 64 ARFSGSGRTDFLTINPEVDADVATYCCQGNEDPTFGTGRLETR 112

RESULT 3
 US-10-169-351-32
 Sequence 32; Application US/10169351
 Patent No. US20030157090A1
 GENERAL INFORMATION:
 APPLICANT: BENVENUTO, EUGENIO
 APPLICANT: FRANKONI, ROBERTA
 APPLICANT: DESIDERIO, ANGIOLA

APPLICANT: TAVADOKSAI, PARASKEVI
 TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
 WHICH INCLUDE THEM
 FILE REFERENCE: 4161-4
 CURRENT APPLICATION NUMBER: US/10/169,351
 PRIOR FILING DATE: 2000-12-29
 PRIOR APPLICATION NUMBER: PCT/IT00/00564
 PRIOR FILING DATE: 2000-12-29
 PRIOR APPLICATION NUMBER: IT RM93A000803
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: Patentl Ver. 2.1
 SEQ ID NO 32: 112
 TYPE: PRT
 STRANDNESS: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: VL-F8 amino
 acid sequence
 US-10-169-351-32

Query Match 90.1%; Score 526; DB 12; Length 112;
 Best Local Similarity 93.6%; Pred. No. 5.6e-42;
 Matches 102; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

0y 4 LTGSPALAVLQGNATISCSASVDYGVNPMWQIQIQPPKLLVYASMLESGI 63
 Db 4 LTGSPALAVLQGNATISCSASVDYGVNPMWQIQIQPPKLLVYASMLESGI 63

0y 64 ARFSGSGRTDFLTINPEVDADVATYCCQGNEDPTFGTGRLETR 112
 Db 64 ARFSGSGRTDFLTINPEVDADVATYCCQGNEDPTFGTGRLETR 112

RESULT 4
 US-10-169-351-49
 Sequence 49; Application US/10169351
 Publication No. US20030157090A1
 GENERAL INFORMATION:
 APPLICANT: BENVENUTO, EUGENIO
 APPLICANT: FRANKONI, ROBERTA
 APPLICANT: DESIDERIO, ANGIOLA
 APPLICANT: TAVADOKSAI, PARASKEVI
 TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
 WHICH INCLUDE THEM
 FILE REFERENCE: 4161-4
 CURRENT APPLICATION NUMBER: US/10/169,351
 PRIOR FILING DATE: 2000-12-29
 PRIOR APPLICATION NUMBER: PCT/IT00/00564
 PRIOR FILING DATE: 2000-12-29
 PRIOR APPLICATION NUMBER: IT RM93A000803
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: Patentl Ver. 2.1
 SEQ ID NO 49: 112
 TYPE: PRT
 STRANDNESS: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: ecFV(F8)
 amino acid sequence
 US-10-169-351-49

Query Match 90.1%; Score 526; DB 12; Length 252;
 Best Local Similarity 93.6%; Pred. No. 5.6e-42;
 Matches 102; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

0y 4 LTGSPALAVLQGNATISCSASVDYGVNPMWQIQIQPPKLLVYASMLESGI 63
 Db 144 LTGSPALAVLQGNATISCSASVDYGVNPMWQIQIQPPKLLVYASMLESGI 203

0y 64 ARFSGSGRTDFLTINPEVDADVATYCCQGNEDPTFGTGRLETR 112
 Db 64 ARFSGSGRTDFLTINPEVDADVATYCCQGNEDPTFGTGRLETR 112

DB 204 AAFSGSGSRDFTLTINPVADAVVYCOQSNEDPFTGSGTKLEIKR 252

RESULT 5
US-09-144-886-80
Sequence 80, Application US/09144886
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Ameradocfer, Peter
TITLE OF INVENTION: Biotinylated Monoclonal Antibodies That Neutralize
FILE REFERENCE: 2500.117050
CURRENT APPLICATION NUMBER: US/09/144,886
PRIORITY FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 80
LENGTH: 112
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-80
Query Match 89.9%; Score 525; DB 10; Length 112;
Best Local Similarity 92.7%; Pred. No. 2,9e-42;
Matches 101; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 LTQSPASLVSLQDQATISCSASVDSYGVNPMWYQIQCPQPKLLIYASNLSSGIP 63
DB 4 LTQSPASLVSLQDQATISCSASVDSYGVNPMWYQIQCPQPKLLIYASNLSSGIP 63
QY 64 AAFSGSGSRDFTLTINPVADAVVYCOQSNEDPFTGSGTKLEIKR 112
DB 64 AAFSGSGSRDFTLTINPVADAVVYCOQSNEDPFTGSGTKLEIKR 112

RESULT 6
US-09-144-886-97
Sequence 97, Application US/09144886
Patent No. US0201511441
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Ameradocfer, Peter
TITLE OF INVENTION: Biotinylated Monoclonal Antibodies That Neutralize
FILE REFERENCE: 2500.117050
CURRENT APPLICATION NUMBER: US/09/144,886
PRIORITY FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 97
LENGTH: 112
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-97
Query Match 89.2%; Score 531; DB 10; Length 112;
Best Local Similarity 89.4%; Pred. No. 3.1e-41;
Matches 100; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 LTQSPASLVSLQDQATISCSASVDSYGVNPMWYQIQCPQPKLLIYASNLSSGIP 63
DB 4 LTQSPASLVSLQDQATISCSASVDSYGVNPMWYQIQCPQPKLLIYASNLSSGIP 63
QY 64 AAFSGSGSRDFTLTINPVADAVVYCOQSNEDPFTGSGTKLEIKR 112
DB 64 AAFSGSGSRDFTLTINPVADAVVYCOQSNEDPFTGSGTKLEIKR 112

RESULT 7
US-10-169-351-103
Sequence 103, Application US/10169351
Publication No. US20030157090A1
GENERAL INFORMATION:
APPLICANT: BERKOWITZ, ROBERTO
APPLICANT: BERKOWITZ, ROBERTO
APPLICANT: DESIDERIO, ANICOLA
TITLE OF INVENTION: STABILIZING PEPTIDES: POLYPEPTIDES AND ANTIBODIES
FILE REFERENCE: 4161-4
CURRENT APPLICATION NUMBER: US/10/169,351
PRIORITY FILING DATE: 2002-10-29/00554
PRIOR FILING DATE: 2004.12.15/00554
PRIOR APPLICATION NUMBER: IT RM99A000803
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 103
LENGTH: 112
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: VL-P8 amino
US-10-169-351-103
Query Match 88.0%; Score 514; DB 12; Length 112;
Best Local Similarity 92.7%; Pred. No. 3.1e-41;
Matches 101; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 LTQSPASLVSLQDQATISCSASVDSYGVNPMWYQIQCPQPKLLIYASNLSSGIP 63
DB 4 LTQSPASLVSLQDQATISCSASVDSYGVNPMWYQIQCPQPKLLIYASNLSSGIP 63
QY 64 AAFSGSGSRDFTLTINPVADAVVYCOQSNEDPFTGSGTKLEIKR 112
DB 64 AAFSGSGSRDFTLTINPVADAVVYCOQSNEDPFTGSGTKLEIKR 112

RESULT 8
US-09-144-886-84
Sequence 84, Application US/09144886
Patent No. US0201511441
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Ameradocfer, Peter
TITLE OF INVENTION: Biotinylated Monoclonal Antibodies That Neutralize
FILE REFERENCE: 2500.117050
CURRENT APPLICATION NUMBER: US/09/144,886
PRIORITY FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 84
LENGTH: 112
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone
US-09-144-886-84
Query Match 89.8%; Score 513; DB 10; Length 112;
Best Local Similarity 87.9%; Pred. No. 3.9e-41;
Matches 99; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 LTQSPASLVSLQDQATISCSASVDSYGVNPMWYQIQCPQPKLLIYASNLSSGIP 63
DB 4 LTQSPASLVSLQDQATISCSASVDSYGVNPMWYQIQCPQPKLLIYASNLSSGIP 63

Db 4 LTGSPASLAVSQGATISCRASSESVSYGSMSPHMYQKQFQOPPLLITVYASNLSSGVP 63
 Oy 64 AAFSGSGSRDPTLTITNPEVADVVATYTCOSNEBPTFGGTGTALETR 112
 Db 64 AAFSGSGSRDPTLTITNPEVADVVATYTCOSNEBPTFGGTGTALETR 112

RESULT 9
 US-09-144-886-86
 Sequence 86, Application US/09144886
 Patent No. US2002015511A1
 GENERAL INFORMATION:
 APPLICANT: Marks, James D
 APPLICANT: Marks, James D
 TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
 TITLE OF INVENTION: Botulinum Neurotoxins
 FILE REFERENCE: 2500.117050 US/09/144.886
 CURRENT FILING DATE: 1998-08-31
 NUMBER OF SEQ ID NOS: 98
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 2
 LENGTH: 112
 TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone

US-09-144-886-86
 Query Match 87.8%; Score 513; DB 10; Length 112;
 Best Local Similarity 89.0%; Pred. No. 3.9e-11;
 Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 Oy 4 LTGSPASLAVSQGATISCRASSESVSYGSMSPHMYQKQFQOPPLLITVYASNLSSGVP 63
 Db 4 LTGSPASLAVSQGATISCRASSESVSYGSMSPHMYQKQFQOPPLLITVYASNLSSGVP 63
 Db 64 AAFSGSGSRDPTLTITNPEVADVVATYTCOSNEBPTFGGTGTALETR 112

RESULT 10
 US-09-144-886-85
 Sequence 85, Application US/09144886
 Patent No. US2002015511A1
 GENERAL INFORMATION:
 APPLICANT: Marks, James D
 APPLICANT: Marks, James D
 TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
 TITLE OF INVENTION: Botulinum Neurotoxins
 FILE REFERENCE: 2500.117050 US/09/144.886
 CURRENT FILING DATE: 1998-08-31
 NUMBER OF SEQ ID NOS: 99
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 85
 LENGTH: 112
 TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone

US-09-144-886-85
 Query Match 87.8%; Score 509; DB 10; Length 112;
 Best Local Similarity 89.0%; Pred. No. 9.3e-11;
 Matches 97; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 Oy 4 LTGSPASLAVSQGATISCRASSESVSYGSMSPHMYQKQFQOPPLLITVYASNLSSGVP 63
 Db 4 LTGSPASLAVSQGATISCRASSESVSYGSMSPHMYQKQFQOPPLLITVYASNLSSGVP 63
 Db 4 LTGSPASLAVSQGATISCRASSESVSYGSMSPHMYQKQFQOPPLLITVYASNLSSGVP 63

Oy 64 AAFSGSGSRDPTLTITNPEVADVVATYTCOSNEBPTFGGTGTALETR 112
 Db 64 AAFSGSGSRDPTLTITNPEVADVVATYTCOSNEBPTFGGTGTALETR 112

RESULT 11
 US-09-881-823-2
 Sequence 2, Application US/09881823
 Patent No. US2001015668A1
 GENERAL INFORMATION: 6868A1
 APPLICANT: SHI, WENYUAN
 APPLICANT: ANDERSON, MAXWELL
 APPLICANT: TRIN, XIAOSHEE
 APPLICANT: WINS, LETHIA
 APPLICANT: CHEN, LI
 TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
 TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries
 CURRENT FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: US/07378.577
 NUMBER OF SEQ ID NOS: 32-08-20
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 2
 TYPE: PRT
 ORGANISM: Murine
 US-09-881-823-2

Query Match 86.5%; Score 505; DB 9; Length 134;
 Best Local Similarity 89.1%; Pred. No. 2.7e-40;
 Matches 98; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 Oy 3 VTGSPASLAVSQGATISCRASSESVSYGSMSPHMYQKQFQOPPLLITVYASNLSSGVP 62
 Db 23 VTGSPASLAVSQGATISCRASSESVSYGSMSPHMYQKQFQOPPLLITVYASNLSSGVP 62
 Db 63 AAFSGSGSRDPTLTITNPEVADVVATYTCOSNEBPTFGGTGTALETR 112
 Db 83 AAFSGSGSRDPTLTITNPEVADVVATYTCOSNEBPTFGGTGTALETR 132

RESULT 12
 US-09-144-886-94
 Sequence 94, Application US/09144886
 Patent No. US2002015511A1
 GENERAL INFORMATION:
 APPLICANT: Marks, James D
 APPLICANT: Marks, James D
 TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
 TITLE OF INVENTION: Botulinum Neurotoxins
 FILE REFERENCE: 2500.117050 US/09/144.886
 CURRENT FILING DATE: 1998-08-31
 NUMBER OF SEQ ID NOS: 99
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 94
 LENGTH: 112
 TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: BONT/A clone

US-09-144-886-94
 Query Match 85.4%; Score 499; DB 10; Length 112;
 Best Local Similarity 88.0%; Pred. No. 8.1e-40;
 Matches 95; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
 Oy 4 LTGSPASLAVSQGATISCRASSESVSYGSMSPHMYQKQFQOPPLLITVYASNLSSGVP 63
 Db 4 LTGSPASLAVSQGATISCRASSESVSYGSMSPHMYQKQFQOPPLLITVYASNLSSGVP 63

Db 4 LTQSPALVSLVLCQKATISCRASREVSYGSGNPMHWYQKQCPPELLIYLSNLSRGVP 63
 Oy 64 ARFGSGSRTDFLTINVEADPWATYYCOSNEDPFTFGGTRLEIK 111
 Db 64 ARFGSGSRTDFLTINVEADPWATYYCOSNEDPFTFGGTRLEIK 111

RESULT 13
 US-09-810-502-36
 / Sequence 36, Application US/09810502
 / Publication No. US20030161832AC
 / GENERAL INFORMATION:
 / APPLICANT: Padina, Eduardo A.
 / INVENTOR: Padina, Eduardo A.
 / TITLE OF INVENTION: METHOD FOR SELECTING THE IMMUNOGENICITY
 / NUMBER OF SEQUENCES: 38
 / CORRESPONDENCE ADDRESS: 38
 / STREET: P.O. Box 2000, 126 B, Lincoln Ave.
 / CITY: Rahway
 / STATE: NJ
 / COUNTRY: USA
 / FILING DATE: 01-Aug-1997
 / PRIORITY DATE: 01-Aug-1997
 / FILING DATE: 01-Mar-1996
 / APPLICATION NUMBER: 08/109,187
 / PRIORITY DATE: 13-Aug-1993
 / FILING DATE: 17-May-1991
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Hand, J. Mark
 / REGISTRATION NUMBER: 36, 545
 / TELEPHONE: 732-594-3505
 / TELECOMMUNICATION INFORMATION: 184100C
 / TELEFAX: 732-594-4120
 / INFORMATION FOR SEQ ID NO. 36:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 112 amino acids
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MOLECULE TYPE: peptide
 / SEQUENCE DESCRIPTION: SEQ ID NO. 36:
 US-09-810-502-36

Query Match 84.6%; Score 494; DB 9; Length 112;
 Best Local Similarity 87.3%; Pred. No. 2,4e-39;
 Matches 96; Mismatches 8; Indels 0; Gaps 0;

Oy 3 VTQSPALVSLVLCQKATISCRASREVSYGSGNPMHWYQKQCPPELLIYLSNLSRG 62
 Db 3 VTQSPALVSLVLCQKATISCRASREVSYGSGNPMHWYQKQCPPELLIYLSNLSRG 62
 Oy 63 PARFGSGSRTDFLTINVEADPWATYYCOSNEDPFTFGGTRLEIK 112
 Db 63 PARFGSGSRTDFLTINVEADPWATYYCOSNEDPFTFGGTRLEIK 112

RESULT 14
 US-10-160-506-81
 / Publication No. US20030161832AC
 / GENERAL INFORMATION:
 / APPLICANT: Bander, Neil H.
 / INVENTOR: BROSCH AND COMPOSITIONS FOR TREATING OR PREVENTING
 / TITLE OF INVENTION: METHOD FOR IDENTIFYING SPECIFIC FOR
 / TITLE OF INVENTION: METHOD FOR IDENTIFYING SPECIFIC FOR
 / FILE REFERENCE: 10448-162001
 / CURRENT APPLICATION NUMBER: US/10/160,506
 / PRIOR APPLICATION NUMBER: 02-09-23,100
 / PRIOR FILING DATE: 2001-09-20
 / PRIOR FILING DATE: 2002-03-08
 / NUMBER OF SEQUENCES: 60/362,612
 / SOFTWARE: Patched for Windows Version 4.0
 / SEQ ID NO 81
 / LENGTH: 112
 / ORGANISM: Mus musculus

US-10-160-506-81
 Query Match 83.5%; Score 487.5; DB 12; Length 112;
 Best Local Similarity 87.3%; Pred. No. 9e-39;
 Matches 96; Mismatches 4; Indels 1; Gaps 1;

Oy 3 VTQSPALVSLVLCQKATISCRASREVSYGSGNPMHWYQKQCPPELLIYLSNLSRG 62
 Db 3 VTQSPALVSLVLCQKATISCRASREVSYGSGNPMHWYQKQCPPELLIYLSNLSRG 62
 Oy 63 PARFGSGSRTDFLTINVEADPWATYYCOSNEDPFTFGGTRLEIK 111
 Db 63 PARFGSGSRTDFLTINVEADPWATYYCOSNEDPFTFGGTRLEIK 112

RESULT 15
 US-10-160-351-48
 / Sequence 48, Application US/10169351
 / Publication No. US20030157090A1
 / GENERAL INFORMATION:
 / APPLICANT: RYUNGO
 / APPLICANT: PRANKON, ROSELLA
 / APPLICANT: DESIDERIO, ANGIOLA
 / TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
 / FILE REFERENCE: 4161-4
 / CURRENT APPLICATION NUMBER: US/10/160,351
 / PRIOR FILING DATE: 2002-10-29
 / PRIOR FILING DATE: 2000-12-29
 / PRIOR FILING DATE: 1999-12-30
 / NUMBER OF SEQUENCES: 118
 / SOFTWARE: Patchin ver. 2.1
 / SEQ ID NO 48
 / LENGTH: 108
 / ORGANISM: Artificial Sequence
 / OTHER INFORMATION: Description of Artificial Sequence: VV-CWV/2G
 US-10-160-351-48

Query Match 82.0%; Score 479; DB 12; Length 108;
 Best Local Similarity 87.2%; Pred. No. 6e-38;
 Matches 95; Mismatches 3; Indels 4; Gaps 1;

Oy 4 LTQSPALVSLVLCQKATISCRASREVSYGSGNPMHWYQKQCPPELLIYLSNLSRGVP 63
 Db 4 LTQSPALVSLVLCQKATISCRASREVSYGSGNPMHWYQKQCPPELLIYLSNLSRGVP 63

Fri Nov 7 09:40:22 2003

us-09-661-992b-86_copy_138_249.rapb

Page 6

Db 4 LTQSPALAVSLQZQNTISGRASBY---HNVMNTQQRQGPPELLYRALNLSGIP 59

QY 64 ARPSGSGSRPTFTLTINPEADVDATYCCQSNEDPLFTGTGLEIR 112

Db 60 ARPSGSGSRPTFTLTINPEADVDATYCCQSRPPTGQGTGLEIR 108

Search completed: November 7, 2003, 08:16:54

Job time : 99.243 secs

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-117-33

Query Match 89.7% Score 524, DB 1, Length 131,
Best Local Similarity 92.7% Pcd. No. 6, 5e-51,
Matches 101, Conservative 3, Mismatches 5, Indels 0, Gaps 0,

QY 3 VLOGSPALVSGGATTCGASSTSYGYNHWHVQIQCPPLLITRANSEGI 62
DB 23 VLQSPVSLVSGGATTCGASSTSYGYNHWHVQIQCPPLLITRANSEGI 82
DB 63 PARFGSGSRDPTLTINVEADVAITYCOQSNEDPTFGGKLEIK 111
DB 83 PARFGSGSRDPTLTINVEADVAITYCOQSNEDPTFGGKLEIK 131

RESULT 2
US-08-436-717-33

/ Sequence 33, Application US/08436717

/ Patent No. 5882544

/ GENERAL INFORMATION:

/ APPLICANT: TOSCHITA, Masayuki

/ APPLICANT: SUTO, Koh

/ APPLICANT: KIMURA, Masayuki

/ APPLICANT: SUTO, Koh

/ APPLICANT: SUTO, Koh

/ APPLICANT: SUTO, Koh

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/ APPLICANT: SUTO, Koh

/ APPLICANT: SUTO, Koh

Query Match 89.7% Score 524, DB 2, Length 131,
Best Local Similarity 92.7% Pcd. No. 6, 5e-51,
Matches 101, Conservative 3, Mismatches 5, Indels 0, Gaps 0,

QY 3 VLOGSPALVSGGATTCGASSTSYGYNHWHVQIQCPPLLITRANSEGI 62
DB 23 VLQSPVSLVSGGATTCGASSTSYGYNHWHVQIQCPPLLITRANSEGI 82
DB 63 PARFGSGSRDPTLTINVEADVAITYCOQSNEDPTFGGKLEIK 111
DB 83 PARFGSGSRDPTLTINVEADVAITYCOQSNEDPTFGGKLEIK 131

RESULT 3
US-08-621-751A-10

/ Sequence 10, Application US/08621751A

/ Patent No. 5882544

/ GENERAL INFORMATION:

/ APPLICANT: Chung N.

/ APPLICANT: Landolf, Nicholas P.

/ APPLICANT: Martin, Ulrich

/ APPLICANT: Martin, Ulrich

/ APPLICANT: Martin, Ulrich

/ APPLICANT: Martin, Ulrich

/ APPLICANT: Martin, Ulrich

/ APPLICANT: Martin, Ulrich

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/ APPLICANT: Martin, Ulrich

/ APPLICANT: Martin, Ulrich

/ APPLICANT: Martin, Ulrich

Query Match 89.7% Score 521, DB 2, Length 131,
Best Local Similarity 92.7% Pcd. No. 1, 4e-50,
Matches 101, Conservative 2, Mismatches 6, Indels 0, Gaps 0,

QY 3 VLOGSPALVSGGATTCGASSTSYGYNHWHVQIQCPPLLITRANSEGI 62
DB 23 VLQSPVSLVSGGATTCGASSTSYGYNHWHVQIQCPPLLITRANSEGI 82
DB 63 PARFGSGSRDPTLTINVEADVAITYCOQSNEDPTFGGKLEIK 111
DB 83 PARFGSGSRDPTLTINVEADVAITYCOQSNEDPTFGGKLEIK 131

RESULT 4
US-08-111-080-18

/ Sequence 18, Application US/111080

/ Patent No. 5882544

/ GENERAL INFORMATION:

/ APPLICANT: Chung N.

/ APPLICANT: Landolf, Nicholas P.

/ APPLICANT: Martin, Ulrich

/ APPLICANT: Martin, Ulrich

/ APPLICANT: Martin, Ulrich

/ APPLICANT: Martin, Ulrich

/ APPLICANT: Martin, Ulrich

/ APPLICANT: Martin, Ulrich

/ APPLICANT: Martin, Ulrich

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/ APPLICANT: Martin, Ulrich

/ APPLICANT: Martin, Ulrich

FILING DATE: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/07111
 FILING DATE: 24-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/039,457
 FILING DATE: 22-APR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: BORN, MICHAEL F.
 REGISTRATION NUMBER: 25,447
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 714-8300
 TELEFAX: 28-3856
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-211-980-18
 Query Match 87.8%; Score 513; DB 1; Length 121;
 Best Local Similarity 89.1%; Pred. No. 9,9e-50;
 Matches 98; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 3 VTGSPSLAVSLGQATITCSASVDYGVNFWNTQIQPQPKLLIYASNLSSGI 62
 DB 3 VTGSPSLAVSLGQATITCSASVDYGVNFWNTQIQPQPKLLIYASNLSSGV 62
 QY 63 PARPSSGSRDPTLTIPYEDADVATYYCCQSNEDPLFPGTGRLEIR 112
 DB 63 PARPSSGSRDPTLTIPYEDADVATYYCCQSNEDPLFPGTGRLEIR 112
 RESULT 7
 US-09-661-992b-22
 Sequence 22; Application US/08211980
 Patent No. 5665569
 GENERAL INFORMATION:
 APPLICANT: Tsumura
 TITLE OF INVENTION: HIV Immunotherapeutics
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 STREET: 6100 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 08/09/11,980
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA: PCT/US92/07111
 FILING DATE: 24-AUG-1992
 PRIOR APPLICATION DATA: US 08/039,457
 APPLICATION NUMBER: US 08/039,457
 ATTORNEY/AGENT INFORMATION:
 NAME: BORN, MICHAEL F.
 REGISTRATION NUMBER: 25,447
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 714-8300
 TELEFAX: 28-3856
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-661-992b-22

TELEPHONE: (312) 474-6300
 TELEFAX: 28-3856
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-211-980-22
 Query Match 87.8%; Score 513; DB 1; Length 121;
 Best Local Similarity 89.1%; Pred. No. 9,9e-50;
 Matches 98; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 3 VTGSPSLAVSLGQATITCSASVDYGVNFWNTQIQPQPKLLIYASNLSSGI 62
 DB 3 VTGSPSLAVSLGQATITCSASVDYGVNFWNTQIQPQPKLLIYASNLSSGV 62
 QY 63 PARPSSGSRDPTLTIPYEDADVATYYCCQSNEDPLFPGTGRLEIR 112
 DB 63 PARPSSGSRDPTLTIPYEDADVATYYCCQSNEDPLFPGTGRLEIR 112
 RESULT 8
 PCT-US92-07111-17
 Sequence 17; Application PCT/US92/07111
 Patent No. 5665569
 GENERAL INFORMATION:
 APPLICANT: Ono, Tsuneya
 TITLE OF INVENTION: HIV Immunotherapeutics
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 STREET: 6100 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 07/28/92
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/748,562
 FILING DATE: 07/28/92
 ATTORNEY/AGENT INFORMATION:
 NAME: Roland, Greeta E.
 REGISTRATION NUMBER: 35,302
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 346-5750
 TELEFAX: (312) 984-9740
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US92-07111-17
 Query Match 87.8%; Score 513; DB 5; Length 121;
 Best Local Similarity 89.1%; Pred. No. 9,9e-50;
 Matches 98; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 3 VTGSPSLAVSLGQATITCSASVDYGVNFWNTQIQPQPKLLIYASNLSSGI 62

DB 3 VTGSSALVSLVGLGATISCSHSSVSDVSNPFWHVCQKQSPFLVYANSLSSGI 62
 QY 63 PARFGSSSRITPLTINPVDADVAVYCCNSHSDVSNPFWHVCQKQSPFLVYANSLSSGI 112
 DB 63 PARFGSSSRITPLTINPVDADVAVYCCNSHSDVSNPFWHVCQKQSPFLVYANSLSSGI 112

RESULT 9

Sequence 18, Application PC/TUS9307967

GENERAL INFORMATION:

APPLICANT: Ohio, Tumeys

ADDRESSER: Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIA TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILE NAME: PCT/US93/07967

FILE DATE: 22-APR-1993

FILE TIME: 10:00:00

FILE SIZE: 1000000

FILE TYPE: 1

FILE EXTENSION: .PCT

FILE CONTENTS: 1

FILE DESCRIPTION: 1

FILE COMMENTS: 1

FILE SECURITY: 1

FILE PERMISSIONS: 1

FILE ATTRIBUTES: 1

FILE METADATA: 1

FILE HISTORY: 1

FILE LOGS: 1

FILE AUDIT: 1

FILE BACKUP: 1

FILE RECOVERY: 1

FILE MAINTENANCE: 1

FILE MONITORING: 1

FILE REPORTING: 1

FILE TROUBLESHOOTING: 1

FILE SUPPORT: 1

FILE TRAINING: 1

FILE DOCUMENTATION: 1

FILE LITERATURE: 1

FILE RESEARCH: 1

FILE DEVELOPMENT: 1

FILE TESTING: 1

FILE DEPLOYMENT: 1

FILE OPERATIONS: 1

FILE SUPPORT: 1

NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
 STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606

RESULT 10

Sequence 22, Application PC/TUS9307967

GENERAL INFORMATION:

APPLICANT: Ohio, Tumeys

ADDRESSER: Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIA TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILE NAME: PCT/US93/07967

FILE DATE: 24-NOV-1992

FILE TIME: 10:00:00

FILE SIZE: 1000000

FILE TYPE: 1

FILE EXTENSION: .PCT

FILE CONTENTS: 1

FILE DESCRIPTION: 1

FILE COMMENTS: 1

FILE SECURITY: 1

FILE HISTORY: 1

FILE LOGS: 1

FILE AUDIT: 1

FILE BACKUP: 1

FILE RECOVERY: 1

FILE MAINTENANCE: 1

FILE MONITORING: 1

FILE REPORTING: 1

FILE TROUBLESHOOTING: 1

FILE SUPPORT: 1

FILE TRAINING: 1

FILE DOCUMENTATION: 1

FILE LITERATURE: 1

FILE RESEARCH: 1

FILE DEVELOPMENT: 1

FILE TESTING: 1

FILE DEPLOYMENT: 1

FILE OPERATIONS: 1

FILE SUPPORT: 1

FILE TRAINING: 1

FILE DOCUMENTATION: 1

FILE LITERATURE: 1

NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
 STREET: 6300 Sears Tower, 233 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606

RESULT 11

Sequence 22, Application PC/TUS9307967

GENERAL INFORMATION:

APPLICANT: Ohio, Tumeys

ADDRESSER: Borun

STREET: 6300 Sears Tower, 233 S. Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIA TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILE NAME: PCT/US93/07967

FILE DATE: 24-NOV-1992

FILE TIME: 10:00:00

FILE SIZE: 1000000

FILE TYPE: 1

FILE EXTENSION: .PCT

FILE CONTENTS: 1

FILE DESCRIPTION: 1

FILE COMMENTS: 1

FILE SECURITY: 1

FILE HISTORY: 1

FILE LOGS: 1

FILE AUDIT: 1

FILE BACKUP: 1

FILE RECOVERY: 1

FILE MAINTENANCE: 1

FILE MONITORING: 1

FILE REPORTING: 1

FILE TROUBLESHOOTING: 1

FILE SUPPORT: 1

FILE TRAINING: 1

FILE DOCUMENTATION: 1

FILE LITERATURE: 1

FILE RESEARCH: 1

FILE DEVELOPMENT: 1

FILE TESTING: 1

FILE DEPLOYMENT: 1

FILE OPERATIONS: 1

FILE SUPPORT: 1

FILE TRAINING: 1

FILE DOCUMENTATION: 1

FILE LITERATURE: 1

SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US 08/039,457
 FILING DATE: 08/31/11, 080
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA: US 07/746,562
 FILING DATE: 22-AUG-1993
 PRIOR APPLICATION NUMBER: PCT/US92/07111
 APPLICATION NUMBER: PCT/US92/07111
 PRIOR APPLICATION DATA: US 08/039,457
 FILING DATE: 22-AUG-1993
 APPLICATION NUMBER: PCT/US92/07111
 REGISTRATION NUMBER: 25,447
 TELEPHONE: (312) 474-0448
 TELEFAX: (312) 474-0448
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-111-080-26

Query Match 97.3% Score 510; DB 1; Length 120;
 Query Similarity 89.1% Pos 2, Le 49, Indels 0; Gaps 0;
 Matches 99; Conservative 5; Mismatches 7; Indels 0;
 QY 3 VTGSPASVAVGQDQATISCASSVSQVFNQNTQIQFQPKLLTVASNLSEGI 62
 DB 3 VTGSPASVAVGQDQATISCASSVSQVFNQNTQIQFQPKLLTVASNLSEGI 62
 QY 63 PARFGSGGRTFTLTINPEVDVAVTYTCQGNEDLTLPQGTGRLTLE 112
 DB 63 PARFGSGGRTFTLTINPEVDVAVTYTCQGNEDLTLPQGTGRLTLE 112

RESULT 13
 US-08-211-980-26
 Sequence 26, Application US/08211980
 Patent No. 5665169
 GENERAL INFORMATION:
 APPLICANT: Ohio, Temuya
 TITLE OF INVENTION: HIV Immunotherapeutics
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS: O'Toole, Gerstein, Murray &
 ADDRESSER: Borum
 STREET: 6100 Sears Tower, 213 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 ZIP: 60606
 COUNTRY: USA
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: US 08/039,457
 FILING DATE: 08/21/11, 980
 APPLICATION NUMBER: 424
 PRIOR APPLICATION DATA:
 FILING DATE: 24-AUG-1992
 APPLICATION NUMBER: PCT/US92/07111
 APPLICATION NUMBER: US 08/039,457

FILING DATE: 22-APR-1993
 ATTORNEY/AGENT INFORMATION:
 REGISTRATION NUMBER: 25,447
 REFERENCE/DOCKET NUMBER: 31629
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-0448
 TELEFAX: (312) 474-0448
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-211-980-26

Query Match 89.1% Score 510; DB 1; Length 120;
 Query Similarity 89.1% Pos 2, Le 49, Indels 0; Gaps 0;
 Matches 99; Conservative 5; Mismatches 7; Indels 0;
 QY 3 VTGSPASVAVGQDQATISCASSVSQVFNQNTQIQFQPKLLTVASNLSEGI 62
 DB 3 VTGSPASVAVGQDQATISCASSVSQVFNQNTQIQFQPKLLTVASNLSEGI 62
 QY 63 PARFGSGGRTFTLTINPEVDVAVTYTCQGNEDLTLPQGTGRLTLE 112
 DB 63 PARFGSGGRTFTLTINPEVDVAVTYTCQGNEDLTLPQGTGRLTLE 112

RESULT 13
 US-08-211-980-26
 Sequence 26, Application PCT/US93/07967
 GENERAL INFORMATION:
 APPLICANT: Ohio, Temuya
 TITLE OF INVENTION: HIV Immunotherapeutics
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
 STREET: 6100 Sears Tower, 213 S. Wacker Drive
 CITY: Chicago
 STATE: Illinois
 ZIP: 60606
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA: PCT/US93/07967
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/07111
 FILING DATE: 08/03/93, 457
 APPLICATION NUMBER: 424
 PRIOR APPLICATION DATA:
 FILING DATE: 22-APR-1993
 APPLICATION NUMBER: PCT/US92/07111
 REGISTRATION NUMBER: 25,447
 TELEPHONE: (312) 474-0448
 TELEFAX: (312) 474-0448
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 120 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: protein
PCT-US91-07967-26

Query Match Similarity 87.3%; Score 510; DB 3; Length 120;
Matches 98; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 3 VLTGSPASLAVSLGQATATSCASBSYDGYGPMHWYQIQFQPPKLLTPASNLSEGI 62
Db 3 VLTGSPASLAVSLGQATATSCASBSYDGYGPMHWYQIQFQPPKLLTPASNLSEGI 62
Qy 63 PARFSGSSRTDFLTINPVEDVAVYYCCQSNEDPFTFGGTLEIKR 112
Db 63 PARFSGSSRTDFLTINPVEDVAVYYCCQSNEDPFTFGGTLEIKR 112

RESULT 14
US-09-661-992b-86-11
Sequence 11; Application US/0827053
Patent No. 5607847

GENERAL INFORMATION:

TITLE OF INVENTION: Recombinant human anti-human immunodeficiency
virus antibody.

NUMBER OF SEQUENCES: 16

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: Release #1.0, Version #1.25 (ERO)

APPLICATION NUMBER: US/08/275,053

PRIOR APPLICATION DATA: PCT/GB93/01798

INFORMATION FOR SEQ ID NO. 11

SEQUENCE CHARACTERISTICS: 11

LENGTH: 111 amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-275-053-11

Query Match 87.0%; Score 508; DB 1; Length 111;

Best Local Similarity 89.0%; Pred. No. 3,2e-49;

Matches 97; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 3 VLTGSPASLAVSLGQATATSCASBSYDGYGPMHWYQIQFQPPKLLTPASNLSEGI 62
Db 3 VLTGSPASLAVSLGQATATSCASBSYDGYGPMHWYQIQFQPPKLLTPASNLSEGI 62
Qy 63 PARFSGSSRTDFLTINPVEDVAVYYCCQSNEDPFTFGGTLEIKR 111
Db 63 PARFSGSSRTDFLTINPVEDVAVYYCCQSNEDPFTFGGTLEIKR 111

RESULT 15

US-09-665-059-13

Sequence 13; Application US/0906509

Patent No. 606881

GENERAL INFORMATION:

APPLICANT: SINO, Ken-Ichiro

APPLICANT: SINO, Ken-Ichiro

APPLICANT: SINO, Ken-Ichiro

APPLICANT: SINO, Ken-Ichiro

APPLICANT: SINO, Ken-Ichiro

APPLICANT: SINO, Ken-Ichiro

APPLICANT: SINO, Ken-Ichiro

APPLICANT: SINO, Ken-Ichiro

APPLICANT: SINO, Ken-Ichiro

APPLICANT: SINO, Ken-Ichiro

APPLICANT: SINO, Ken-Ichiro

APPLICANT: SINO, Ken-Ichiro

COUNTRY: USA
212-42214

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/065,059

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: BRUCE Ph.D., Daniel

RESEARCH/DOCTOR NUMBER: 40356-151

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-518-5100

TELEFAX: 703-518-5100

INFORMATION FOR SEQ ID NO. 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 112 amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-065-059-13

Query Match 85.6%; Score 500; DB 3; Length 112;

Best Local Similarity 87.3%; Pred. No. 2,9e-48;

Matches 96; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 3 VLTGSPASLAVSLGQATATSCASBSYDGYGPMHWYQIQFQPPKLLTPASNLSEGI 62
Db 3 VLTGSPASLAVSLGQATATSCASBSYDGYGPMHWYQIQFQPPKLLTPASNLSEGI 62
Qy 63 PARFSGSSRTDFLTINPVEDVAVYYCCQSNEDPFTFGGTLEIKR 112
Db 63 PARFSGSSRTDFLTINPVEDVAVYYCCQSNEDPFTFGGTLEIKR 112

Search completed: November 7, 2003, 07:30:11

Job time: 17.4486 sec

```
! FINDPATTERNS on geneseq: * allowing 0 mismatches
!
! 1 CXYGNSPFGFAYXC November 7, 2003 07:46 ..
!
! AAB20444 ct: 623 len: 16 ! AAB20444 Anti-FIX/FIXa antibody CDS, 6/200
!
! 1: CXYGNSPFGFAYXC
! CXYGNSPFGFAYXC
!
Database searched:
Geneseq-A1, Release 13.0, Released on 199un2003, Formatted on 150ul2003
Total finds: 1
Total length: 158,726,570
Total sequences: 1,107,863
CPU time: 02:53.22
```

```
!!SEQUENCE LIST 1.0
! FINDPATTERNS on geneseq.* allowing 0 mismatches
!
! CXYGNPQGFANYXC
November 7, 2003 07:51 ..

GENSEQP00015.AAB20444 Ck: 623 len: 16 finds: 1 ! AAB20444 Anti-FIX/TKA anti-
\End of list

Databases searched:
Genseq.ab, Release 13.0, Released on 15Jun2003, Formatted on 15Jul2003

Total finds: 1
Total length: 159,726,570
Total sequences: 1,107,863
CPU time: 05:00.84
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11AA SEQUENCE 1.0
ID _AA020444 standard; Peptide; 16 AA.
XX
AC AA020444;
XX
DT 21-JUN-2001 (first entry)
XX
DE Anti-FIX/FIXa antibody CDR3.
XX
KW Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant;
XX Factor VIII cofactor; blood coagulation disorder; haemophilia A;
XX haemorrhagic diathesis; haemostatic; amolytic; therapy; mouse;
XX complementarily determining region; CDR.
OS
MS mus musculus.
XX
XX Key Location/Qualifiers
FR Misc-difference /note= "any amino acid"
FT
FT Misc-difference 3 /note= "any amino acid"
FT
FT Misc-difference /note= "any amino acid"
FT
FT Misc-difference 15 /note= "any amino acid"
XX
XX WO200119992-A2.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-EP08936.
XX
XX 14-SEP-1999; 99AT-0002576.
XX
XX (BAXT) BAXTER AG.
XX
XX Schelflinger F, Kerschbaum R, Falkner F, Dornier F;
XX WPI: 2001-290356/30.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
XX increasing amolytic activity of factor IXa, and for treating blood
XX coagulation disorders such as haemophilia A and haemorrhagic diathesis -
XX
XX Claim 7; Page 74; 13pp; English.
XX
XX The present sequence is that of complementarily determining
XX region 3 (CDR3) of an antibody having anti-Factor IX (FIX) or
XX anti-activated factor IX (FIXa) activity. Such antibodies
XX and their derivatives (including those that comprise the present
XX amino acid sequence) are useful for the treatment of blood
XX coagulation disorders, such as haemophilia A and haemorrhagic
XX activating activity. Administration of the antibodies or their
XX derivatives leads to an increase in the procoagulant activity of
XX FIXa, even in the presence of PVIa inhibitors. This allows for
XX the treatment of haemorrhagic diathesis, haemophilia A and
XX in the case of PVIa inhibitor patients. The antibodies or their
XX derivatives are used in a claimed pharmaceutical composition for
XX treating patients with blood coagulation disorders, especially
XX haemophilia A and haemorrhagic diathesis.
XX
XX Sequence 16 AA:
XX
AA020444 Length: 16 November 7, 2003 09:14 Type: P Check: 623 ..
1 CXYGNSPRG FAXXC

Quest - Quick User-directed Expression Search Tool
Release 5.4

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.

```

1 seqids [AA] ID seqids are preliminary pattern
2
3 followed by
4
5 C
6 any character
7 any character
8 yzmpskgfay
9 any character
10 any character
11 C
12

```

Data bank : Issued_AA , all entries

Format Options:	File Options:
Nucleic acid code matching	Indirect file
Find non-matching hits only	Sequence or key file
Report key used	List of hits
Note position of hit	Hit display
Display full annotations	Name and annotations
Sequence context	

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

-- Search Statistics --

```

Times:          CPU          Total Elapsed
           00:01:34.06      00:01:37.00

Number of sequences searched:      338807
Number of sequence hits:           0
Number of separate matches:        0
Number of sequence hits saved:     0

```

! FINDPATTERNS on plr:* allowing 0 mismatches
! 1 CXXYNSPGXGVXXC

November 7, 2003 07:41 ..

Databases searched:

NBRF, Release 76.1, Released on 12May2003, Formatted on 10Jun2003

Total finds: 0
Total sequences: 96,148,642
Total sequences: 283,308
CPU time: 54.01

! FINDPATTERNS on swp:* allowing 0 mismatches
! 1 CXXYSPFGRVXKC November 7, 2003 07:42 ..

Databases searched:

SWISS-PROT, Release 41.1, Released on 6Jun2003, Formatted on 9Jun2003
SPRTRMBL, Release 23.0, Released on 7Mar2003, Formatted on 7Mar2003

Total finds: 0
Total length: 305,079,309
Total sequences: 358,388
CPU time: 03:26.92

GenCode version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 1.1534 seconds

653,278 Million cell updates/sec

Title: US-09-661-992b-105

Sequence: 1 CXXVNSPCGFAKXC 16

Scoring table: BLAST62

Gapop 10.0 , Gapext 0.5

Searched: 127663 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127663

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 88

Listing first 45 summaries

Database: SwissProt, 41.1*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
2	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
3	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
4	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
5	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
6	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
7	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
8	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
9	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
10	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
11	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
12	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
13	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
14	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
15	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
16	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
17	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
18	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
19	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
20	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
21	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
22	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
23	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
24	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
25	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
26	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
27	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
28	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
29	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
30	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
31	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
32	53.8	723	1	S21C_MOUSE	QBK078 mus musculus
33	53.8	723	1	S21C_MOUSE	QBK078 mus musculus

34	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
35	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
36	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
37	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
38	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
39	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
40	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
41	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
42	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
43	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
44	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
45	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
46	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
47	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
48	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
49	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
50	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
51	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
52	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
53	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
54	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
55	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
56	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
57	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
58	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
59	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
60	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
61	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
62	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
63	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
64	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
65	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
66	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
67	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
68	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
69	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
70	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
71	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
72	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
73	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
74	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
75	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
76	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
77	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
78	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
79	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
80	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
81	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
82	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
83	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
84	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
85	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
86	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
87	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
88	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
89	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
90	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
91	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
92	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
93	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
94	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
95	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
96	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
97	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
98	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
99	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor
100	37	46.2	572	1	LAC3_HUMAN	002079 thnatephor

DR	pfam: pf0772; S-Adomet synthet; 1.
DR	Pfam: PF0772; S-Adomet synthet; 1.
DR	TIGRfam: TIGRf01034; mEET_1.1.5.
DR	PROSITE: PS00376; ADOMET SYNTHETASE 1.1.
DR	PROSITE: PS00377; ADOMET SYNTHETASE 2.1.
CC	Metal-binding: The gamma-carbon methionine; ATP-binding; Magnesium; Potassium;
KM	Metal-binding
FT	NP BIND 130 35
FT	METHAL 30 35 MAGNESIUM (BY SIMILARITY).
FT	METHAL 36 35 POTASSIUM (BY SIMILARITY).
FT	METHAL 38 35 MAGNESIUM (EX SIMILARITY).
FT	METHAL 39 35 POTASSIUM (EX SIMILARITY).
FT	BINDING 158 158 ACP (POTENTIAL).
FT	SEQUENCE 395 AA; 42366 MW; 8CF39C9B93A1A0FC CACCA4;
QY	Query Match 50.0%; Score 40; DB 1; Length 395;
QY	Best Local Similarity 53.8%; Pred. No. 11;
QY	Matches 7; Conservative 1; Mismatches 5; Gaps 0
DB	91 YDSSKGFDTXTC 103
RESULT 14	
NR	MARK_RAT_PAT STANDARD; PRT 395 AA.
NR	MARK_RAT_PAT (181829)
AD	01-NOV-1990 (Rel. 16; Created)
DT	01-NOV-1990 (Rel. 16; Last sequence update)
DT	5-MAR-2003 (Rel. 42; Last annotation update)
DD	01-NOV-1990 (Rel. 16; Last version update) NCBI 2.5.1.6 (Methionine
DB	adenosyltransferase) [Adomet synthetase] (Met 11).
GN	MATRA OF NMSG.
OS	Rattus norvegicus (Rat).
OC	Mammalia; Artiodactyla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OK	NCBI TaxId:101616;
RS	11
RS	Sequence from N.A.
RS	STRAIN:RAT_NA_TISSUE:Kidney;
RS	HITOKU.T.; Horikawa K.; Tanaka K.;
RS	"Structure of the rat methionine adenosyltransferase 2a gene and its promoter.";
RS	J Biol. Chem. 269:451-450 (1994).
CC	-1- FUNCTION CATALYZES THE FORMATION OF S-ADENOSYL METHIONINE FROM
CC	METHIONINE AND ATP.
CC	-1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC	COSMOETHANOL ADENOSYL-L-methionine + adenosine or cobalt-, and
CC	L-potassium ion per substrate (by similarity?)
CC	-1- PATHWAY: Activated methyl cycle.
CC	-1- TISSUE: Kidney.
CC	-1- SUBCELLULAR LOCATION: IN MAWELIAN TISSUES, THERE ARE THREE DISTINCT
CC	FORMS OF ADOMET SYNTH. DESIGNATED AS ALPHA, BETA AND GAMMA. ALPHA
CC	AND BETA ARE EXPRESSED ONLY IN ADULT LIVER, WHILE GAMMA IS WIDELY
CC	DISTRIBUTED IN EXTRASPLANCHIC TISSUES. IN ADDITION THE GAMMA FORM
CC	REPLACES BY THE ALPHA AND BETA FORMS DURING DEVELOPMENT.
CC	-1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC	This SwissProt entry was produced through a collaboration between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no restrictions on its

[illegible]

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DR      HSSP; P04384; 1XHE     69357  

DR      Incepp; ICR00213; S-Adomet_synth.  

DR      Pfam; PF00438; S-Adomet_synd2; 1.  

DR      Pfam; PF00772; S-Adomet_synd2; 1.  

DR      Pfam; PF00773; S-Adomet_synd3; 1.  

DR      Trnaseq; T000004; S-Adomet_synd3; 1.  

DR      PROSITE; PS00377; ADOMET_SYNTHETASE_1; 1.  

DR      PROSITE; PS00376; ADOMET_SYNTHETASE_2; 1.  

DR      Hypothetical protein; Transferase; One-carbon metabolism; Magnesium;  

DR      NP_BIND    beta-binding; Multispecific; ATP-binding.  

DR      METAL      19      19      MAGNESIUM (BY SIMILARITY) .  

DR      METAL      45      45      POTASSIUM (BY SIMILARITY) .  

DR      METAL      271     271     POTASSIUM (BY SIMILARITY) .  

DR      FT          271     271     ATP (POTENTIAL) .  

DR      BINDING    147     147     CRCE4;  

DR      SEQUENCE   404 AA; 44034 MW; 4f7891333b4e268 CRC64;  

Query Match                               50.0%; Score 40; DB 1; Length 404;  

Matches 7; Conservative 1; Mismatches 5; Gaps 0;  

DQ      4 YONSPTKATKXC 16  

DB      80 YDSSSKEDYKTC 92

```



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RM SEQUENCE FROM N.A.
RM TISSUE:Ovary;
RM MEDLINE:97121433; PubMed:9620293;
RM "Molecular cloning of a c-myc complementary element binding protein: An
RM RT evolutionarily conserved protein that interacts with the cytoplasmic
RM RT polyadenylation element of c-mos mRNA."
RM Proc. Natl. Acad. Sci. U.S.A. 93:14602-14607(1996).
RM PubMed:93108443; Cpub:
RM MIM:108443; Cpub:
RM MIM:108443; Cpub:
RM SMART:SM00360; Rfam:1.
RM SPOSITE:PS50102; Rfam:1.
RM SEQUENCE 561 AA; 62255 MW; 36CF42B1AC70A377 CRC64;
SQ
Query Match 52.5%; Score 42; DB 13; Length 561;
Best Local Similarity 52.8%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CXXYNSPKGFY 13
Db 344 CPROKMANOYV 356

RESURF 14
OC GDEDS; PRELIMINARY; PRT; 559 AA.
AC GDEDS;
RT 01-MAR-2001 (TREMBL:rel_16, Created)
RT 01-MAR-2001 (TREMBL:rel_16, Last sequence update)
DE Cytoplasmic polyadenylation element binding protein.
CN CPEB.
OC Mus musculus (Mouse);
OC Charassius auratus (Goldfish);
OC Drosophila melanogaster (Fruit fly);
OC Actinopterygii:Neogobius;
OC Cyprinidae; Carassius.
NCBI_TaxID:7957;
RM SEQUENCE FROM N.A.
RM Karem Y., Yamashita M., Ogawa K., Nishihama Y.;
RM "Goldfish cytoplasmic polyadenylation element binding protein
RM (CPEB): its interaction with CPE of cyclin B mRNA and phosphorylation
RM RT Sublited JDN-2000 To the EMBL/Genbank/DBJ databases.
RM EMBL: AB045534; BAB15051.1; -.
RM InterPro: IPR000504; Rfam_rec_mot.
RM PROSITE: PS50102; Rfam:1.
RM SEQUENCE 559 AA; 62122 MW; 05507CESD1568144 CRC64;
SQ
Query Match 52.5%; Score 42; DB 13; Length 559;
Best Local Similarity 52.8%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CXXYNSPKGFY 13
Db 344 CPROKMANOYV 356

RESURF 15
ID P70166; PRELIMINARY; PRT; 561 AA.
AC P70166;
RT 01-MAR-1997 (TREMBL:rel_02, Created)
RT 01-MAR-1997 (TREMBL:rel_02, Last sequence update)
DE Cytoplasmic polyadenylation element-binding protein (CPEB).
CN CPEB.
OC Mus musculus (Mouse);
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID:10090;
RM [1]

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RP SEQUENCE FROM N.A.
RP TISSUE:Ovary;
RP MEDLINE:97121433; PubMed:9620293;
RP "Molecular cloning of a c-myc complementary element binding protein: An
RP RT evolutionarily conserved protein that interacts with the cytoplasmic
RP RT polyadenylation element of c-mos mRNA."
RP Proc. Natl. Acad. Sci. U.S.A. 93:14602-14607(1996).
RP PubMed:93108443; Cpub:
RP MIM:108443; Cpub:
RP MIM:108443; Cpub:
RP SMART:SM00360; Rfam:1.
RP SPOSITE:PS50102; Rfam:1.
RP SEQUENCE 561 AA; 62255 MW; 36CF42B1AC70A377 CRC64;
SQ
Query Match 52.5%; Score 42; DB 13; Length 561;
Best Local Similarity 52.8%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 1 CXXYNSPKGFY 13
Db 350 CPROKMANOYV 362

```

Search completed: November 7, 2003, 07:34:37
 Job time : 6.37637 sec8

CC 14-SEP-1999; 99AFT-0001576.
 CC (BAXT) BAXTER AG.
 CC Scheeflinger F, Kerschbaum R, Faltner F, Donner F;
 CC WPI; 2001-290356/30.
 CC New factor IX/factor IXa antibodies and their derivatives useful for
 CC increasing antidiolytic activity of factor IXa and for treating blood
 CC coagulation disorders such as haemophilia A and haemorrhagic diathesis -
 CC Claim 7; Page 74; 138pp; English.
 CC The present sequence is that of complementarily determining
 CC region 3 (CDR3) of an antibody having anti-factor IX (FIX) or
 CC anti-activated factor IX (FIXa) activity. Such antibodies
 CC are useful for the treatment of haemorrhagic disorders, such as
 CC CDR3 peptide) have Factor VIII (FVIII) cofactor activity or FIXa
 CC activating activity. Administration of the antibodies or their
 CC derivatives leads to an increase in the procoagulant activity of
 CC Factor VIII or FIXa, respectively, and thus to a rapid blood
 CC rapid blood coagulation even in the absence of FVIII or FIXa, and
 CC in the case of FVIII inhibitor patients. The antibodies or their
 CC derivatives are used in a claimed pharmaceutical composition for
 CC haemophilia A and haemorrhagic diathesis, especially
 CC Sequence 16 M;
 CC Query Match 90.0%; Score 72; DB 22; Length 16;
 CC Best Local Similarity 100.0%; Pred.No. 2.9e-05;
 CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC 1 CXYGNSPGPAHXKC 16
 CC 1 CXYGNSPGPAHXKC 16
 CC Db
 CC 1 CXYGNSPGPAHXKC 16
 CC RESULT 2
 CC AAB20433 standard; Protein; 242 AA.
 CC AAB20433;
 CC 21-JUN-2001 (first entry)
 CC Anti-FIX/FIXa antibody 193/AD3 scFv.
 CC Factor IX, FIX, Factor IXa, FIXa, scFv, antibody, procoagulant;
 CC Factor VIII cofactor, blood coagulation disorder; haemophilia;
 CC haemorrhagic diathesis; haemostatic; amido/lytic; therapy; mouse;
 CC Characteric - Mus musculus.
 CC Characteric - Synthetic.
 CC Key Location/Qualifiers
 CC Protein /AAB20433 WH
 CC Region 98-108
 CC Peptide /AAB20433 CDR3
 CC /AAB20433 Linker
 CC 135-242
 CC Protein /AAB20433 WH
 CC 223-231 CDR3
 CC /AAB20433 CDR3
 CC Region
 CC W0200119992-A2.
 CC 22-MAR-2001.
 CC 14-SEP-1999; 99AFT-0001576.
 CC (BAXT) BAXTER AG.
 CC Scheeflinger F, Kerschbaum R, Faltner F, Donner F;

PF 13-SEP-2000; 2000WO-EP08936.
 PF 14-SEP-1999; 99AFT-0001576.
 PF (BAXT) BAXTER AG.
 PF Scheeflinger F, Kerschbaum R, Faltner F, Donner F;
 PF WPI; 2001-290356/30.
 PF New factor IX/factor IXa antibodies and their derivatives useful for
 PF increasing antidiolytic activity of factor IXa, and for treating blood
 PF coagulation disorders such as haemophilia A and haemorrhagic diathesis -
 PF Claim 8; Fig 14; 138pp; English.
 PF The present sequence is that of a single chain Fv (scFv) derivative
 PF of an antibody having anti-factor IX (FIX) or anti-activated factor IX
 PF variable regions of 193/AD3 joined by an artificial, flexible linker
 PF peptide. The scFv was obtained by PCR amplification of cDNA for
 PF 193/AD3 WH and VH regions and cloning in vector pM2. 193/AD3 is
 PF a heavy chain variable region of an antibody (coagulation factor IXa)
 PF CDR3 peptide) have Factor VIII (FVIII) cofactor activity or FIXa
 PF activating activity. Administration of the antibodies or their
 PF derivatives leads to an increase in the procoagulant activity of
 PF Factor VIII or FIXa, respectively, and thus to a rapid blood
 PF rapid blood coagulation even in the absence of FVIII or FIXa, and
 PF in the case of FVIII inhibitor patients. The antibodies or their
 PF derivatives are used in a claimed pharmaceutical composition for
 PF haemophilia A and haemorrhagic diathesis, especially
 PF Sequence 242 AA;
 PF Query Match 82.5%; Score 66; DB 22; Length 242;
 PF Best Local Similarity 84.6%; Pred.No. 0.0061;
 PF Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 PF 1 CXYGNSPGPAHXKC 13
 PF 96 CXYGNSPGPAHXKC 108
 PF Db
 PF 96 CXYGNSPGPAHXKC 108
 PF RESULT 3
 PF AAB20388 standard; Peptide; 10 AA.
 PF AAB20388;
 PF 21-JUN-2001 (first entry)
 PF Anti-FIX/FIXa antibody 193/AD3 CDR3.
 PF Factor IX, FIX, Factor IXa, FIXa, antibody, procoagulant;
 PF Factor VIII cofactor, blood coagulation disorder; haemophilia A;
 PF haemorrhagic diathesis; haemostatic; amido/lytic; therapy; mouse;
 PF Complementarily determining region; CDR.
 PF Mus musculus.
 PF W0200119992-A2.
 PF 22-MAR-2001.
 PF 13-SEP-2000; 2000WO-EP08936.
 PF 14-SEP-1999; 99AFT-0001576.
 PF (BAXT) BAXTER AG.
 PF Scheeflinger F, Kerschbaum R, Faltner F, Donner F;

XX MFI: 2001-29056/30.

XX New factor IX/factor IXa antibodies and their derivatives useful for
XX increasing antithrombotic activity of Factor IXa, and for treating blood
XX coagulation disorders such as hemophilia A and hemorrhagic diathesis
XX
XX Claim 7: Page 74, 138pp; English.

XX The present sequence is that of complementarity determining region
XX 3 (CDR3) of the heavy chain of an antibody expressed by mouse
XX hybridoma 193/AB3. This antibody has anti-Factor IX (FIX) or
XX anti-activated Factor IX (aFIX) activity. It is an example of
XX their derivatives (including those that comprises the present CDR3
XX peptide) have Factor VIIIa (FVIIIa) cofactor activity or FIXa
XX activating activity. Administration of the antibodies or their
XX derivatives, especially FVIIIa, is useful for regulating activity of
XX FIXa in the presence of FVIIIa in the blood of a patient with
XX rapid blood coagulation even in the absence of FVIII or FVIIIa, and
XX in the case of FVIII inhibitor patient. The antibodies or their
XX derivatives are used as a clinical pharmaceutical composition for
XX treatment of hemophilia B, hemorrhagic diathesis, especially
XX hemophilia A and hemorrhagic diathesis.

XX Sequence 10 AA;

XX Query Match 72.5%; Score 58; DB 22; Length 10;

XX Best Local Similarity 100.0%; Pred. No. 0.0038;
XX Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 4 YXNSPGFAY 13

XX 1 YXNSPGFAY 10

XX DB

XX AA059884 standard; Protein, 365 AA.

XX AA059884;

XX 20-NOV-1998 (first entry)

XX Amino acid sequence of the cDNA clone Bcl-1ike (HA1G29).

XX Bcl-1ike (HA1G29); chronic inflammatory disease; Allergic reaction;
XX Immunological disorders; autoimmune diseases; anti-infectious agent.

XX Homo sapiens.

XX MO8031007-82.

XX 23-JUL-1998.

XX 21-JUN-1998; 98MO-US00960.

XX 21-JUN-1997; 97US-0034205.

XX 21-JUN-1997; 97US-0034204.

XX (AACC)- AUCLAND UNIVERSITIES LTD.

XX (HBM)- HUMAN GENOME SCI INC.

XX Feng P., Gentz FL, Kristensen GM, Ni J, Rosen CH;

XX Su JF;

XX MFI: 1998-414099/75.

XX N-5805; AA041525.

XX New isolated polypeptides and encoded polypeptides - used to
XX develop products for treating e.g. inflammatory diseases,
XX infectious, immunological disorders, autoimmune diseases, allergies
XX or tumors

XX Claim 1: Fig 12a-12d; 120pp; English.

XX This is the amino acid sequence of the cDNA clone Bcl-1ike (HA1G29),
XX used in the method of the invention. The products of the clone can be
XX used for the treatment of inflammatory diseases, autoimmune diseases,
XX inflammatory diseases, immunological disorders, autoimmune diseases,
XX inflammatory diseases, various allergic, and anti-infectious agents.
XX The products can also be used for detection and diagnosis.

XX Sequence 365 AA;

XX Query Match 55.0%; Score 44; DB 19; Length 365;

XX Best Local Similarity 53.8%; Pred. No. 0.0038;
XX Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

XX 1 CXXYNSPGFAY 13

XX 264 CXXYNSPGFAY 276

XX DB

XX AA055556 standard; Protein, 365 AA.

XX AA055556;

XX 15-JUN-2003 (first entry)

XX Human novel secreted protein gene 120 polypeptide #1.

XX Human; secreted protein; autoimmune disease; chemocytosis;
XX rheumatoid arthritis; hypersproliferative disorder; breast neoplasm;
XX liver neoplasm; cardiovascular disorder; cardiac arrest; skin aging;
XX nervous system disorders; Alzheimer's disease; infection;
XX ocular disorder; corneal infection; wound healing; tissue regeneration;
XX epithelial cell proliferation; organ transplantation; food additive;
XX preservative; nutritional.

XX Homo sapiens.

XX US6420526-B1.

XX 16-JUL-2002.

XX 08-SEP-1998; 98US-0149476.

XX 07-MAR-1997; 97US-038623P.

XX 07-MAR-1997; 97US-040161P.

XX 07-MAR-1997; 97US-040162P.

XX 07-MAR-1997; 97US-040338P.

XX 07-MAR-1997; 97US-040338P.

XX 07-MAR-1997; 97US-040338P.

XX 07-MAR-1997; 97US-040338P.

XX 07-MAR-1997; 97US-040338P.

XX 07-MAR-1997; 97US-040338P.

XX 07-MAR-1997; 97US-040338P.

XX 07-MAR-1997; 97US-040338P.

XX 07-MAR-1997; 97US-040338P.

XX 07-MAR-1997; 97US-040338P.

XX 07-MAR-1997; 97US-040338P.

XX 07-MAR-1997; 97US-040338P.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from *Pitheophila*. The invention is
CC useful in developmental biology and in elucidating cell signaling and
CC cell-cell interactions in higher eukaryotes for the development of
CC diagnostic tests for the detection of the presence of a specific gene
CC discloses genomic DNA sequences (AB16176-AB16511), expressed DNA
CC sequences (AB16180-AB16175) and the encoded proteins
CC (AB16177-AB16179). This patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pub/published_pct_sequences.

XX Sequence 2515 AA;

XX Query March

Best Local Similarity 51.2%; Score 41; DB 22; Length 2515;

XX Matches

7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX 4 CXYGSPKGP 11

|||||

DB 2171 YGNSKSP 2178

XX RESULT 9

XX AB076564

XX AB076564 standard; Protein; 107 AA.

XX AC AB076564;

XX 05-MAY-2002 (first entry)

XX HCV E1 antigen monoclonal antibody #52.

XX human, HCV; hepatitis C virus; E1 antigen; monoclonal antibody; vaccine;

XX hepatotropic; Fpb; hypervariable region; E2 antigen; antibody.

XX Homo sapiens.

XX OS Homo sapiens

XX WC020060954-A1.

XX 08-MAY-2002.

XX 14-JUN-2002; 2002WO-0200044.

XX 12-JUN-2001; 2001US-260889P.

XX (KARO) KAROLINSKA INNOVATIONS AB.

XX Drakenberg K, Persson MA;

XX WPI; 2002-608902/65.

XX Vaccine comprising a human monoclonal antibody against hepatitis C

XX virus (HCV) E1 or E2 antigen, useful for treating or preventing HCV

XX infection.

XX Disclosure; Page 56; 6app; English.

XX The invention relates to a human monoclonal antibody or its antigen

XX binding fragments, which exhibit immunological binding affinity for a

XX hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence

XX homologous to the binding portion of a human antibody Fab molecule from a

XX human monoclonal antibody library.

XX antibodies or antigen binding fragments against HCV E1 or E2 antigen or

XX its hypervariable region is useful in treating or preventing HCV

XX infection in a subject. Sequences AB076513-AB076568 represent human

XX monoclonal antibodies against HCV E1 antigen.

XX Sequence 107 AA;

XX Query March

Best Local Similarity 50.0%; Score 40; DB 23; Length 107;

XX 63.6%; Pred. No. 45;

XX 50.0%; Score 40; DB 23; Length 107;

XX 63.6%; Pred. No. 45;

XX 50.0%; Score 40; DB 23; Length 107;

XX 63.6%; Pred. No. 45;

XX 50.0%; Score 40; DB 23; Length 107;

XX 63.6%; Pred. No. 45;

XX 50.0%; Score 40; DB 23; Length 107;

XX 63.6%; Pred. No. 45;

XX 50.0%; Score 40; DB 23; Length 107;

XX 63.6%; Pred. No. 45;

XX 50.0%; Score 40; DB 23; Length 107;

XX 63.6%; Pred. No. 45;

XX 50.0%; Score 40; DB 23; Length 107;

XX 63.6%; Pred. No. 45;

XX 50.0%; Score 40; DB 23; Length 107;

XX 63.6%; Pred. No. 45;

XX 50.0%; Score 40; DB 23; Length 107;

XX 63.6%; Pred. No. 45;

XX 50.0%; Score 40; DB 23; Length 107;

XX 63.6%; Pred. No. 45;

XX 50.0%; Score 40; DB 23; Length 107;

XX 63.6%; Pred. No. 45;

Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX 1 CXYGSPKGP 11

|||||

DB 88 CQGYSPKGP 98

XX RESULT 10

XX AB076206

XX AB076206 standard; Protein; 136 AA.

XX AC AB076206;

XX 26-FEB-2003;

XX 10-OCT-2002 (first entry)

XX Human immunoprecipitate to HCV E2 glycoprotein F2b variable region #53.

XX Viruslike human immunoprecipitate; immunoprecipitate; envelope glycoprotein;

XX human, hepatitis C virus; HCV; E2 glycoprotein.

XX NS3 protein; viral infection.

XX Homo sapiens.

XX OS Homo sapiens

XX WC020059340-A1.

XX 01-MAY-2002.

XX 25-JAN-2002; 2002WO-0202303.

XX 26-JAN-2001; 2001US-264451P.

XX (SCEI) SCEIPES R&S INST.

XX Matsuyama T, Jones IM, Burton DR, Fox RI;

XX WPI; 2002-599801/64.

XX H-TSDB; AB092705.

XX New human immunoprecipitate with binding specificity for carrying

XX envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C virus

XX (HCV), for diagnosing or treating patients having or suspected of

XX having HCV infection.

XX Claim 10; Fig 12; 30app; English.

XX The present invention relates to human immunoprecipitates, produced by a

XX phage transduced cell library. The present sequence is one such

XX phage transduced cell library. The present sequence is one such

XX phage transduced cell library. The present sequence is one such

XX phage transduced cell library. The present sequence is one such

XX phage transduced cell library. The present sequence is one such

XX cell binding and complex neutralising epitopes, while NS3 is thought to

XX be involved in viral replication and assembly. The present sequence is

XX for diagnosing and treating a patient having or suspected to be having

XX HCV infection.

XX Sequence 136 AA;

XX Query March

Best Local Similarity 46.2%; Pred. No. 59;

XX Matches

1; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

XX 1 CXYGSPKGP 13

|||||

DB 89 CQGYSPKGP 101

|||||

XX RESULT 11

XX AB043671

XX AB043671 standard; Protein; 261 AA.

XX AC AB043671;

XX 26-FEB-2003 (first entry)

XX Methionine adenosyltransferase II alpha clone MGC.2907.
 XX
 XX Neuroprotective; immunomodulatory; cancer; chromosome 20p11.2;
 XX cyclo-oxygenase; anti-inflammatory; growth; survival; medicinal; ADOS;
 XX K16000366 standard; Protein; 291 AA.
 XX
 XX amorphotropic lateral sclerosis; autoimmune disorder; inflammation;
 XX vulnerability.
 XX
 XX Homo sapiens.
 XX
 XX M0200231111-12.
 XX
 XX 18-MAR-2002.
 XX
 XX 11-OCT-2001; 2001MO-US27760.
 XX
 XX 12-OCT-2000; 2000US-0687537.
 XX
 XX (HSE)-1 HXRD INC.
 XX
 XX
 XX Tang YF, Liu C, Zhou P, Abusdi V, Zhang J, Zhao QH, Ren F;
 XX Xue M, Yang Y, Weinman F, Dermane R;
 XX NFI, 2002-436237/45.
 XX
 XX N-550B; AB066925.
 XX
 XX New polypeptides and their encoded proteins, useful as nutritional
 XX sources or supplements, or in gene therapy, particularly for treating
 XX wounds, Alzheimer's disease, amorphotropic lateral sclerosis, cancer or
 XX inflammation.
 XX
 XX Claim 20; SEQ ID # 574; 357bp + sequence listing; English.
 XX
 XX The invention relates to 446 newly isolated polynucleotide sequences.
 XX The activity of polynucleotides of the invention may be described as,
 XX anti-inflammatory, immunomodulatory, cyclo-oxygenase and
 XX anti-inflammatory. Compositions comprising nucleic acids of the invention
 XX and/or polypeptides or their encoded proteins, or as nutritional sources or
 XX supplements, these are useful in gene therapy, particularly for treating
 XX wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
 XX amorphotropic lateral sclerosis, autoimmune disorders, cancer or
 XX inflammation, and research methods. The polypeptides are also useful in
 XX diagnosis and research methods. The polypeptides are also useful in
 XX the invention.
 XX The sequence data for this patent did not form part of the printed
 XX publication, but was obtained in electronic format directly from WIPO
 XX at fip.wipo.int/pub/published_pat_sequences.
 XX
 XX
 XX Sequence 261 AA;
 XX
 XX Query Match 50.0%; Score 40; DB 23; Length 261;
 XX Best Local Similarity 53.8%; Pred. No. 1.1e+02;
 XX Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 XX
 XX 4 YGNSEPKFYATXC 16
 XX
 XX 92 YDSSNCPYFATC 104
 XX
 XX
 XX RESULT 12
 XX AB063366
 XX K1600366 standard; Protein; 291 AA.
 XX
 XX AB063366;
 XX
 XX 26-MAR-2002 (first entry)
 XX
 XX Drosophila melanogaster polypeptide SEQ ID NO 16990.
 XX
 XX Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical.

XX
 XX Drosophila melanogaster.
 XX
 XX M0200171042-42.
 XX
 XX 27-SEP-2001.
 XX
 XX 23-MAR-2001; 2001MO-US092311.
 XX
 XX 23-MAR-2000; 2000US-131637P.
 XX
 XX 11-JUL-2000; 2000US-0644150.
 XX
 XX (PSE)-1 PE CORP NY.
 XX
 XX Venter JC, Adams M, Li PMD, Myers EW;
 XX NFI, 2001-655860/75.
 XX
 XX N-550B; AB070469.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 XX genes from Drosophila and for elucidating cell signalling and cell-cell
 XX interactions.
 XX
 XX Disclosure; SEQ ID NO 16990; 21bp + sequence listing; English.
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 XX useful in developmental biology and in elucidating cell signalling and
 XX cell-cell interactions in higher eukaryotes for the development of
 XX insecticides, therapeutics and pharmaceutical drugs. The invention
 XX relates to a nucleic acid detection reagent, expressed DNA
 XX sequences (AB01840-AB01847) and the encoded proteins
 XX (AB057737-AB072021).
 XX The sequence data for this patent did not form part of the printed
 XX publication, but was obtained in electronic format directly from WIPO
 XX at fip.wipo.int/pub/published_pat_sequences.
 XX
 XX
 XX Sequence 291 AA;
 XX
 XX Query Match 50.0%; Score 40; DB 23; Length 291;
 XX Best Local Similarity 77.8%; Pred. No. 1.3e+02;
 XX Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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 XX 5 GNSPKFYAT 13
 XX
 XX 119 GNSPKFYAT 127
 XX
 XX
 XX RESULT 13
 XX AA055075
 XX K1600366 standard; Protein; 385 AA.
 XX
 XX AA055075;
 XX
 XX 23-JUN-2000 (first entry)
 XX
 XX Candida albicans polypeptide sequence # 43.
 XX
 XX Candida albicans infection; growth; survival; medicinal; ADOS;
 XX vulvovaginitis; immunocompromised patient; treat.
 XX
 XX Candida albicans.
 XX
 XX BP962401-42.
 XX
 XX 01-MAR-2000.
 XX
 XX 23-DEC-1998; 98EP-0310694.
 XX
 XX 14-DEC-1998; 98GB-0017796.
 XX
 XX (JNMC) JANSSEN PHARM NV.

DB 148 CDSGSHPMKRN 160

RESULT 2
US-10-153-688-120
/ Sequence 696, Application US/01015668
/ Publication No. US2003009216A1
/ GENERAL INFORMATION:
/ FILE REFERENCE: P2002P2
/ TITLE OF INVENTION: 166 Human secreted proteins
/ APPLICANT: HONDA, Goichi
/ APPLICANT: HONDA, Goichi
/ APPLICANT: MURAHATSU, Shuji
/ APPLICANT: ISHIZAWA, Kenya
/ TITLE OF INVENTION: State Activating Gene
/ CURRENT APPLICATION NUMBER: US/10/153,666
/ PRIOR FILING DATE: 2002-05-24
/ PRIOR APPLICATION NUMBER: US 60/293,172
/ PRIOR APPLICATION NUMBER: US 60/316,331
/ PRIOR FILING DATE: 2001-08-31
/ PRIOR APPLICATION NUMBER: US 60/328,403
/ PRIOR APPLICATION NUMBER: JP 2001-157043
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: JP 2001-312175
/ PRIOR FILING DATE: 2001-10-10
/ NUMBER OF SEQ ID NOS: 488
/ SEQ ID NO 126: cshpmkrn ver. 2.0
/ LENGTH: 306
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-153-689-120

Query Match 55.0%; Score 44; DB 15; Length 306;
Best Local Similarity 53.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
DB 205 CDSGSHPMKRN 217

RESULT 3
US-09-609-391-696
/ Sequence 696, Application US/09809391
/ Publication No. US2003009491A1
/ GENERAL INFORMATION:
/ FILE REFERENCE: P2002P2
/ TITLE OF INVENTION: 166 Human secreted proteins
/ APPLICANT: HONDA, Goichi
/ APPLICANT: HONDA, Goichi
/ APPLICANT: MURAHATSU, Shuji
/ APPLICANT: ISHIZAWA, Kenya
/ TITLE OF INVENTION: State Activating Gene
/ CURRENT APPLICATION NUMBER: US/09/809,391
/ PRIOR FILING DATE: 2002-05-24
/ PRIOR APPLICATION NUMBER: US 60/293,172
/ PRIOR APPLICATION NUMBER: US 60/316,331
/ PRIOR FILING DATE: 2001-08-31
/ PRIOR APPLICATION NUMBER: US 60/328,403
/ PRIOR APPLICATION NUMBER: JP 2001-157043
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: JP 2001-312175
/ PRIOR FILING DATE: 2001-10-10
/ NUMBER OF SEQ ID NOS: 761
/ SEQ ID NO 126: cshpmkrn ver. 2.0
/ LENGTH: 365
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-609-391-696

Query Match 55.0%; Score 44; DB 11; Length 365;
Best Local Similarity 53.8%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
DB 264 CDSGSHPMKRN 276

RESULT 4
US-09-661-992b-171-696
/ Sequence 696, Application US/09882171
/ Publication No. US2003017588A1
/ GENERAL INFORMATION:
/ FILE REFERENCE: P2002P2
/ TITLE OF INVENTION: 166 Human secreted proteins
/ APPLICANT: HONDA, Goichi
/ APPLICANT: HONDA, Goichi
/ APPLICANT: MURAHATSU, Shuji
/ APPLICANT: ISHIZAWA, Kenya
/ TITLE OF INVENTION: State Activating Gene
/ CURRENT APPLICATION NUMBER: US/09/882,171
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 09/680,391
/ PRIOR APPLICATION NUMBER: 09/149,476
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: PCT/US98/04493
/ PRIOR FILING DATE: 1998-03-06
/ PRIOR APPLICATION NUMBER: 60/040,162
/ PRIOR APPLICATION NUMBER: 60/040,333
/ PRIOR FILING DATE: 1997-03-07
/ PRIOR APPLICATION NUMBER: 60/038,621
/ PRIOR APPLICATION NUMBER: 60/040,626
/ PRIOR FILING DATE: 1997-03-07
/ PRIOR APPLICATION NUMBER: 60/040,534
/ PRIOR APPLICATION NUMBER: 60/040,336
/ PRIOR FILING DATE: 1997-03-07
/ PRIOR APPLICATION NUMBER: 60/040,163
/ PRIOR APPLICATION NUMBER: 60/047,600
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,615
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,597
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,502
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,632
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,583
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,617
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,618
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,503
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,592
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,584
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,500
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,597
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,492
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,598
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,613
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,582
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,596
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,612
/ PRIOR FILING DATE: 1997-05-23
/ PRIOR APPLICATION NUMBER: 60/047,632
/ PRIOR FILING DATE: 1997-05-23


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APPLICANT: Butten, D.
TITLE OF INVENTION: Anticardiolipin antibodies to glucose-6-phosphate isomerase and their particles
FILE REFERENCE: 1361.000501; US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 3
TYPE: PRT
ORGANISM: Homo sapiens
US-09-828-708-3

Query Match
Best Local Similarity 54.5%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 CXXGSSPKPF 11
82 CQGVSSPKPF 92

RESULT 6
US-09-828-708-7
Patent No. US0202164753A1
GENERAL INFORMATION:
APPLICANT: Dietzel, H.
APPLICANT: Dietzel, H.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Anticardiolipin antibodies to glucose-6-phosphate isomerase and their particles
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SEQ ID NO: 1
LENGTH: 105
TYPE: PRT
US-09-828-708-7

Query Match
Best Local Similarity 54.5%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 CXXGSSPKPF 11
82 CQGVSSPKPF 92

RESULT 7
US-08-844-215-10
Sequence 10, Application US/08844215
Publication No. US2002006443A1
GENERAL INFORMATION:
APPLICANT: PERSON, MRS AREL.
APPLICANT: ALANDER, TOBIAS ERIK
TITLE OF INVENTION: HERMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 1
CORRESPONDENCE ADDRESS:
ADDRESSES: ROBINS & ASSOCIATES
STREET: 50 WINDLEFIELD ROAD, SUITE 200
STATE: MA 02128
COUNTRY: USA
ZIP: 02128
COMPILED BY: MARIANNE POHLM
MEDIUM TYPE: Floppy disk

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COMPILED: IBM PC compatible
SOFTWARE: Research Release A1.0, Version A1.30
CURRENT APPLICATION DATA: US/08/844,215
APPLICATION NUMBER: US/08/844,215
FILING DATE: 17 APR 1997
PRIORITY DATE: 17 APR 1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/633,109
FILING DATE: 19 APR 1996
APPLICANT: PERSON, MRS AREL.
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,538
REFERENCE/DOCNO NUMBER: 80146,002
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7812
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE: 107 amino acids
LENGTH: 107 amino acids
STRANDNESS: single
TYPE: amino acid
MOLECULE TYPE: polypeptide
US-08-844-215-10

Query Match
Best Local Similarity 54.5%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 CXXGSSPKPF 11
88 CQGVSSPKPF 98

RESULT 8
US-10-269-805-32
Sequence 32, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPEPTIN-2 SPECIFIC BINDING AGENTS
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/388,604
PRIOR FILING DATE: 2001-10-11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 32
LENGTH: 108
TYPE: PRT
US-10-269-805-32

Query Match
Best Local Similarity 54.5%; Pred. No. 42;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

1 CXXGSSPKPF 11
89 CQGVSSPKPF 99

RESULT 9
US-10-269-805-36
Sequence 36, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPEPTIN-2 SPECIFIC BINDING AGENTS
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/388,604
PRIOR FILING DATE: 2001-10-11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
LENGTH: 108
TYPE: PRT
US-10-269-805-36

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/ CURRENT FILING DATE: 2002-10-10
/ PRIOR APPLICATION NUMBER: US 09/764,903
/ PRIOR FILING DATE: 2001-10-11
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: Patent version 3.1
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-661-992b-105

Query Match Similarity: 47.5%; Score 38; DB 15; Length 108;
Best Local Similarity: 54.5%; Pct. No. 42;
Matches: 6; Conservative: 2; Mismatches: 3; Indels: 0; Gaps: 0;

Cy 1 CXXYNSPKG 11
Db 89 CORTISPRF 99

RESULT 10
US-09-764-903-39
/ Patent No. US09764903
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Polynucleotides, Proteins, and Antibodies
/ FILE REFERENCE: P1228
/ CURRENT FILING DATE: 2001-01-17
/ PRIOR APPLICATION NUMBER: US/09/764,903
/ NUMBER OF SEQ ID NOS: 67
/ SOFTWARE: Patent Ver. 2.0
/ SEQ ID NO 39
/ SEQ ID NO 39
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-764-903-39

Query Match Similarity: 47.5%; Score 38; DB 9; Length 211;
Best Local Similarity: 46.2%; Pct. No. 84;
Matches: 4; Conservative: 3; Mismatches: 4; Indels: 0; Gaps: 0;

Cy 4 YONSPPQYXXC 16
Db 3 HNSVDSQFQWCC 15

RESULT 11
US-09-978-295A-226
/ Sequence 226 Application US/09978295A
/ GENERAL INFORMATION:
/ APPLICANT: Ashkenazi, Avi
/ TITLE OF INVENTION:
/ APPLICANT: Baker Kevin P.
/ FILE REFERENCE: P1228
/ CURRENT FILING DATE: 2001-01-17
/ PRIOR APPLICATION NUMBER: US/09/764,903
/ NUMBER OF SEQ ID NOS: 67
/ SOFTWARE: Patent Ver. 2.0
/ SEQ ID NO 39
/ SEQ ID NO 39
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-978-295A-226

Query Match Similarity: 47.5%; Score 38; DB 9; Length 211;
Best Local Similarity: 46.2%; Pct. No. 84;
Matches: 4; Conservative: 3; Mismatches: 4; Indels: 0; Gaps: 0;

Cy 4 YONSPPQYXXC 16
Db 3 HNSVDSQFQWCC 15

APPLICANT: Reuhl, Nicholas F.
APPLICANT: Reuhl, Nicholas F.
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Umada, Daniel Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS
CURRENT FILING DATE: US/09/978,295A
CURRENT APPLICATION NUMBER: 09/978585
PRIOR APPLICATION NUMBER: 09/978585
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062520
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062429
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065364
PRIOR FILING DATE: 1997-12-01
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077452
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077661
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077691
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079329
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079669
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 TITLE REFERENCE: P26301227
 CURRENT APPLICATION NUMBER: US/09/979,697
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/662350
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/664249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/665311
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/666364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/677450
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/677632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/677641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/677791
 PRIOR FILING DATE: 1998-03-22
 PRIOR APPLICATION NUMBER: 60/678004
 PRIOR FILING DATE: 1998-03-13
 PRIOR APPLICATION NUMBER: 60/678886
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/678936
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/678910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/678939
 PRIOR FILING DATE: 1998-03-25
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 PRIOR FILING DATE: 1998-04-01
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 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/681070
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/681049

PRIOR APPLICATION NUMBER: 60/681071
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/681195
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/681203
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/681229
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/681995
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/681817
 PRIOR FILING DATE: 1998-04-15
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 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/681838
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/681992
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 PRIOR FILING DATE: 1998-04-22
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 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: 60/683362
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/683495
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 PRIOR FILING DATE: 1998-04-28
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 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/683545
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/683554
 PRIOR FILING DATE: 1998-04-28
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 PRIOR FILING DATE: 1998-04-28
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 PRIOR APPLICATION NUMBER: 60/683560
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/683742
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/683836
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/684414
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/684441
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/684639
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/684640
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/684598
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/684600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/684627

PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081955
 PRIOR FILING DATE: 1998-04-15
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 PRIOR APPLICATION NUMBER: 60/081828
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/085688
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/085659
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082804
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 PRIOR FILING DATE: 1998-04-22
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 PRIOR FILING DATE: 1998-04-28
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 PRIOR APPLICATION NUMBER: 60/085318
 PRIOR FILING DATE: 1998-05-11

PRIOR APPLICATION NUMBER: 60/085323
 PRIOR FILING DATE: 1998-05-11
 PRIOR APPLICATION NUMBER: 60/085582
 PRIOR FILING DATE: 1998-05-15
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697
 Query March 42.5% Score 38; PB 10; Length 351.
 Best Local Similarity 42.2%; Pctd. No. 1,4ee02;
 Matches 6; Consensativity 3; Mismatches 4; Indels 0; Gaps 0;
 4 YONSPPHYXNC 16
 143 HGVSPFOMGCC 155
 Db
 RESULT 14
 US-09-999-832a-226
 Sequence 226, Application US/999832A
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Ben-David
 APPLICANT: Demireva, Nac
 APPLICANT: Eston, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filaret, Allen
 APPLICANT: Guo, Wei-Qiang
 APPLICANT: Guder, Hanspeter
 APPLICANT: Gertelman, Mary B.
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gutney, Nathan L.
 APPLICANT: Kijavitt, Yvar J.
 APPLICANT: Kijavitt, Yvar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Paoletti, Nicholas P.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Kimberly A.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William L.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ACID SEQUENCES OF INVENTION
 FILE REFERENCE: P63091063 Amending the Same
 CURRENT APPLICATION NUMBER: US/09/999-832a
 PRIOR FILING DATE: 2001-10-14
 PRIOR APPLICATION NUMBER: 60/118585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/044245
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066564

PRIOR FILING DATE	1997-11-21
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PRIOR FILING DATE	1998-04-09
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PRIOR FILING DATE	1998-04-15

PRIOR FILING DATE: 1998-04-21
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 PRIOR APPLICATION NUMBER: 60/085689
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 PRIOR FILING DATE: 1998-05-15
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 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15

PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697
 Query Match
 Best Local Similarity 46.3% Score 38, DB 11, length 351,
 Best Local 6, Conservative 3, Mismatches 4, Indels 0, Gaps 0
 Matches 6
 QY 4 YGSMKRYXCC 16
 DB 143 HGVSP08F08M08C 155

Search completed: November 7, 2003, 08:16:55
 Job time: 15.0347 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 ; Search time 2.3498 Second

(without alignments)
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 Perfect score: 80

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Scoring table: BLOSUM62

[illegible]

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Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by

and is derived by analysis of the total score distribution.

SUMMARIES

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2	44	48.8	106	4	US-09-026-700-12

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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4	38	47.5	1.119	US-08-107-936-19	Sequence 16, App
5	38	47.5	1.119	US-08-107-936-19	Sequence 19, App
6	38	47.5	1.119	US-08-107-936-19	Sequence 20, App
7	38	47.5	1.119	US-08-107-936-22	Sequence 20, App
8	38	47.5	1.119	US-08-107-936-22	Sequence 21, App
9	38	47.5	1.119	US-08-107-936-22	Sequence 37, App
10	38	47.5	1.119	US-08-107-936-22	Sequence 19, App
11	38	47.5	1.119	US-08-160-804-19	Sequence 20, App
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15	38	47.5	1.119	US-08-160-804-19	Sequence 28, App
16	38	47.5	1.119	US-08-160-804-19	Sequence 28, App
17	38	47.5	1.119	US-08-160-804-19	Sequence 28, App
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45	35	42.8	US-08-766-8584-33	Sequence 33, Appl 1
44	35.5	44.4	US-08-039-2322-4	Sequence 4, Appl 1
43	37.0	43.2	US-08-185-4321-9	Sequence 4, Appl 1
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41	37.0	43.2	US-08-185-4321-9	Sequence 4, Appl 1
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US-09-149-476-696
 RESULT 1
 Patent No. 6,966,420 Application US/09149476
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 FILE REPRESENTATION: 16 human secreted proteins
 CURRENT FILING DATE: 1998-09-08
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60/040,462
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60/040,333
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60/038,421
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60/040,426
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60/040,334
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60/040,463
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60/047,600
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60/047,615
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60/047,597
 EARLIER FILING DATE: 1997-05-23
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 EARLIER APPLICATION NUMBER: 60/047,517
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60/047,503
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60/047,594
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60/047,581
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60/047,584
 EARLIER FILING DATE: 1997-05-23

ALIGNMENTS

EARLIER APPLICATION NUMBER: 60/057,669
 EARLIER FILING DATE: 1997-09-05
 EARLIER APPLICATION NUMBER: 60/049,610
 EARLIER FILING DATE: 1997-06-13
 EARLIER APPLICATION NUMBER: 60/061,060
 EARLIER FILING DATE: 1997-10-02
 EARLIER FILING DATE: 1997-10-02

Query Match 55.0%; Score 44; DB 4; Length 365;
 Best Local Similarity 53.8%; Pctd. No. 9.6;
 Matches 77; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXYGNSPKXEN 13
 DB 264 CXYGNSPKXEN 276

RESULT 2
 US-09-625-799b-15
 GENERAL INFORMATION: Application US/09025769B
 Patent No. 6300064

GENERAL INFORMATION:
 APPLICANT: Knapik, Achia
 ATTORNEY/AGENT INFORMATION: P
 APPLICANT: Knapik, Achia
 APPLICANT: 1149, Vic
 APPLICANT: Ge, Liming
 APPLICANT: Motorola, Simon
 APPLICANT: Motorola, Simon
 APPLICANT: Motorola, Simon
 TITLE OF INVENTION: Protein (poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESS: Motorola, Inc., 1300 N. 17th St., Sec 9, c/o Fish & Neave
 STREET 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021

COMPUTER READABLE FORM:
 MODERN TYPE: FOLGY disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
 CURRENT APPLICATION DATA: 09/025,769B
 FILING DATE: 1998-FEB-1598
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 NAME: James F. Haley, Jr., Eng.

REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MOPRHO/5
 TELEPHONE: (212)596-9000
 TELEFAX: (212)596-9090
 INFORMATION FOR SEQ ID NO: 16:
 STRAND: 16
 LENGTH: 109 amino acids
 TYPE: amino acid
 MODSUS TYPE: none
 US-09-625-799b-16

Query Match 48.8%; Score 39; DB 4; Length 109;
 Best Local Similarity 43.6%; Pctd. No. 19;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CXYGNSPKXEN 11
 DB 89 CXYGNSPKXEN 99

RESULT 3

US-09-615-109-7
 Sequence 7; Application US/08635109
 Patent No. 6538114

GENERAL INFORMATION:
 APPLICANT: Petron, Marc A. N.
 ATTORNEY/AGENT INFORMATION: P
 APPLICANT: Petron, Marc A. N.
 APPLICANT: 1149, Vic
 TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESS: RED & ROBIN
 STREET: 285 Hamilton Avenue, Suite 200
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94301

COMPUTER READABLE FORM:
 MODERN TYPE: FOLGY disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: 08/635,109
 FILING DATE: 19-APR-1996
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION: P
 REGISTRATION NUMBER: 2300-6146
 REFERENCE/DOCKET NUMBER: 38,548
 TELEPHONE: (415) 327-4231
 TELEFAX: (415) 327-4231
 INFORMATION FOR SEQ ID NO: 7:
 STRAND: 7
 LENGTH: 109
 TYPE: amino acid
 MODSUS TYPE: none
 US-08-615-109-7

COMPUTER READABLE FORM:
 MODERN TYPE: FOLGY disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: 08/635,109
 FILING DATE: 19-APR-1996
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION: P
 REGISTRATION NUMBER: 2300-6146
 REFERENCE/DOCKET NUMBER: 38,548
 TELEPHONE: (415) 327-4231
 TELEFAX: (415) 327-4231
 INFORMATION FOR SEQ ID NO: 7:
 STRAND: 7
 LENGTH: 109
 TYPE: amino acid
 MODSUS TYPE: none
 US-08-615-109-7

Query Match 47.5%; Score 38; DB 4; Length 107;
 Best Local Similarity 45.5%; Pctd. No. 27;
 Matches 67; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXYGNSPKXEN 11
 DB 89 CXYGNSPKXEN 99

GENERAL INFORMATION: Biopharmaceutical, Inc.
 APPLICANT: 104 Hamilton Court
 APPLICANT: Menlo Park, California 94025
 APPLICANT: United States of America
 APPLICANT: 1345 Avenue of the Americas
 APPLICANT: New York, New York 10105
 APPLICANT: United States of America
 TITLE OF INVENTION: RECOMBINANT HUMAN ANT-ILK26
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESS: Felice & Lynch
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10022

COMPUTER READABLE FORM:
 MODERN TYPE: FOLGY disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: 08/635,109
 FILING DATE: 19-APR-1996
 CLASSIFICATION: 435

MEDION TYPE: 3.5 inch
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 6.0/ASCII standard
 CURRENT APPLICATION NUMBER: US/08/207/996
 APPLICATION NUMBER: US/08/207/996
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Paequalina, Patricia A.
 ADDRESS: 1345 Avenue of the Americas
 REFERENCE/DOCKET NUMBER: LUD-5363
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-688-9200
 FAX: 212-688-9200
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-207-996-18
 Query Match 47.5%; Score 38; DB 1; Length 119;
 Best Local Similarity 46.2%; Pred. No. 30;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CXXYNSPKSFYV 13
 Db 96 CARRDDPMWV 108
 RESULT 5
 US-08-207-996-19
 Application US/08207996
 Patent No. 5646253
 GENERAL INFORMATION:
 APPLICANT: Scogen Biopharmaceuticals, Inc.
 ADDRESS: 1345 Avenue of the Americas
 APPLICANT: United States of America
 APPLICANT: 1345 Avenue of the Americas
 APPLICANT: New York City 10105
 APPLICANT: United States of America
 TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LX26
 ANTIBODIES
 INVENTOR: FELIX L. LYNCH
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felix & Lynch
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10022
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 6.0/ASCII standard
 CURRENT APPLICATION NUMBER: US/08/207/996
 APPLICATION NUMBER: US/08/207/996
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Paequalina, Patricia A.
 ADDRESS: 1345 Avenue of the Americas
 REFERENCE/DOCKET NUMBER: LUD-5363
 TELEPHONE: 212-688-9200
 FAX: 212-688-9200
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-207-996-20
 Query Match 47.5%; Score 38; DB 1; Length 119;
 Best Local Similarity 46.2%; Pred. No. 30;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CXXYNSPKSFYV 13
 Db 96 CARRDDPMWV 108
 RESULT 7

LENGTH: 119 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-207-996-19
 Query Match 47.5%; Score 38; DB 1; Length 119;
 Best Local Similarity 46.2%; Pred. No. 30;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CXXYNSPKSFYV 13
 Db 96 CARRDDPMWV 108
 RESULT 6
 US-08-207-996-20
 Application US/08207996
 Patent No. 5646253
 GENERAL INFORMATION:
 APPLICANT: Scogen Biopharmaceuticals, Inc.
 ADDRESS: 1345 Avenue of the Americas
 APPLICANT: United States of America
 APPLICANT: 1345 Avenue of the Americas
 APPLICANT: New York City 10105
 APPLICANT: United States of America
 TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LX26
 ANTIBODIES
 INVENTOR: FELIX L. LYNCH
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felix & Lynch
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10022
 COMPUTER READABLE FORM:
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WordPerfect 6.0/ASCII standard
 CURRENT APPLICATION NUMBER: US/08/207/996
 APPLICATION NUMBER: US/08/207/996
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Paequalina, Patricia A.
 ADDRESS: 1345 Avenue of the Americas
 REFERENCE/DOCKET NUMBER: LUD-5363
 TELEPHONE: 212-688-9200
 FAX: 212-688-9200
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-207-996-20
 Query Match 47.5%; Score 38; DB 1; Length 119;
 Best Local Similarity 46.2%; Pred. No. 30;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 CXXYNSPKSFYV 13
 Db 96 CARRDDPMWV 108
 RESULT 7

US-08-207-996-21
 Sequence 21, Application US/08207996
 Patent No. 5646253
 GENERAL INFORMATION:
 APPLICANT: Scigen Biopharmaceuticals, Inc.
 APPLICANT: 1014 Hamilton Court
 APPLICANT: Menlo Park, California 94025
 APPLICANT: United States of America
 APPLICANT: 144 Avenue of the Americas
 APPLICANT: New York, New York 10105
 APPLICANT: United States of America
 TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LX26
 CLASSIFICATION: 530
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Falte & Lynch
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10022
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-688-3884
 TELEFAX: 212-688-3884
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 LENGTH: 119 amino acids
 STANDARDS: single
 MOLECULAR TYPE: DNN (genomic)
 US-08-207-996-21

Query Match 47 54; Score 38; DB 1; Length 119;
 Overall Similarity 47 54; 2; Mismatches
 Matches 6; Conservative 2; Indels 0; Gaps 0;

Db 96 CARRIDDPANFY 108

RESULT 9
 US-08-207-996-22
 Sequence 22, Application US/08207996
 Patent No. 5646253
 GENERAL INFORMATION:
 APPLICANT: Scigen Biopharmaceuticals, Inc.
 APPLICANT: 1014 Hamilton Court
 APPLICANT: Menlo Park, California 94025
 APPLICANT: United States of America
 APPLICANT: 144 Avenue of the Americas
 APPLICANT: New York, New York 10105
 APPLICANT: United States of America
 TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LX26
 CLASSIFICATION: 530
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Falte & Lynch
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10022
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-688-3884
 TELEFAX: 212-688-3884
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 LENGTH: 119 amino acids
 STANDARDS: single
 MOLECULAR TYPE: protein
 US-08-207-996-22

CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10022
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-688-3884
 TELEFAX: 212-688-3884
 INFORMATION FOR SEQ ID NO: 22:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 LENGTH: 119 amino acids
 STANDARDS: single
 MOLECULAR TYPE: protein
 US-08-207-996-22

Query Match 47 54; Score 38; DB 1; Length 119;
 Overall Similarity 47 54; 2; Mismatches
 Matches 6; Conservative 2; Indels 0; Gaps 0;

Db 96 CARRIDDPANFY 108

RESULT 9
 US-08-207-996-27
 Sequence 27, Application US/08207996
 Patent No. 5646253
 GENERAL INFORMATION:
 APPLICANT: Scigen Biopharmaceuticals, Inc.
 APPLICANT: 1014 Hamilton Court
 APPLICANT: Menlo Park, California 94025
 APPLICANT: United States of America
 APPLICANT: 144 Avenue of the Americas
 APPLICANT: New York, New York 10105
 APPLICANT: United States of America
 TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LX26
 CLASSIFICATION: 530
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Falte & Lynch
 STREET: 805 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10022
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-688-3884
 TELEFAX: 212-688-3884
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 LENGTH: 119 amino acids
 STANDARDS: single
 MOLECULAR TYPE: protein
 US-08-207-996-27

CORRESPONDENCE ADDRESS:
 WILLIAM J. HARRIS
 STREET 805 THIRD AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 ZIP: 10022 S.A.
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA: 08/760 840A
 FILING DATE: 05-DEC-1996
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 FILING NUMBER: 08-MAR-1995
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: HARRIS, NO. 595248man D.
 REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NH/SLH
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-688-9200
 TELEFAX: 212-688-9200
 INFORMATION FOR SEQ ID NO: 20:
 LENGTH: 119 amino acids
 STRANDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-760-840A-21
 Query Match 47.5%; Score 38; DB 2; Length 119;
 Best Local Similarity 46.2%; Pred. No. 30;
 Matches 0; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Cy 1 CXXYSGSPGMYAT 13
 Db 96 CARI8DDPMWAK 108

RESULT 11
 ? Sequence 21, Application US/08760840A
 ? Patent No. 5952484
 ? GENERAL INFORMATION:
 ? INVENTOR: WILLIAM J. HARRIS;
 ? APPLICANT: WILLIAM J. HARRIS;
 ? APPLICANT: WOLFGANG J. BETTIG;
 ? APPLICANT: PIAT GARTH-CHESA;
 ? PRIORITY NUMBER: 08/08760 840A
 ? TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-L26 ANTIBODIES
 ? NUMBER OF SEQUENCES: 31
 ? CORRESPONDENCE ADDRESS:
 ? WILLIAM J. HARRIS
 ? STREET 805 THIRD AVENUE
 ? CITY: NEW YORK
 ? STATE: NEW YORK
 ? ZIP: 10022 S.A.
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: floppy disk
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Wordperfect
 ? CURRENT APPLICATION DATA: 08/760 840A
 ? FILING DATE: 05-DEC-1996
 ? CLASSIFICATION: 536

PRIOR APPLICATION DATA:
 FILING NUMBER: 08-MAR-1995
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: HARRIS, NO. 595248man D.
 REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NH/SLH
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-688-9200
 TELEFAX: 212-688-9200
 INFORMATION FOR SEQ ID NO: 21:
 LENGTH: 119 amino acids
 STRANDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-760-840A-21
 Query Match 47.5%; Score 38; DB 2; Length 119;
 Best Local Similarity 46.2%; Pred. No. 30;
 Matches 0; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Cy 1 CXXYSGSPGMYAT 13
 Db 96 CARI8DDPMWAK 108

RESULT 11
 ? Sequence 22, Application US/08760840A
 ? Patent No. 5952484
 ? GENERAL INFORMATION:
 ? INVENTOR: WILLIAM J. HARRIS;
 ? APPLICANT: WILLIAM J. HARRIS;
 ? APPLICANT: WOLFGANG J. BETTIG;
 ? APPLICANT: PIAT GARTH-CHESA;
 ? PRIORITY NUMBER: 08/08760 840A
 ? TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-L26 ANTIBODIES
 ? NUMBER OF SEQUENCES: 31
 ? CORRESPONDENCE ADDRESS:
 ? WILLIAM J. HARRIS
 ? STREET 805 THIRD AVENUE
 ? CITY: NEW YORK
 ? STATE: NEW YORK
 ? ZIP: 10022 S.A.
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: floppy disk
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: Wordperfect
 ? CURRENT APPLICATION DATA: 08/760 840A
 ? FILING DATE: 05-DEC-1996
 ? PRIOR APPLICATION DATA:
 ? FILING NUMBER: 08-MAR-1995
 ? CLASSIFICATION: 536
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: HARRIS, NO. 595248man D.
 ? REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NH/SLH
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 212-688-9200
 ? TELEFAX: 212-688-9200
 ? INFORMATION FOR SEQ ID NO: 22:
 ? LENGTH: 119 amino acids
 ? STRANDNESS: unknown

TOPOLOGY: unknown
 W01: 100% identity
 US-08-760-840A-22

Query Match 47.5%; Score 38; DB 2; Length 119;
 Meet Local Similarity 46.2%; Pred. No. 30;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXXVNSPFGKAY 13
 DB 96 CANR00DPWPMF1 108

RESULT 15
 US-08-760-840A-28
 US-08-760-840A-28 Application US/08760840A

GENERAL INFORMATION:
 APPLICANT: PAUL WALLACE;
 APPLICANT: 1811 HUNTER HARBIS;
 APPLICANT: 101500001; BETTING;
 APPLICANT: PILLAR GRIN-CHESA;
 APPLICANT: Lloyd J. Old
 APPLICANT: 101500001; BETTING;
 NUMBER OF SECTIONS: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSER: false & Lynch
 STREET: 405 Third Avenue
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 DATE: 1002
 COMMENTS: 1002; 1002; 1002; 1002;
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION:
 CURRENT APPLICATION:
 APPLICATION NUMBERS: US/08/760,840A
 FILING DATE: 05-DEC-1996
 PRIOR APPLICATION DATE:
 APPLICATION NUMBER: PCT/US 95/01094
 FILING DATE: 08-MAR-1995
 CLASSIFICATION: 536
 NAME: 1002; 1002; 1002; 1002;
 REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
 TELEPHONE: 212-688-3880
 TELEFAX: 212-688-3884
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULAR WEIGHT: 1002
 US-08-760-840A-28

Query Match 47.5%; Score 38; DB 2; Length 119;
 Meet Local Similarity 46.2%; Pred. No. 30;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXXVNSPFGKAY 13
 DB 96 CANR00DPWPMF1 108

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GenoCore version 5.1.6

ON protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 2.0721 Seconds

(without alignment)

142,584 Million data updates/sec

File: US-09-661-992b-106

Percent score: 82

Sequence: 1 PRRNRMALYKSCSD 16

Scoring table: BLOSUM62

Gapop 10.0 / Gapext 0.5

Searched: 20308 seqs, 9616682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter 45 summaries

Database:

1: P131*

2: P132*

3: P133*

4: P134*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the local score distribution.

SUMMARIES

Result	Score	Query	Length	DB	ID	Description
1	82	106.0	2351	1	E2H7	coagulation factor
2	76	92.7	2351	1	E2H7	coagulation factor
3	76	92.7	2351	1	E2H7	coagulation factor
4	70	85.4	2133	3	P131*	coagulation factor
5	44	53.7	275	2	B33412	streptococcal 3'-p
6	42	51.2	220	2	S44966	lmb protein - Str
7	42	51.2	220	2	S44966	lmb protein - Str
8	41	50.0	1120	2	T13211	hypothetical prote
9	40	48.8	76	2	A37957	hypothetical prote
10	40	48.8	76	2	A37957	hypothetical prote
11	39	47.6	573	2	B56639	protein ttrp 16 tl
12	39	47.6	573	2	B56639	protein ttrp 16 tl
13	39	47.6	160	2	T44703	lipopolysaccharide
14	39	47.6	505	2	A37642	sugar transporter
15	39	47.6	505	2	A37642	sugar transporter
16	39	47.6	505	2	A37642	sugar transporter
17	39	47.6	1058	2	A59311	hypothetical prote
18	39	47.6	1058	2	A59311	hypothetical prote
19	39	47.6	1058	2	A59311	hypothetical prote
20	39	47.6	1058	2	A59311	hypothetical prote
21	39	47.6	1058	2	A59311	hypothetical prote
22	39	47.6	1058	2	A59311	hypothetical prote
23	39	47.6	1058	2	A59311	hypothetical prote
24	39	47.6	1058	2	A59311	hypothetical prote
25	39	47.6	1058	2	A59311	hypothetical prote
26	39	47.6	1058	2	A59311	hypothetical prote
27	39	47.6	1058	2	A59311	hypothetical prote
28	39	47.6	1058	2	A59311	hypothetical prote
29	39	47.6	1058	2	A59311	hypothetical prote
30	39	47.6	1058	2	A59311	hypothetical prote
31	39	47.6	1058	2	A59311	hypothetical prote
32	39	47.6	1058	2	A59311	hypothetical prote
33	39	47.6	1058	2	A59311	hypothetical prote
34	39	47.6	1058	2	A59311	hypothetical prote
35	39	47.6	1058	2	A59311	hypothetical prote
36	39	47.6	1058	2	A59311	hypothetical prote
37	39	47.6	1058	2	A59311	hypothetical prote
38	39	47.6	1058	2	A59311	hypothetical prote
39	39	47.6	1058	2	A59311	hypothetical prote
40	39	47.6	1058	2	A59311	hypothetical prote
41	39	47.6	1058	2	A59311	hypothetical prote
42	39	47.6	1058	2	A59311	hypothetical prote
43	39	47.6	1058	2	A59311	hypothetical prote
44	39	47.6	1058	2	A59311	hypothetical prote
45	39	47.6	1058	2	A59311	hypothetical prote

ALIGNMENTS

30	37	45.1	394	2	A45989	proteasome assembly
31	37	45.1	394	2	A45989	proteasome assembly
32	37	45.1	456	2	T46221	hypothetical prote
33	37	45.1	552	2	T33760	apilipoglycan-1-phos
34	37	45.1	717	2	B72208	conserved hypocher
35	37	45.1	772	2	G99327	hypothetical 91.8K
36	37	45.1	772	2	G99327	hypothetical 91.8K
37	37	45.1	776	2	T20644	hex factor asgrega
38	37	45.1	1243	2	S60138	hex factor asgrega
39	37	45.1	1243	2	S60138	hex factor asgrega
40	36	43.9	89	1	S45609	Shg9-like toxin 1
41	36	43.9	89	2	S01033	Shg9-like toxin 1
42	36	43.9	89	2	S01033	Shg9-like toxin 1
43	36	43.9	89	2	S01033	Shg9-like toxin 1
44	36	43.9	89	2	S01033	Shg9-like toxin 1
45	36	43.9	89	2	S01033	Shg9-like toxin 1

A/Cross-references: EMBL:U94781; NID:g2444173; PIDN:AAB71526.1; PID:g2444174

General:

A; genre: my1; name:

C/Superfamily: myosin heavy chain 95F; myosin motor domain homology

F;120-782/Domain: myosin motor domain homology <MMO>

Query Match 50.04: Score 41: DB 2: Length 1120.

Best Local Similarity	EO 08	Pred	No.	Denign	Lazv?

Matchbox 7, Coonemohine 3, 11/21/61

matches 1; conservative 3; mismatches 4; indels 0;

1. **Introduction**
 2. **Background**
 3. **Methods**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Figure 1**
 10. **Figure 2**
 11. **Figure 3**
 12. **Figure 4**
 13. **Figure 5**
 14. **Figure 6**
 15. **Figure 7**
 16. **Figure 8**
 17. **Figure 9**
 18. **Figure 10**
 19. **Figure 11**
 20. **Figure 12**
 21. **Figure 13**
 22. **Figure 14**
 23. **Figure 15**
 24. **Figure 16**
 25. **Figure 17**
 26. **Figure 18**
 27. **Figure 19**
 28. **Figure 20**
 29. **Figure 21**
 30. **Figure 22**
 31. **Figure 23**
 32. **Figure 24**
 33. **Figure 25**
 34. **Figure 26**
 35. **Figure 27**
 36. **Figure 28**
 37. **Figure 29**
 38. **Figure 30**
 39. **Figure 31**
 40. **Figure 32**
 41. **Figure 33**
 42. **Figure 34**
 43. **Figure 35**
 44. **Figure 36**
 45. **Figure 37**
 46. **Figure 38**
 47. **Figure 39**
 48. **Figure 40**
 49. **Figure 41**
 50. **Figure 42**
 51. **Figure 43**
 52. **Figure 44**
 53. **Figure 45**
 54. **Figure 46**
 55. **Figure 47**
 56. **Figure 48**
 57. **Figure 49**
 58. **Figure 50**
 59. **Figure 51**
 60. **Figure 52**
 61. **Figure 53**
 62. **Figure 54**
 63. **Figure 55**
 64. **Figure 56**
 65. **Figure 57**
 66. **Figure 58**
 67. **Figure 59**
 68. **Figure 60**
 69. **Figure 61**
 70. **Figure 62**
 71. **Figure 63**
 72. **Figure 64**
 73. **Figure 65**
 74. **Figure 66**
 75. **Figure 67**
 76. **Figure 68**
 77. **Figure 69**
 78. **Figure 70**
 79. **Figure 71**
 80. **Figure 72**
 81. **Figure 73**
 82. **Figure 74**
 83. **Figure 75**
 84. **Figure 76**
 85. **Figure 77**
 86. **Figure 78**
 87. **Figure 79**
 88. **Figure 80**
 89. **Figure 81**
 90. **Figure 82**
 91. **Figure 83**
 92. **Figure 84**
 93. **Figure 85**
 94. **Figure 86**
 95. **Figure 87**
 96. **Figure 88**
 97. **Figure 89**
 98. **Figure 90**
 99. **Figure 91**
 100. **Figure 92**
 101. **Figure 93**
 102. **Figure 94**
 103. **Figure 95**
 104. **Figure 96**
 105. **Figure 97**
 106. **Figure 98**
 107. **Figure 99**
 108. **Figure 100**
 109. **Figure 101**
 110. **Figure 102**
 111. **Figure 103**
 112. **Figure 104**
 113. **Figure 105**
 114. **Figure 106**
 115. **Figure 107**
 116. **Figure 108**
 117. **Figure 109**
 118. **Figure 110**
 119. **Figure 111**
 120. **Figure 112**
 121. **Figure 113**
 122. **Figure 114**
 123. **Figure 115**
 124. **Figure 116**
 125. **Figure 117**
 126. **Figure 118**
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 208. **Figure 200**
 209. **Figure 201**
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 213. **Figure 205**
 214. **Figure 206**
 215. **Figure 207**
 216. **Figure 208**
 217. **Figure 209**

[illegible]

```

A1gene: g91uh
A1map position: circular chromosome
Query Match: Score 39; DB 2; length 512;
Mismatch: 47; 68;
Identical Similarity: 60.0%; Read No.: 3;
Methods: 4; Conservative; 4; Mismatches
Qy 1 PRRSPAL1 10
Db 189 PRRSPAL1 198

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 1.1534 Seconds

440000 alignments
655.978 Million cell updates/sec

Title:

Sequence: US-03-661-992b-106

Scoring table: BLASTNCALUSCSD 16

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum March 08

Maximum March 08

Listing first 45 summaries

Database: SwissProt_41.1*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

RESULTS

Result No	Score	Query	Length	ID	Description
1	82	100.0	2351	P86_HUMAN	P00451 homo sapien
2	76	82.7	2113	P86_HUMAN	P00451 mus musculu
3	70	76.2	2113	P86_HUMAN	P00451 mus musculu
4	41	50.0	324	CHIF_MOUSE	G09263 mus musculu
5	39	47.6	160	1 COOL_WTILE	G09263 mus musculu
6	39	46.3	150	1 COOL_WTILE	G09263 mus musculu
7	39	45.1	150	1 COOL_WTILE	G09263 mus musculu
8	37	45.1	150	1 COOL_WTILE	G09263 mus musculu
9	36.5	44.5	650	1 BHEG_BOVI	P03366 bovine hemo
10	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
11	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
12	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
13	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
14	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
15	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
16	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
17	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
18	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
19	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
20	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
21	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
22	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
23	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
24	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
25	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
26	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
27	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
28	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
29	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
30	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
31	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
32	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu
33	36	43.9	149	1 SIBB_MOUSE	G09263 mus musculu

Result No	Score	Query	Length	ID	Description
34	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
35	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
36	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
37	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
38	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
39	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
40	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
41	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
42	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
43	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
44	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
45	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
46	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
47	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
48	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
49	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
50	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
51	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
52	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
53	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
54	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
55	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
56	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
57	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
58	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
59	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
60	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
61	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
62	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
63	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
64	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
65	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
66	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
67	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
68	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
69	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
70	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
71	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
72	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
73	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
74	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
75	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
76	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
77	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
78	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
79	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
80	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
81	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
82	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
83	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
84	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
85	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
86	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
87	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
88	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
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90	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
91	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
92	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
93	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
94	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
95	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
96	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
97	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
98	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
99	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee
100	35	42.7	144	1 OUR_CHRE	G09233 chimpanzee

[illegible]

[illegible][illegible]

QY 5 ORNTALTVNSC 15
 DB 154 ORNTSLTSLSC 164

RESULT 15

ID DUS4.CHICK STANDARD; PRT; 375 AA.

DT 16-OCT-2001 (Prt) 40 (Created)

DT 16-OCT-2001 (Rel) 40 (Last sequence update)

DT 28-FEB-2003 (Rel) 41 (Last annotation update)

DB Dual specificity protein phosphatase 4 (EC 3.1.3.48) (EC 3.1.3.16)

DR Dual specificity protein phosphatase 4 (EC 3.1.3.48) (EC 3.1.3.16)

DS Dual specificity protein kinase phosphatase-2 (GAF) kinase

GN DUSP4 OR KKP2

OS Gallus gallus (Chicken)

OC Archaea; Bacteria; Eukaryota; Vertebrata; Eumetazoa; Galliformes; Phasianidae; Phasianinae;

OC Gallus

OC NCBI_TaxID=9031

PP SEQUENCE FROM N.A.

RX STEARIN-White Leghorn;

RC MEDLINE=20379359; PubMed=10918612;

RA Fu S.-L.; Wahn A.; Vogt P.K.;

RT transformed by "v-jun"; overexpression of genes upregulated in cells

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DB 202 GYTMALTVNS 211
 Search completed: November 7, 2003, 07:28:11
 Job time : 3.15354 secs

Query Match 43.9% Score 36; DD 1; Length 375;
 Mismatches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

5 ORNTALTVNS 14


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RESULT 2
Q14806 PRELIMINARY; PRT; 2343 AA.
O14806;
AC O14806;
DT 01-JUN-1998 (TRIMBLrel. 05, Created)
DE BEET LOCAL SIMILARITY 53.7%; Score 44; DB 16; Length 275;
DN Factor VIII.
FS.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Carnifera; Vertebrata; Euteleostomi;
NCBI_TaxId=9615;
LN [1]
SEQUENCE FROM N.A.
RA Cameron C., Nolley C., Hoyle S., Medlyn L., Hough C., Kamise S.,
RA Giles A., Allcrop D.,
RA "The canine factor VIII cDNA and 5' flanking sequence."
RA Shiba-Tanihara, 1993) to the EMBL/Genbank/DBJ databases.
OC Eukaryota; Metazoa; Chordata; Carnifera; Vertebrata; Euteleostomi;
DN EMBL; AF045234; AB049123.1; J01159 C DOKA1NG.
DR HSPF; P00451; ICRG.
DR InterPro; IPRO01117; Ox-carboxide.
DR PROSITE; PS00754; PS_P8_Type_C_2.
DR Pfam; PF00399; Ox-carboxide_3.
DR PIRam; P00754; PS_P8_Type_C_2.
DR SMART; S000231; P586C2.1.
DR DMD; D00000; P586C2.2.
DR PROSITE; PS01286; P586C2.2.
DR PROSITE; PS00079; MULTIDOMAIN_OXIDASE1.3.
SQ
SEQUENCE 2343 AA; 265829 MW; A85FA5E7C3B399 CRC64;

Query Match
Best Local Similarity 93.8%; Score 77; DB 6; Length 2343;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 PIRNCMTALXVSSCD 16
DB 710 PIRNCMTALXVSSCN 725

RESULT 3
Q912N7 PRELIMINARY; PRT; 275 AA.
ID Q912N7;
DT 01-MAR-2001 (TRIMBLrel. 16, Created)
DT 01-MAR-2001 (TRIMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRIMBLrel. 23, Last annotation update)
OS Streptomyces 3'-phosphotransferase.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
AC Pseudomonadaceae; Pseudomonas.
LN [1]_TaxId=287;
SEQUENCE FROM N.A.
RA STRAIN:PCN 15697 / PM01;
RA Pseudomonas fluorescens Pf0-1 (2)
RA Steyer C.X., Phan X.-O., Berrill L., Mizoguchi S.D., Hartner P.,
RA Hickey M.J., Britman F.S.L., Hittinger W.O., Kowalik D.J., Lagroix W.,
RA Garber R.L., Goller S.N., Folger K.R., Kass A., Leebig K., Lim R.N.,
RA Smith K., Soule S.N., Folger K.R., Kass A., Leebig K., Lim R.N.,
RA Reizer J., Saiter M.R., Hancock R.E.W., Lory S., Olsen M.V.,
RA "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RA opportunistic pathogen."
RA Nierman M.C., White O., Olson M.V., Davis A.A., Clayton M.,
RT EMBL; AB004612; AB005247.1; --
DR InterPro; IPR006748; AMP_6_hmr.
DR Pfam; PF04655; AMP_6_hmr.
DR TransDecoder; Complete proteome.

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SQ SEQUENCE 275 AA; 31144 MW; 476F0AC0A1FE0068 CRC64;

Query Match
Best Local Similarity 53.7%; Score 44; DB 16; Length 275;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 PIRNCMTALXVSSCD 16
DB 34 PIRNCMTALXVSSCN 48

RESULT 4
Q88376 PRELIMINARY; PRT; 265 AA.
AC Q88376;
DT 01-JUN-2002 (TRIMBLrel. 21, Created)
DT 01-JUN-2002 (TRIMBLrel. 21, Last sequence update)
DE BEET LOCAL SIMILARITY 53.7%; Score 44; DB 16; Length 275;
DN MAP kinase MAP2B.
OS Homo sapiens (Human).
GN MAPK5.
OC Cyta sactiva (Rice).
OC Eukaryota; Viridiplantae; Scrophylales; Embryophyta; Trachophyta;
OC Eukaryota; Viridiplantae; Scrophylales; Embryophyta; Trachophyta;
OC Eukaryota; Viridiplantae; Scrophylales; Embryophyta; Trachophyta;
OC Eukaryota; Viridiplantae; Scrophylales; Embryophyta; Trachophyta;
OC NCBI_TaxId=4510;
LN [1]
SEQUENCE FROM N.A.
RA Xiong L., Qi M., Yang Y.,
RA "Molecular cloning and characterization of a novel MAP kinase,
RA MAPK5, in rice."
RA EMBL; AF076884; AF076884.1; --
DR HSPF; P24941; IYU1.
DR Genset; Q88376; --
DR InterPro; IPR000719; Prot_kinase.
DR PROSITE; PS00001; PROTEIN_KINASE_ATP_1.
DR PROSITE; PS00001; PROTEIN_KINASE_ATP_1.
DR PROSITE; PS00001; PROTEIN_KINASE_ATP_1.
DR PROSITE; PS00001; PROTEIN_KINASE_ATP_1.
SQ
SEQUENCE 265 AA; 30817 MW; 62AB27A1A7998F8C CRC64;

Query Match
Best Local Similarity 52.4%; Score 43; DB 10; Length 265;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 PIRNCMTALXVSSCD 16
DB 56 PIRNCMTALXVSSCN 71

RESULT 5
ID Q8NGJ0 PRELIMINARY; PRT; 311 AA.
AC Q8NGJ0;
DT 01-OCT-2002 (TRIMBLrel. 22, Created)
DT 01-OCT-2002 (TRIMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRIMBLrel. 22, Last annotation update)
OS Homo sapiens (Human).
GN Seven transmembrane helix receptor.
OC Eukaryota; Metazoa; Chordata; Carnifera; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Carnifera; Vertebrata; Euteleostomi;
OC NCBI_TaxId=9606;
LN [1]_TaxId=9606;
SEQUENCE FROM N.A.
RA Gough J., Gough J., Gough J., Gough J., Gough J., Gough J.,
RA Tansini, Sero, Chubert-Roe, Gough J., Gough J., Gough J.,
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes."
RT EMBL; AB065728; AB065728.1; --
DR InterPro; IPR000276; GPCR_GPCRs.
DR Pfam; PF00001; 7tm_1; 1.

```

PRINTS; P800237; GPCRINTEGRIN.
DR PROSITE; P800237; G PROTEIN RECP P.1; 1.
DR PROSITE; P800237; G PROTEIN RECP P.1; 1.
KW Reciprocal; Transmembrane.
SO SEQUENCE 311 AA; 3468 MW; C680187C342C7DM CRC64;

Query Match
Best Local Similarity 75.0%; Pred. No. 11; Length 311;

Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 42 NCBI/NTL/NCSS 53

RESULT 6

OGWGA8 PRELIMINARY; PRT; 312 AA.

AC GSWGA8; 2002 (TREMURel. 20. Created)
DT 01-MAR-2003 (TREMURel. 20. Last annotation update)
DT 01-MAR-2003 (TREMURel. 23. Last annotation update)
DE Olfactory receptor MOR174-1.
OS Mus musculus (Mouse).
OC Mammalia; Eutheria; Rodentia; Sciurinae; Muridae; Murinae; Mus.
NCB1_TaxId=10090;
LN 1)
SR SEQUENCE FROM N.A.
RA Zhang X.; Riverain S.J.;
RT "The olfactory receptor gene superfamily of the mouse."
RL Nat. Neurosci. 0:0-0(2002).

RP SEQUENCE FROM N.A.
RA Adams M.;
RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072248; AAL60907.1; -
DR DDBJ; AF072248; AAL60907.1; -
DR Ffam; P800031; 7C6.1; GPCR, Anodan.

DR PRINTS; P800237; GPCRINTEGRIN.
DR PROSITE; P800237; G PROTEIN RECP P.1; 1.
DR PROSITE; P800237; G PROTEIN RECP P.2; 1.

SO SEQUENCE 312 AA; 3468 MW; 9AA6C0D87080A74 CRC64;

Query Match
Best Local Similarity 52.4%; Score 43; DB 11; Length 312;

Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Db 42 NCBI/NTL/NCSS 53

RESULT 7

OG4372 PRELIMINARY; PRT; 220 AA.

AC OG4372; 1996 (TREMURel. 01. Created)
DT 01-NOV-1996 (TREMURel. 01. Last sequence update)
DT 01-DEC-2001 (TREMURel. 13. Last annotation update)
DE LAR protein.
OS Streptococcus lincolnensis.
OC Bacteria; Firmicutes; Bacillales; Streptococcales;
OC Streptococcaceae; Streptococcaceae; Streptococcaceae;
NCB1_TaxId=1915;
LN 1)
SR SEQUENCE FROM N.A.

RA Mendicino-P. Schmidt H.; Zhang H.Z.; Piesberg W.;
RT "Molecular characterization of the lincomycin production gene cluster
of Streptococcus lincolnensis 78-11;"
Mol. Microbiol. 16:1137-1156(1995).
DR EMBL; X79146; CA55765.1; -
DR DDBJ; X79146; CA55765.1; -
DR Ffam; P800031; 7C6.1; GPCR, Anodan.

DR PROSITE; P800237; G PROTEIN RECP P.1; 1.
SO SEQUENCE 220 AA; 23491 MW; 59184145A16A87 CRC64;

Query Match
Best Local Similarity 64.3%; Pred. No. 11; Length 220;

Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 158 NCBI/NTL/NCSS 171

RESULT 8

OG3M7 PRELIMINARY; PRT; 221 AA.

AC OG3M7; 2001 (TREMURel. 19. Created)
DT 01-DEC-2001 (TREMURel. 19. Last annotation update)
DT 01-MAR-2003 (TREMURel. 23. Last annotation update)
DE CWP-NeuNc synthetase.
OS Mus musculus (Mouse).
OC Mammalia; Eutheria; Rodentia; Sciurinae; Muridae; Murinae; Mus.
NCB1_TaxId=1917;
LN 1)
SR SEQUENCE FROM N.A.

RA Gilbert M.; Michoniewicz J.; Karwinski M.-P.; Cunningham A.;
RT "Molecular basis for the variation in the lipi-oligosaccharide of
the mucosal pathogen, Campylobacter jejuni: Biochemistry of sialylated
glycoside moieties in the core oligosaccharide."
J. Biol. Chem. 276:10000-10006(2001).
DR EMBL; AF072248; AAL60907.1; -
DR DDBJ; AF072248; AAL60907.1; -
DR Ffam; P800031; 7C6.1; GPCR, Anodan.

DR PRINTS; P800237; GPCRINTEGRIN.
DR PROSITE; P800237; G PROTEIN RECP P.1; 1.
DR PROSITE; P800237; G PROTEIN RECP P.2; 1.

SO SEQUENCE 221 AA; 24915 MW; CC777F801A2A864 CRC64;

Query Match
Best Local Similarity 51.2%; Score 42; DB 2; Length 221;

Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
Db 118 NCBI/NTL/NCSS 163

RESULT 9

OG33M2 PRELIMINARY; PRT; 221 AA.

AC OG33M2; 2001 (TREMURel. 19. Created)
DT 01-DEC-2001 (TREMURel. 19. Last sequence update)
DT 01-MAR-2003 (TREMURel. 23. Last annotation update)
DE CWP-NeuNc synthetase (CWP-NeuNc synthetase).
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Spirochaetobacteriales; Campylobacteriales;
OC Campylobacteraceae; Campylobacteraceae;
NCB1_TaxId=1917;
LN 1)
SR SEQUENCE FROM N.A.

RA Query P.; Szymanski C.M.; Pendergast M.H.; Hickey T.B.; Swing C.P.;
RT "Phase Variation of Campylobacter jejuni 81-176 Lipooligosaccharide
affects virulence."

DR EMBL; X79146; CA55765.1; -
DR DDBJ; X79146; CA55765.1; -
DR Ffam; P800031; 7C6.1; GPCR, Anodan.

GenCode version 5.1.6
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OM protein - protein search, using sw model

Run on: November 7, 2003, 07:30:19 / Search time 14.0347 seconds

155,759 Million Cell updates/sec

Title: US-09-661-992b-106

RefSeq score: 12

Sequence: 1 PRKSRKRLTKALVSSCD 16

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 644079 seqs, 117479392 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing filter: 45 summaries

Database: Published applications 3A*

1: /cgn2_6/prodata/2/pubpa/US07_PIRCOMB.pep.*
2: /cgn2_6/prodata/2/pubpa/PCR_NEM_PUB.pep.*
3: /cgn2_6/prodata/2/pubpa/US06_NEM_PUB.pep.*
4: /cgn2_6/prodata/2/pubpa/US07_NEM_PUB.pep.*
5: /cgn2_6/prodata/2/pubpa/US07_NEM_PUB.pep.*
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16: /cgn2_6/prodata/2/pubpa/US10C_NEM_PUB.pep.*
17: /cgn2_6/prodata/2/pubpa/US10C_PIRCOMB.pep.*
18: /cgn2_6/prodata/2/pubpa/US06_PIRCOMB.pep.*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the best matching protein, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	82	100.0	1438	14	US-10-006-097-1	Sequence 1, App1
2	82	100.0	1438	14	US-10-006-097-1	Sequence 1, App1
3	82	100.0	1438	14	US-10-006-097-1	Sequence 1, App1
4	82	100.0	1438	14	US-10-006-097-1	Sequence 1, App1
5	82	100.0	1438	14	US-10-006-097-1	Sequence 1, App1
6	82	100.0	1438	14	US-10-006-097-1	Sequence 1, App1
7	82	100.0	1438	14	US-10-006-097-1	Sequence 1, App1
8	82	100.0	1438	14	US-10-006-097-1	Sequence 1, App1
9	82	100.0	1438	14	US-10-006-097-1	Sequence 1, App1
10	82	100.0	1438	14	US-10-006-097-1	Sequence 1, App1
11	82	100.0	1438	14	US-10-006-097-1	Sequence 1, App1
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13	82	100.0	1438	14	US-10-006-097-1	Sequence 1, App1
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43	82	100.0	1438	14	US-10-006-097-1	Sequence 1, App1
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45	82	100.0	1438	14	US-10-006-097-1	Sequence 1, App1

15	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
16	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
17	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
18	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
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20	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
21	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
22	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
23	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
24	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
25	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
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31	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
32	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
33	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
34	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
35	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
36	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
37	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
38	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
39	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
40	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
41	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
42	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
43	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
44	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1
45	70	85.4	1443	12	US-10-131-510A-39	Sequence 39, App1

ALIGNMENTS

RESULT 1
US-10-006-097-1
Sequence 1, Application US/10006091
GENERAL INFORMATION:
APPLICANT: Cho, Myung-Sam
APPLICANT: Kwon, Shun-Yuan
APPLICANT: Yoo, Seung-Ho
APPLICANT: Yoo, Seung-Ho
TITLE OF INVENTION: Expression System for Factor VIII
FILE REFERENCE: NMR-7155-1; US/10/006-091
CURRENT PUBLICATION: NMR-7155-1; US/10/006-091
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1: 1438
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES: Sequence
OTHER INFORMATION: Description of Artificial Sequence: Derived from
US-10-006-097-1
Query Match: 100.0%; Score 82, DB 14; Length 1438;
Best Local Similarity 100.0%; Pred. No. 4,68-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB: 697 PRKSRKRLTKALVSSCD 16
US-10-006-097-1
Sequence 1, Application US/10006091
GENERAL INFORMATION:
US-10-006-097-1
Sequence 1, Application US/10006091
GENERAL INFORMATION:

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/ APPLICANT: Cho, Myung-Sam
/ APPLICANT: Cho, Shun-Yuen
/ APPLICANT: Yee, Hean-Han
/ TITLE OF INVENTION: Expression System for Factor VIII
/ FILE REFERENCE: US-10/047/257
/ CURRENT FILING DATE: 2002-03-15
/ PRIOR APPLICATION NUMBER: US-10/047/257
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: Patent Ver. 2.0
/ SEQ ID NO: 148
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ ORGANISM INFORMATION: Description of Artificial Sequence: Derived from
/ OTHER INFORMATION: Human Factor VIII sequence
US-10-047-257-1

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Query Match
/ Sequence 1, Application US/10225900
/ Similarity 100.0%; Score 82; DB 14; Length 1438;
/ Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 697 FNNGGTALLVNSD 712

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RESULT 3
US-10-225-900-1
/ Sequence 1, Application US/10225900
/ Publication No. US200300775241
/ TITLE OF INVENTION: Expression System for Factor VIII
/ APPLICANT: Cho, Myung-Sam
/ APPLICANT: Yee, Hean-Han
/ APPLICANT: Yee, Shun-Yuen
/ FILE REFERENCE: US-7255
/ CURRENT FILING DATE: 2002-03-15
/ PRIOR APPLICATION NUMBER: US-10/225,900
/ CURRENT FILING DATE: 2002-03-15
/ PRIOR FILING DATE: 1998-12-10
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: Patent Ver. 2.0
/ SEQ ID NO: 148
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ ORGANISM INFORMATION: Description of Artificial Sequence: Derived from
/ OTHER INFORMATION: Human Factor VIII sequence
US-10-225-900-1
Query Match
/ Sequence 1, Application US/10225900
/ Similarity 100.0%; Score 82; DB 15; Length 1438;
/ Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 697 FNNGGTALLVNSD 712

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/ APPLICANT: Munson, Keith
/ TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII and
/ FILE REFERENCE: 35057/204375
/ CURRENT FILING DATE: 2002-03-15
/ PRIOR APPLICATION NUMBER: 09/689,430
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 60/158,780
/ PRIOR FILING DATE: 2000-09-12
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 2
/ TYPE: PRT
/ ORGANISM: Homo sapiens B-domain deleted factor VIII
/ ORGANISM INFORMATION: Homo sapiens BDD FVIII
US-10-095-718-2

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Query Match
/ Sequence 2, Application US/09957641
/ Similarity 100.0%; Score 82; DB 10; Length 1471;
/ Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 716 FNNGGTALLVNSD 731

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RESULT 5
US-09-957-641-2
/ Sequence 2, Application US/09957641
/ Publication No. US20020182870A1
/ GENERAL INFORMATION:
/ TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII
/ APPLICANT: Munson, Keith
/ FILE REFERENCE: 75-00
/ CURRENT APPLICATION NUMBER: US/09/957,641
/ CURRENT FILING DATE: 2001-09-16
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: US-09/23460
/ PRIOR FILING DATE: 2000-09-19
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: Patent Ver. 2.0
/ SEQ ID NO: 2
/ LENGTH: 2332
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ ORGANISM INFORMATION: Homo sapiens BDD FVIII
US-09-957-641-2
Query Match
/ Sequence 2, Application US/10131510A
/ Similarity 100.0%; Score 82; DB 10; Length 2332;
/ Conservative 16; Mismatches 0; Indels 0; Gaps 0;
Db 697 FNNGGTALLVNSD 712

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RESULT 4
US-10-095-718-2
/ Sequence 2, Application US/10095718
/ Publication No. US2002013156A1
/ GENERAL INFORMATION:
/ TITLE OF INVENTION: Adeno-Associated Virus Vectors Encoding Factor VIII
/ APPLICANT: Munson, Keith
/ APPLICANT: Cho, Shun-Yuen
/ APPLICANT: Yee, Hean-Han
/ APPLICANT: Yee, Shun-Yuen
/ FILE REFERENCE: 75-950
/ CURRENT FILING DATE: 2002-07-10
/ PRIOR FILING DATE: 2001-09-15
/ PRIOR APPLICATION NUMBER: 09/315,179
/ PRIOR FILING DATE: 1999-05-20
/ PRIOR APPLICATION NUMBER: U.S. 09/037,601

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[illegible]

1 APPLICATION NUMBER: US 06/087/11155
 2 FILING DATE: 1997-06-26
 3 APPLICATION NUMBER: US 08/670,707
 4 FILING DATE: 1996-06-26
 5 ATTORNEY/AGENT INFORMATION: See 1,
 6 REGISTRATION NUMBER: 27,994
 7 REFERENCE/DOCID NUMBER: 75-95K
 8 TELECOMMUNICATION INVENTION:
 9 TELEPHONE: 303/499-8089
 10 TELEFAX: 303/499-8089
 11 TITLE: Sequence of the Murine Factor VIII CNA
 12 JOURNAL: Genomics
 13 PAGES: 374-379
 14 DATE: 1993
 15 RELEVANT RESIDUES IN SEQ ID NO: 6: FROM 1 TO 2319
 16 US-10-187-319-4
 17 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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1 Publication No. US2000068765A1
 2 GENERAL INFORMATION:
 3 APPLICANT: Lollar, John S.
 4 TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
 5 NUMBER OF SEQUENCES: 40
 6 COMPLETION DATE: 1997-06-26
 7 ADDRESS: Greendale, Winner and Sullivan, P.C.
 8 STREET: 5370 Manhattan Circle Suite 201
 9 CITY: Boulder
 10 STATE: Colorado
 11 COUNTRY: USA
 12 ZIP: 80303
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ON protein - protein search, using sw model

Run on: November 7, 2003, 07:21:18 / Search time 2.3498 Seconds

(without alignments)

289,099 million cells updated/sec

Title: US-09-661-992b-106

RefSeq score: 82

Sequence: 1 FNNRMTALYNSCD 16

Scoring table: BIOSW62

Gapop 10.0 / Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Minimum Match 0%

Listing first 45 summaries

Database:

1: Issued Patent, AA*

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4	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
5	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
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7	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
8	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
9	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
10	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
11	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
12	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
13	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
14	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
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16	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
17	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
18	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
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23	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
24	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
25	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
26	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl
27	82	100.0	1	US-08-683-8399-1	Sequence 1, Appl

SDWARTIS

Pred No. is the number of results predicted by chance to have a
local score of at least as high as the one observed.
and is derived by analysis of the local score distribution.

28	76	92.7	2319	4	US-09-523-666-28	Sequence 28, Appl
29	76	92.7	2319	5	US-09-523-666-28	Sequence 29, Appl
30	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
31	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
32	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
33	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
34	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
35	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
36	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
37	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
38	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
39	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
40	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
41	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
42	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
43	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
44	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl
45	70	85.4	367	1	US-08-684-0048-2	Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-09-209-916-1
Sequence 1, Application US/09209916
GENERAL INFORMATION:
APPLICANT: Cho, Myung-Sam
INVENTOR: Cho, Myung-Sam
APPLICANT: Yes, Helena
TITLE OF INVENTION: Expression System for Factor VIII
FILE REFERENCE: W88-7555, US/09/709, 916
CURRENT FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 148
SEQ ID NO: 149
SEQ ID NO: 150
OTHER INFORMATION: Description of Artificial Sequence: Derived from
US-09-209-916-1
OTHER INFORMATION: human factor VIII sequence
Query Match 100.0% Score 82.1 DB 4, Length 1488,
Best Local Similarity 100.0% Pred. No. 1.4e-06,
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 FNNRMTALYNSCD 16
697 FNNRMTALYNSCD 12
US-08-683-8399-3
Sequence 3, Application US/086838399
GENERAL INFORMATION:
APPLICANT: Ill, Charles R. et al.
INVENTOR: Ill, Charles R. et al.
TITLE OF INVENTION: Use of Viral Cis-Acting Post-Transcriptional
Regulatory Sequences to Increase Expression of
NUMBER OF SEQ ID NOS: 18
CORRESPONDENCE ADDRESSES:
ADDRESS: LAMAR & COCKFIELD
CITY: Baton Rouge
STATE: Louisiana
COUNTRY: USA
EPI: 02109-1075

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COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,839B
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Remillard, Jane E.
REGISTRATION NUMBER: 38,872
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1471 amino acids
TYPE: amino acid
TOPOLOGY: linear
WPM: 663-839B-3; protein
US-08-663-839B-3

Query Match 100.0%; Score 82; DB 1; Length 1471,
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Or 1 FRNKGWTKLVKSSCD 16
Db 716 FRNKGWTKLVKSSCD 731

RESULT 3
US-07-864-004B-4
Sequence 4, Application US/07864004B
Patent No. 5364771
GENERAL INFORMATION:
APPLICANT: Lollar, John S.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/864,004B
TITLE OF INVENTION: Hybrid human/porcine Factor VIII
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES: 6 Cody
STREET: 1100 Peachtree Street
CITY: Atlanta
STATE: Georgia
ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/864,004B
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Patel, Patricia L.
REGISTRATION NUMBER: 11,384
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6508
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2332 amino acids
TYPE: amino acid
STRANDNESS: single

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TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Liver cDNA sequence
US-07-864-004B-4

Query Match 100.0%; Score 82; DB 1; Length 2332,
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Or 1 FRNKGWTKLVKSSCD 16
Db 697 FRNKGWTKLVKSSCD 712

RESULT 4
US-08-251-937A-4
Sequence 4, Application US/08251937A
Patent No. 5364771
GENERAL INFORMATION:
APPLICANT: Lollar, John S.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/251,937A
TITLE OF INVENTION: Hybrid human/porcine Factor VIII
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES: 6 Cody
STREET: 1100 Peachtree Street
CITY: Atlanta
STATE: Georgia
ZIP: 30309
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/251,937A
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/864,004
FILING DATE: 07-APR-1992
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 28,476
TELEPHONE: (404) 815-6508
TELEFAX: (404) 815-6508
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2332 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Liver cDNA sequence
US-08-251-937A-4

Query Match 100.0%; Score 82; DB 1; Length 2332,
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 PNNRGNALNVSSCD 16
 Db 697 PNNRGNALNVSSCD 712

RESULT 5
 / Sequence 2: Application US/08212133A
 / Patent No. 5663060

/ GENERAL INFORMATION:
 / APPLICANT: Kollis, John S.
 / INVENTOR: Kollis, John S.
 / TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
 / NUMBER OF SEQUENCES: 12
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: 100 Peachtree Street
 / CITY: Atlanta
 / STATE: Georgia
 / ZIP: 30309

/ COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: IBM PC compatible
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/212 133A
 / FILING DATE: 18-Jul-1994
 / CLASSIFICATION: 435

/ PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/864,004
 / FILING DATE: 07-SEP-1992
 / ATTORNEY/AGENT:
 / NAME: Patel, Pateel Ltd.
 / REGISTRATION NUMBER: 31,284
 / TELEPHONE: 404-572-6508
 / TELEFAX: 404-572-6555
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 2332 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MODIFICATION: none
 / HYPOTHEetical: YES
 / ANTI-SENSE: NO
 / FRAGMENT TYPE: N-terminal
 / ORIGIN: human
 / ORGANISM: Homo sapien
 / TISSUE TYPE: Liver cDNA sequence

US-08-212-133A-2
 Query Match 100.0%; Score 82; DB 1; Length 2332;
 Best Local Similarity 100.0%; Pred.No.2,5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNNRGNALNVSSCD 16
 Db 697 PNNRGNALNVSSCD 712

RESULT 6
 / Sequence 2: Application US/08275944A

/ Patent No. 5663195
 / APPLICANT: YONEMURA, Hiroshi
 / INVENTOR: YONEMURA, Hiroshi
 / APPLICANT: Tajima, Yoshitaka
 / INVENTOR: Tajima, Yoshitaka
 / APPLICANT: Sugawara, Masaharu
 / INVENTOR: Masuda, Kenichi

/ TITLE OF INVENTION: PROCESS FOR PREPARING HUMAN COAGULATION
 / NUMBER OF SEQUENCES: 11
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: Foley & Lardner
 / STREET: 3000 K Street, N.W., Suite 500
 / CITY: Washington
 / STATE: USA
 / COUNTRY: USA

/ ZIP: 20007-5109
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: IBM PC compatible
 / SOFTWARE: Patentin Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/276,594A
 / FILING DATE: 18-Jul-1994
 / CLASSIFICATION: 435

/ PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 07/950,191
 / FILING DATE: 07-SEP-1992
 / ATTORNEY/AGENT:
 / APPLICATION NUMBER: JP 243262/1991
 / FILING DATE: 24-SEP-1991
 / NAME: WERNER, Harold C.
 / REGISTRATION NUMBER: 25,268
 / TELEPHONE: (202)672-5308
 / TELEFAX: (202)672-5399

/ INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 2332 amino acids
 / TYPE: amino acid
 / MODIFICATION: none
 / TOPOLOGY: linear

US-08-276-594A-2
 Query Match 100.0%; Score 82; DB 1; Length 2332;
 Best Local Similarity 100.0%; Pred.No.2,5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PNNRGNALNVSSCD 16
 Db 697 PNNRGNALNVSSCD 712

RESULT 7
 / Sequence 2: Application US/08474503

/ Patent No. 574446
 / APPLICANT: Emory University
 / INVENTOR: HALL, David
 / TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
 / NUMBER OF SEQUENCES: 12
 / CORRESPONDENCE ADDRESS:
 / ADDRESS: Kiplerick & Cody
 / STREET: 100 Peachtree Street, Suite 2800
 / CITY: Atlanta
 / STATE: Georgia
 / COUNTRY: US

/ ZIP: 30309
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/474,503
 / FILING DATE: 07-JUN-1995

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: KATE, JOHN S., 29, 476
 REFERENCE/DOCKET NUMBER: EMU06CIP(13)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-815-6500
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2332 amino acids
 TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYDROTHERMAL: YES
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 TISSUE TYPE: Liver, CDNA sequence
 US-08-474-503-2

Query Match 100.0%; Score 82; DB 1; Length 2332;
 Beat Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 697 FNNNGWTLALNVSSCD 16

RESULT 8
 Sequence 2, Application US/08670707A
 Patent No. 5859204
 GENERAL INFORMATION:
 APPLICANT: Loliet, John S.
 TITLE OF INVENTION: Single Human/Animal Factor VIII
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Greenlee, Minner and Sullivan, P.C.
 STREET: 5370 Manhattan Circle Suite 201
 CITY: Boulder
 STATE: Colorado
 COUNTRY: USA
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Presentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/670,707A
 FILING DATE: 26-JUN-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/US94/13200
 FILING DATE: 15-NOV-1994
 PRIOR APPLICATION NUMBER: US 08/212,133
 FILING DATE: 11-MAR-1994
 APPLICATION DATA: US 07/864,004
 ATTORNEY/AGENT INFORMATION:
 NAME: Greenlee, Lorraine L.
 REGISTRATION NUMBER: 27,894
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303/499-8080
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2332 amino acids
 TYPE: amino acid
 STRANDNESS: single
 MOLECULE TYPE: protein
 HYDROTHERMAL: YES
 ANTI-SENSE: NO N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 TISSUE TYPE: Liver
 US-08-670-707A-2

Query Match 100.0%; Score 82; DB 2; Length 2332;
 Beat Local Similarity 100.0%; Pred. No. 2.5e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 697 FNNNGWTLALNVSSCD 16

RESULT 9
 US-09-037-601-2
 Sequence 2, Application US/09037601
 Patent No. 5859204
 GENERAL INFORMATION:
 APPLICANT: Loliet, John S.
 TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Greenlee, Minner and Sullivan, P.C.
 STREET: 5370 Manhattan Circle Suite 201
 CITY: Boulder
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Presentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/037,601
 FILING DATE: 26-JUN-1996
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: NO PCT/US94/13200
 FILING DATE: 15-NOV-1994
 PRIOR APPLICATION NUMBER: US 08/212,133
 APPLICATION DATA: US 07/864,004
 APPLICATION NUMBER: US 07/864,004
 FILING DATE: 07-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Greenlee, Lorraine L.
 REGISTRATION NUMBER: 31,878
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 303/499-8080
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2332 amino acids
 TYPE: amino acid
 STRANDNESS: single
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 HYDROTHERMAL: YES
 ANTI-SENSE: NO N-terminal
 FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 TISSUE: Liver
 US-09-037-601-2

Query Match 100.0%; Score 82; DB 3; Length 2332;
 Best Local Similarity 100.0%; Pct. No. 2.5e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FRRNGPMTALVSSCD 16
 DB 697 FRRNGPMTALVSSCD 712

RESULT 10
 Sequence 2: Application US/09315179
 Patent No. 6376463
 GENERAL INFORMATION:

APPLICANT: Lolait, John S
 TITLE: Amino acid modified Factor VIII

CURRENT FILING DATE: 1999-05-20
 EARLIER FILING DATE: 1998-03-10

EARLIER APPLICATION NUMBER: US: 08/670,707
 EARLIER FILING DATE: 1996-06-26

EARLIER APPLICATION NUMBER: PCT/US97/11155
 EARLIER FILING DATE: 1997-05-27

EARLIER APPLICATION NUMBER: 1994-11-15
 EARLIER FILING DATE: 1994-11-15

EARLIER APPLICATION NUMBER: U.S. 07/864,004
 EARLIER FILING DATE: 1992-04-07

NUMBER OF SEQ ID NOS: 40
 SEQ ID NO 2 PatentIn ver. 2.0

LENGTH: 2332
 TYR: PRT

US-09-115-179-2
 ORGANISM: Homo sapiens

Query Match 100.0%; Score 82; DB 4; Length 2332;
 Best Local Similarity 100.0%; Pct. No. 2.5e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FRRNGPMTALVSSCD 16
 DB 697 FRRNGPMTALVSSCD 712

RESULT 11
 Sequence 2: Application US/09523656

Patent No. 6458563
 GENERAL INFORMATION:

APPLICANT: Lolait, John S
 TITLE: Amino acid modified Factor VIII

CURRENT FILING DATE: 2000-03-10
 EARLIER FILING DATE: 1998-03-07

EARLIER APPLICATION NUMBER: 08/670,707
 EARLIER FILING DATE: 1996-06-26

NUMBER OF SEQ ID NOS: 38
 SEQ ID NO 2 PatentIn ver. 2.0

LENGTH: 2332
 TYR: PRT

ORGANISM: Homo sapiens

US-09-523-656-2

Query Match 100.0%; Score 82; DB 4; Length 2332;
 Best Local Similarity 100.0%; Pct. No. 2.5e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FRRNGPMTALVSSCD 16
 DB 697 FRRNGPMTALVSSCD 712

RESULT 12
 Sequence 2: Application FC/TUS910275
 GENERAL INFORMATION:

APPLICANT: Lolait, John S
 TITLE: Amino acid modified Factor VIII

CURRENT FILING DATE: 1999-05-20
 EARLIER FILING DATE: 1998-03-10

EARLIER APPLICATION NUMBER: US: 08/670,707
 EARLIER FILING DATE: 1996-06-26

EARLIER APPLICATION NUMBER: PCT/US97/11155
 EARLIER FILING DATE: 1997-05-27

EARLIER APPLICATION NUMBER: 1994-11-15
 EARLIER FILING DATE: 1994-11-15

EARLIER APPLICATION NUMBER: U.S. 07/864,004
 EARLIER FILING DATE: 1992-04-07

NUMBER OF SEQ ID NOS: 40
 SEQ ID NO 2 PatentIn ver. 2.0

LENGTH: 2332
 TYR: PRT

US-09-115-179-2
 ORGANISM: Homo sapiens

Query Match 100.0%; Score 82; DB 5; Length 2332;
 Best Local Similarity 100.0%; Pct. No. 2.5e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FRRNGPMTALVSSCD 16
 DB 697 FRRNGPMTALVSSCD 712

RESULT 13
 Sequence 2: Application FC/TUS9413200
 GENERAL INFORMATION:

APPLICANT: Lolait, John S
 TITLE: Amino acid modified Factor VIII

CURRENT FILING DATE: 2000-03-10
 EARLIER FILING DATE: 1998-03-07

EARLIER APPLICATION NUMBER: 08/670,707
 EARLIER FILING DATE: 1996-06-26

NUMBER OF SEQ ID NOS: 38
 SEQ ID NO 2 PatentIn ver. 2.0

LENGTH: 2332
 TYR: PRT

ORGANISM: Homo sapiens

Query Match 100.0%; Score 82; DB 5; Length 2332;
 Best Local Similarity 100.0%; Pct. No. 2.5e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FRRNGPMTALVSSCD 16
 DB 697 FRRNGPMTALVSSCD 712

```

1 APPLICANT: Emory University
2 TITLE OF INVENTION: Hybrid Human/Animal Factor VIII
3 NUMBER OF INVENTORS: 12
4 CORRESPONDENCE ADDRESS:
5 ADDRESSER: Aliphatrick & Cooy
6 STREET: 1100 Peachtree Street, Suite 2800
7 CITY: Atlanta
8 STATE: Georgia
9 COUNTRY: US
10 ZIP: 30309
11 COMPUTER READABLE FORM:
12 COMPUTER TYPE: PC COPY disk
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patent In Release #1.0, Version #1.25
15 CURRENT APPLICATION DATA: US/08/121202
16 FILING DATE: 15-NOV-1994
17 CLASSIFICATION:
18 ATTORNEY/AGENT INFORMATION:
19 NAME: M. C. Meindert
20 REGISTRATION NUMBER: 31,544
21 TELEPHONE: (617) 876-5851
22 TELEFAX: (617) 876-5851
23 INFORMATION FOR SEQ ID NO: 2:
24 SEQUENCE CHARACTERISTICS:
25 TYPE: amino acid
26 TOPOLOGY: linear
27 MOLECULE TYPE: protein
28 LENGTH: 2332
29 STRANDNESS: single
30 NUCLEIC ACID TYPE: DNA
31 NUCLEIC ACID TYPE: protein
32 ANTI-SENSE: NO
33 FRAGMENT TYPE: N-terminal
34 ORIGINAL SOURCE:
35 TISSUE TYPE: Liver cDNA sequence
36 PCT-US94-11200-2
37
38 Query Match 100.0% Score 82, DB 5, Length 2332,
39 Best Local Similarity 100.0% Pred. No. 2,6e-06;
40 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
41
42 Db 697 FRANKMALLANSCSD 712
43
44 RESULT 14
45 US-08-121-202-2
46 Sequence 2, Application US/08121202
47 Patent No. 5563045
48 GENERAL INFORMATION:
49 APPLICANT: Pitman, Debra
50 ADDRESSER: Rehembulla, Alimwaz
51 APPLICANT: Mooney, John W.
52 ADDRESSER: Aulman, Randall J.
53 NUMBER OF SEQUENCES: 27
54 CORRESPONDENCE ADDRESS:
55 ADDRESSER: Legal Affairs, Genetics Institute, Inc.
56 CITY: Cambridge
57 STATE: MA
58 COUNTRY: USA
59 ZIP: 02142
60 COMPUTER READABLE FORM:
61 COMPUTER TYPE: Ploppy disk
62 OPERATING SYSTEM: IBM PC compatible
63 SOFTWARE: Patent In Release #1.0, Version #1.25
64 SOFTWARE: Patent In Release #1.0, Version #1.25

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1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/121.202
3 FILING DATE: 14-SEP-1993
4 CLASSIFICATION: C13
5 ATTORNEY/AGENT INFORMATION:
6 NAME: Meindert, M. C.
7 REGISTRATION NUMBER: 31,544
8 TELEPHONE: (617) 876-5851
9 TELEFAX: (617) 876-5851
10 INFORMATION FOR SEQ ID NO: 2:
11 SEQUENCE CHARACTERISTICS:
12 TYPE: amino acid
13 TOPOLOGY: linear
14 MOLECULE TYPE: protein
15 US-08-121-202-2
16
17 Query Match 100.0% Score 82, DB 1, Length 2351,
18 Best Local Similarity 100.0% Pred. No. 2,6e-06;
19 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
20
21 Db 716 FRANKMALLANSCSD 731
22
23 RESULT 15
24 US-08-366-851A-2
25 Sequence 2, Application US/08366851A
26 Patent No. 5681746
27 GENERAL INFORMATION:
28 APPLICANT: Bodner, Mordechai
29 ADDRESSER: Hersh, David Col Tang
30 APPLICANT: Chang, Steven
31 TITLE OF INVENTION: Retroviral Delivery of Full Length Factor VIII
32 NUMBER OF SEQUENCES: 3
33 CORRESPONDENCE ADDRESS:
34 ADDRESSER: Viagene, Inc.
35 CITY: San Diego
36 STATE: California
37 COUNTRY: U.S.A.
38 ZIP: 92121
39 COMPUTER READABLE FORM:
40 COMPUTER TYPE: Floppy disk
41 OPERATING SYSTEM: IBM PC compatible
42 OPERATING SYSTEM: PC-DOS/MS-DOS
43 SOFTWARE: Patent In Release #1.0, Version #1.25
44 CURRENT APPLICATION DATA:
45 FILING DATE: 09/09/96, 851A
46 CLASSIFICATION: 514
47 ATTORNEY/AGENT INFORMATION:
48 NAME: M. C. Meindert
49 REGISTRATION NUMBER: 31,544
50 TELEPHONE: (617) 876-5851
51 TELEFAX: (617) 876-5851
52 INFORMATION FOR SEQ ID NO: 2:
53 SEQUENCE CHARACTERISTICS:
54 TYPE: amino acid
55 LENGTH: 2351
56 TOPOLOGY: linear
57 MOLECULE TYPE: protein
58 US-08-366-851A-2
59
60 Query Match 100.0% Score 82, DB 1, Length 2351,
61 Best Local Similarity 100.0% Pred. No. 2,6e-06;
62 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 PRNCRPTLTXSSCD 16
| | | | | | | | | |
Db 716 PRNCRPTLTXSSCD 731

Search completed: November 7, 2003, 07:30:12
Job time : 3.3498 sec